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Sequence 55, Application US/10409107A
Publication No. US20040053288A1
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, Shigeto
APPLICANT: YAMAMOTO, Kozo
APPLICANT: YAMAMOTO, Kozo
APPLICANT: TARGAMI, Hakuo
ITILE OF INVENTION: Method for estimating therapeutic efficacy of tumor necrosis
TITLE OF INVENTION: Accor
FILE REFERENCE: YAMAI=3
CURRENT FILING DATE: 2003-04-19
PRIOR APPLICATION NUMBER: US/10/409,107A
CURRENT FILING DATE: 2002-04-09
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 100
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
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0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1361 TGAAGATGATCGGGAAACACAA 1382
                   1 TCAAGTGGATGGCGCTGGAGTC 22
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ORGANISM: Artificial Sequence
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Publication No. US20030162796A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim International GmbH
TITLE OF INVENTION: Pharmaceutical composition for the treatment of disorders of
TITLE OF INVENTION: non-human mammals
FILE REFERENCE: Case 12 221
CURRENT APPLICATION NUMBER: US/10/259,451
CURRENT FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 22
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; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-259-451-11
                                                                                                Query Match 0.4%; Score 15.6; DB 1; Length 21; Best Local Similarity 93.8%; Pred. No. 6e+02; Matches 15; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     Sequence 1081, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
JAPPLICANT Briscol Myers Squibb Company
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT APPLICATION NUMBER: 60/251,015
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR PILING DATE: 2000-12-03
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR PILING DATE: 2001-01-23
PRIOR PILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1579
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.4%; Score 15.6; DB 1; Length 22; Best Local Similarity 81.8%; Pred. No. 6.3e+02; Matches 18; Conservative 0; Mismatches 4; Indels
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                 ) OTHER INFORMATION: DNA excision repair protein ERCCS; OTHER INFORMATION: The letter "s" stands for g or c. US-09-782-837-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2326 TGTGTGTGTGTGTGTGTG 2347
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; ORGANISM: Homo sapiens
US-10-005-956-1081
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US-10-259-451-11
FEATURE:
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APPLICANT: GU, Yizhong
APPLICANT: GU, Yongdang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Oligonucleotide
US-10-219-195-35
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0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                       Length 39
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                                                                                                                                                                                 Score 15.6; DB 1;
Pred. No. 1.1e+03;
0; Mismatches 9;
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CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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ORGANISM: Artificial Sequence
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Best Local Similarity 70.0%;
Matches 21; Conservative
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| Sequence 22, Application Us/10455470
| Publication No. US20040170613A1
| GENREAL INFORMATION:
| APPLICANT: Ferrara, Napoleone
| APPLICANT: Hillan, Kenneth J.
| APPLICANT: Le Couter, Jennifer
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR LIVER GROWTH AND LIVER PROTECTION
| FILE REFERENCE: P1849R1US
| CURRENT APPLICATION NUMBER: US/10/455,470
| FILE REPLICATION NUMBER: US/60/386,637
| PRIOR PILING DATE: 2003-06-05
| NUMBER OF SEQ ID NOS: 36
| LENGTH: 22
                                                                                                                                                                                              ; OTHER INFORMATION: Oligonucleotide used as primer for PCR detection of ERK1 mRNA
US-10-409-107A-55
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; Sequence 35, Application US/10219195
; Dublication No. US20030165917A1
; Dublication No. US20030165917A1
; APPLICANT: ULLWAN, EDWIN
; APPLICANT: MU, MING
; APPLICANT: LU, YEN PING
; TITLE OF INVENTION: ISOTHERWAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
; TILE REFERENCE: 3817.05-11
; FILE REFERENCE: 3817.05-11
; FULL REPERENCE: 2002-08-14
; PRIOR PILING DATE: 2002-08-14
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 49
; SOFTHARE: Patentin Ver. 2.1
; SEQ ID NO 35
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ilarity 81.8%; Pred. No. 6.38+02;
Conservative 0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                          855 GGAGGAGCTGGTGGAGGCTGAC 876
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ORGANISM: Artificial sequence
         SOFTWARE: Patentin version 3.2
SEQ ID NO 55
LENGTH: 22
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Matches 18; Conserva
                                                                                                            TYPE: DNA ORGANISM: Artificial
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Publication No. US20030073207A1

Publication No. US20030073207A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICATION: BLOOZYME Pharmaceuticals, Inc.

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate

TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

TITLE OF INVENTION: US/09/848,754A

CURRENT PILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 9645

SEQ ID NO 3493

LENGTH: 17
                                                                                                                                                                                                                                                                            US-09-730-289B-155

i Sequence 155, Application US/09730289B

i Publication No. US20330050259A1

i REDEBAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: McSwiggen, Jim

TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease

FILE REFERENCE: MBHB00-864-A (400/006)

CURRENT APPLICATION NUMBER: US/09/730,289B

CURRENT FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 3897

SOFTWARE: PatentIn version 3.0

SEQ ID NO 155

LENGTH: 17
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                              Score 15.4; DB 1; Length 17;
Pred. No. 5.1e+02;
8; Mismatches 1; Indels
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0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 5.1e+02;
Matches 13; Conservative 3; Mismatches 1; Indels
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                                                                                                                                                       3003 AGTTTTGTTTTAAACT 3019
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1 GUUUAGUUUUAAAACUG 17
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                              Query Match

0.4%;

Best Local Similarity 47.1%;

Matches 8; Conservative 8
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US-09-848-754A-3493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-730-289B-155
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US-10-163-552-649
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US-19-15-1-10-17/1

US-19-15-1-10-17/1

Sequence 711, Application US/0985805

Publication No. US200300004122A1

GENERAL INFORMATION:

APPLICANT: Relegalmen, Lec

APPLICANT: Relegalmen, Lec

APPLICANT: Relegalmen, Lec

APPLICANT: Relegalmen, Lec

APPLICANT: Anderic, Jasenka Matulic

CURRENT APPLICATION NUMBER: 105/925.305

FRIOR PILING DATE: 1099-12-30

FRIOR PILING DATE: 1999-04-28

FRIOR PILING DATE: 1999-04-29

FRIOR PILING DATE: 1999-04-29

FRIOR PILING DATE: 1999-04-29

FRIOR PILING DATE: 1998-04-29

FRIOR PILING DATE: 1998-04-29

FRIOR APPLICATION NUMBER: 60/064,866

FRIOR PILING DATE: 1998-04-29

FRIOR APPLICATION NUMBER: 60/064,866

FRIOR PILING DATE: 1998-04-29

FRIOR PILING DATE: 1998-04-29

FRIOR APPLICATION NUMBER: 60/064,866

FRIOR PILING DATE: 1998-04-29

FRIOR APPLICATION NUMBER: 60/064,866

FRIOR PILING DATE: 1998-04-29

FRIOR PILING DATE: 1998-04-29
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US-09-730-289B-154

Sequence 154, Application US/09730289B

Publication No. US20030050259A1

GENERAL INVORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
FILE REPERENCE: MRH800-864-A (400/006)
CURRENT APPLICATION NUMBER: US/09/730,289B

CURRENT FILING DATE: 2000-12-05
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 3897

SOFTWARE: Patentin Version 3.0

SEQ ID NO 154
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1992 CACCTTCAAGCAGCTGG 2008
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                                                          1 CACCATCAAGCAGCTGG 17
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Best Local Similarity 76.5%;
Matches 13; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                               US-09-825-805-771
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APPLICANT: RESERVANN, BEINDARD
APPLICANT: ROSCHORZ, BITGHL
APPLICANT: ROSCHORZ, BITGHL
APPLICANT: RISPERT, Andreas
ITTLE OF INVENTION: NUCLEIC ACIDS INVOLVED IN THE RESPONDER PHENOTYPE AND APPLICATIONS: TITLE OF INVENTION: THEREOF
ITTLE OF INVENTION: UNMBER: US/10/454,224
CURRENT APPLICATION NUMBER: US/10/454,726A
PRIOR FILING DATE: 1998-11-18
PRIOR PELING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: EP 97 12 0190.0
PRIOR APPLICATION NUMBER: EP 97 12 0190.0
PRIOR PLING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PALENTIN VERSION 3.1
LENGTH: 17
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Publication No. US20040077565A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Racoboryme Pharmaceuticals, Inc.
APPLICANT: Recobedo, Dam
APPLICANT: Bacobedo, Dam
APPLICANT: Brinchcomb, Dam
APPLICA
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Pred. No. 5.1e+02;
2; Mismatches 1; Indels
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                  Sequence 28, Application US/10454224 Publication No. US20040010814A1 GENERAL INFORMATION: APPLICANT: HERRWANN, Bernhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1747 GTGAAGTGGATGGCGCC 1763
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SOFTWARE: Patentin version 3.0
SEQ ID NO 1977
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Best Local Similarity 82.4%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Homo sapiens
US-10-138-674-1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 687
US-10-138-674-2009
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                      APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
TITLE OF INVENTION: HER2
TITLE OF INVENTION: HER2
CURRENT REFERENCE: MBHB01-1653-A (400/014)
CURRENT PILING DATE: 2002-06-06
NUMBER OF SEQ ID NOS: 1997
SOFTWARE: Patentin version 3.0
SEQ ID NO 649
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Pred. No. 5.1e+02;
3; Mismatches 1; Indels
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US-10-061-201-442

Sequence 442. Application US/10061201

Publication No. US2003016622941

GENERAL INFORMATION

FILE REFERENCE: PB0178

CURRENT APPLICATION WUMBER: US/10/061,201

CURRENT FILING DATE: 2002-01-30

PRIOR APPLICATION WUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PRILING DATE: 2001-01-30

PRIOR PLILING DA
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Best Local Similarity 76.5%;
Matches 13; Conservative
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US-10-061-201-442
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US-10-163-552-649
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
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Gaps

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APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Dan
APPLICANT: Pavco, Dan
APPLICANT: ACSWIGGEN, Jim
APPLICANT: SEcobedo, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERBUCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
NUMBER OF SEQ ID NOS: 2002-0-03
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6731
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APPLICANT: Pavco, Pam
APPLICANT: McSuggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138, 674
CURRENT APPLICATION NUMBER: 2002-05-03
NUMBER OF SEQ ID NOS: 2082-2
SOFTWARE: PatentIn version 3.0
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TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 6730
LENGTH: 17
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O.4%; Score 15.4; DB 1;
Best Local Similarity 82.4%; Pred. No. 5.1e+02;
Matches 14; Conservative 2; Mismatches 1;
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; Sequence 6762, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6731, Application US/10138674
Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1611 GTGCATCCACAGGGACC 1627
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CORGANISM: Homo sapiens
US-10-138-674-6730
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CORGANISM: Homo sapiens
US-10-138-674-6731
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                                                        APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Raco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Bacobed, Jam
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Becobed, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 2009
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Publication No. US20040077565A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Baccobed, Dan
APPLICANT: Strinchcomb, Dan
APPLICANT: Strinchcomb, Dan
APPLICANT: Strinchcomb, Dan
APPLICANT: MESCOBED, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
NUMBER OF SEQ ID NOS: 20822
SOPTWARE: Patentin version 3.0
SEQ ID NO 6729
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Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Jaine
APPLICANT: Escobedo, Jaine
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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82.4%; Pred. No. 5.1e+02;
ive 2; Mismatches 1; Indels
Sequence 2009, Application US/10138674 Publication No. US20040077565A1 GENERAL INFORMATION:
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Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-2009
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; ORGANISM: Homo sapiens
US-10-138-674-6729
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Stinchcomb, Dan
APPLICANT: Scinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor FILE REFERENCE: WHENDO-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT PILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 2002-05-03
SOFTWARE: Patentin version 3.0
SEQ ID NO 8260
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0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 5.1e+02;
Matches 9; Conservative 7; Mismatches 1; Indels
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US-10-138-674-8510/c
; Sequence 8510, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                    ; Sequence 8260, Application US/10138674; Publication No. US20040077565A1; GENERAL INFORMATION:
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1 GUGUGUGUGUGGGGUGUG 17
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CRGANISM: Homo sapiens
US-10-138-674-8261
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; ORGANISM: Homo sapiens
US-10-138-674-8260
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Best Local Similarity
Matches 9; Conserv
                                                                    RESULT 694
US-10-138-674-8260
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US-10-138-674-7615

Sequence 7615, Application US/10138674

Sequence 7615, Application US/10138674

Sequence 7615, Application No. US20040077565A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Bacobedo, Jaime
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION NUMBER: US/10/138,674
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20922

SEQ ID NOS: 20922

SEQ ID NO 7615
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Sequence 8259, Application US/10138674

Publication No. US20040077555A1

GENERAL INFORMATION:

APPLICANT: Riboryme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Merhod and Reagent for the Treatment of Diseases or Conditi

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: UNMERR: US/10/138,674

CURRENT APPLICATION NUMBER: US/10/138,674

CURRENT FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20822

SEQ ID NO 8259

LENGTH: 17
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0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 5.1e+02;
Matches 9; Conservative 7; Mismatches 1; Indels
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0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 5.1e+02;
Matches 13; Conservative 3; Mismatches 1; Indels
                                                                      Query Match

0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 5.1e+02;
Matches 9; Conservative 7; Mismatches 1; Indels
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1 GUGACGUCUGGUCUUUU 17
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US-10-138-674-8259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7615
             , ORGANISM: Homo sapiens
US-10-138-674-6762
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## APPLICANT: Ribozyme Pharmaceuticals, Inc.
## APPLICANT: Pavco, Pam
## APPLICANT: Acswigen, Jim
## APPLICANT: Stinchcomb, Dan
## APPLICANT: Brinchcomb, Dan
## APPLICANT: Stinchcomb, Dan
## APPLICANT: Brinchcomb, Dan
## APPLICANT: Stinchcomb, Dan
## APPLICANT: Stinchcomb, Dan
## TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
## TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
## TITLE OF INVENTION: NUMBER: US/10/287,949A
## CURRENT APPLICATION NUMBER: US/10/287,949A
## CURRENT FILING DATE: 2003-04-11
## NUMBER OF SEQ ID NOS: 20822
## SEQ ID NO 1977
## LENGTH APPLICATION
## INVENTION OF THE OF THE
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APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Bacobedon, Jim
APPLICANT: Stinchedomb, Dan
APPLICANT: Escobedo, Jahan
APPLICANT: Escobedo, Jahan
APPLICANT: Becobedo, Jahan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Con
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 8985
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Pred. No. 5.1e+02;
6; Mismatches 1; Indel8
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; Sequence 1977, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8985, Application US/10138674; Publication No. US20040077565A1; GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8954
LENGTH: 17
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Best Local Similarity 88.2%;
Matches 15; Conservative
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Best Local Similarity 58.8
Watches 10, Conservative
                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-138-674-8954
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US-10-138-674-8985
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                                                                                                                                                                                                         TYPE: RNA
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                                                                                 APPLICANT: Stinchcomb, Dam
APPLICANT: Stinchcomb, Dam
APPLICANT: Stinchcomb, Daime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION WUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
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APPLICANT: Bacco, Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: Baccobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-875-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138;674
CURRENT APPLICATION NUMBER: US/10/138;674
NUMBER OF SEQ ID NOS: 2002-05-03
SOFTWARE: Patentin version 3.0
SEQ ID NO 8949
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Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bavco, Pam
APPLICANT: Brobado, Jam
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
APPLICANT: Repension of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refirs OF INVENTION: Method and Reagent for the Treatment of Diseases OF OF INVENTION OF The Treatment of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8949, Application US/10138674
Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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         Pavco, Pam
McSwiggen, Jim
Stinchcomb, Dan
Escobedo, Jaime
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Sequence 6730, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Baccobedo, Dan
APPLICANT: Secobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rely
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0

SEQ ID NO 6730
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Publication No. US20040102389A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bacobedo, Jaime
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rell
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rell
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822
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Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
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Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-10-287-949A-6730
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Forguser 6729, Application US/10287949A

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Paveo, Pam
APPLICANT: Racobedo, Dam
APPLICANT: Bacobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refine Reference:
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: Patentin version 3.0

SEQ ID NO 6729
                                                                                                                                                                                                                                  Sequence 2009, Application US/10287949A

Fublication No. US20040102389A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bacobed, Jame
APPLICANT: Escobed, Jame
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions ReTILE REFERENCE: MENHOD-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT APPLICATION NUMBER: US/10/287,949A

NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0

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0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 5.1e+02;
Matches 14; Conservative 2; Mismatches 1; Indels
82.4%; Pred. No. 5.1e+02;
ive 2; Mismatches 1; Indels
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  Best Local Similarity 82.4
Matches 14; Conservative
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Best Local Similarity 58.8
Matches 10; Conservative
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CORGANISM: Homo sapiens
US-10-287-949A-2009
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ORGANISM: Homo sapiens
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Sequence 8260, Application US/10287949A

Sequence 8260, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bacobed, Jaime
APPLICANT: Escobed, Jaime
APPLICANT: Escobed, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A

NUMBER OF SEQ ID NOS: 20822

SEC ID NO 8260

SEC ID NO 8260
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Sequence 8261, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Bacobedo, Jaine
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re;
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re;
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re;
TITLE OF INVENTION: MORBER: US/10/287,949A

FILE REFERENCE: MEHBOO-876-N (400/049)

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822

SOFTMARE: Patentin version 3 0
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0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 5.1e+02;
Matches 9; Conservative 7; Mismatches 1; Indels
                                                                                                                                                                                  Length 17;
                                                                                                                                                                                                                                                                       1; Indels
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Pred. No. 5.1e+02;
7; Mismatches 1;
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1 GUGUGUGUGUGGGGGG 17
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Best Local Similarity 52.9%;
Matches 9; Conservative
        ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8259
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CORGANISM: Homo sapiens
US-10-287-949A-8261
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US-10-287-949A-8260
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Bublication No. US20040102389A1

GENERAL INFORMATION:
APPLICANT: Rabozyme Pharmaceuticals, Inc.
APPLICANT: Bavco, Pam
APPLICANT: Brinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8259, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ravco, Pam
APPLICANT: Bavco, Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions ITTLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor FILE REFERENCE: WBHBOO-875-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFFWARE: Patentin version 3.0
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-287-949A-7615
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US-10-287-949A-8259
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LENGTH: 17
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APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBHH00-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 2003-2

SOFTWARE: PatentIn version 3.0

LENGTH: 17
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| Sequence 8985, Application US/10287949A
| Publication No. US20040102389A1
| GENERAL INFORMATION:
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: Bacoco, Pam
| APPLICANT: Escobedo, Jaime
| APPLICANT: Escobedo, Jaime
| TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rell
| TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
| TITLE OF INVENTION: Usevels of Vascular Endothelial Growth Factor Receptor
| FILE REFERENCE: MBHB00-976-N (400/049)
| CURRENT APPLICATION NUMBER: US/10/287,949A
| NUMBER OF SEQ ID NOS: 20822
| SOFTWARE: Patentin Version 3.0
| SEQ ID NO 9985
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Sequence 7996, Application US/10723361

Publication No. USZ0040137589A1

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: FRANK, David R.

APPLICANT: RANK, David R.

APPLICANT: RANK, David R.

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANN

FILE REFERENCE: PB0105
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Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 1; Mismatches 1;
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; ORGANISM: Homo sapiens
US-10-287-949A-8985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-287-949A-8954
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US-10-287-949A-8510/c

US-10-287-949A-8510/c

Sequence 8510, Application US/10287949A

Publication No. US20040102389A1

GENERAL INFORMATION:
APPLICANT: Riboxyme Pharmaceuticals, Inc.
APPLICANT: Riboxyme Paramaceuticals, Inc.
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT FILING DATE: 2003-04-11

CURRENT FILING DATE: 2003-04-11

SEQ ID NOS: 20822

SOFTWARE: PatentIn version 3.0

SEQ ID NOS: 20826
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; Sequence 8949, Application No. US20040102389A1
; Publication No. US20040102389A1
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Bacco, Dam
; APPLICANT: Stinchcomb, Dan
APPLICANT: Escobed, Jaim
; APPLICANT: Escobed, Jaim
; APPLICANT: Bacched, Jaim
; APPLICANT: Bacched, Jaim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: UNDER: US/10/287, 949A
; CURRENT APPLICATION NUMBER: US/10/287, 949A
; CURRENT PILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFURARE: PatentIn version 3.0
; SEQ ID NO 8949
; LENGTH: 17
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Pred. No. 5.1e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.4%; Score 15.4; DB 1; Length 17; Best Local Similarity 94.1%; Pred. No. 5.1e+02; Matches 16; Conservative 0; Mismatches 1; Indels
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US-10-287-949A-8954
Sequence 8954, Application US/10287949A
; Publication No. US/30040102389A1
; GENERAL INFORMATION:
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1 GGCAUGGAGUUCUUGGC 17
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Local Similarity 70.6%;
hes 12; Conservative 4
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1 GUGUGUGUGGGUGUG 17
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CORGANISM: Homo sapiens
US-10-287-949A-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8510
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US-10-287-949A-8949
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Best Local Si
Matches 12;
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FILE REFERENCE: 38-10(52679) A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT APPLICATION NUMBER: US 09/754,853
FRIOR APPLICATION NUMBER: US 09/754,853
FRIOR PILING DATE: 2001-01-05
FRIOR FILING DATE: 2001-01-13
FRIOR APPLICATION NUMBER: US 09/855,768
FRIOR APPLICATION NUMBER: US 09/855,768
FRIOR APPLICATION NUMBER: US 09/855,768
FRIOR FILING DATE: 2001-01-13
FRIOR FILING DATE: 2001-05-15
FRIOR FILING DATE: 2001-05-15
FRIOR OF SEQ ID NOS: 4593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2975, Application US/09969373
; Sequence 2975, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679) A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR PRILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NOS: 4593
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Pred. No. 5.5e+02;
0; Mismatches 1;
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                                                                                                                                                        ; Sequence 1877, Application US/09969373
; Patent No. US20020133852A1
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                 18 CCTACACCCAAAGCTGA 2
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Best Local Similarity 94.1
Matches 16; Conservative
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CORGANISM: Glycine max
US-09-969-373-1877
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; ORGANISM: Glycine max
US-09-969-373-2975
                                                                                                                                   US-09-969-373-1877/c
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US-09-263-959-983/c
; Sequence 983, Appl
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APPLICANT: Trent, Jeffrey
APPLICANT: Trent, Jeffrey
APPLICANT: Marcelluc, Jose
TITLE OF INVENTION: Novel Methods and Reagents for the Treatment of Osteoarthritis
FILE REFERENCE: Case-06212
CURRENT APPLICATION NUMBER: US/09/802,207
CURRENT APPLICATION NUMBER: 09/619,175
PRIOR PILING DATE: 2000-07-19
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PARCELL NOS: 30
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 18
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NUMBER OF SEQ ID NOS: 15755
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0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR PLICATION NUMBER: US 09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-26
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Aeomica Sequence Listing Engine SEQ ID NO 7996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09802207
Publication No. US20020086824A1
GENERAL INFORMATION:
APPLICANT: Warman, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2600 CCCACACCCAAAGCTGA 2616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-723-361-7996
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; Patent No. US20020150891A1

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APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSES: Seed and Berry LLP
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                                                                                         Gaps
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                                           Length 18;
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Publication No. US20040157255A1
GENERAL INFORMATION:
APPLICANT: Agus, David
APPLICANT: Shak, Steven
APPLICANT: Baker, Joffre
TITLE OF INVENTION: Gene Expression Markers for Response to TITLE OF INVENTION: Gene Expression Princes
FILE REFERENCE: 39740/0009
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: RELIGIBLY disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
NAME: MCMSters, David D.
REFERENCE/DOCKET NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92010.426C2
TELECOMMUNICATION: NUMBER: PATENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
                                      Score 15.4; DB 1;
Pred. No. 5.5e+02;
0; Mismatches 1;
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Patent No. US20020150891A1
GENERAL INFORMATION:
                                                                                                                                    2337 GTGTGTGTGTGTGCA 2353
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                                                                                                                                                                                     17 Grardidicididada 1
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TELEPAX: (206) 682-6031
INFORMATION FOR SEO ID NO: 42:
SEQUENCE CHARACTERISTICS:
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                                             Query Match
Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 98104-7092
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US-10-773-951-53/c
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US-09-263-959-427
US-10-321-039-716
                                                                                                                                                                                                                                                           RESULT 720
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                        APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Kowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
WUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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APPLICANT: Lyamichev, Victor
APPLICANT: Lukowiak, Andrew
APPLICANT: Lukowiak, Andrew
APPLICANT: Sarvie, Namory
APPLICANT: Sarvie, Namory
APPLICANT: Rurenesky, David
TITLE OF INVENTION: Amplification Methods and Compositions
FILE REPERENCE: FORS-06596
CURRENT APPLICATION NUMBER: US/10/321,039
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 60/329,113
PRIOR APPLICATION NUMBER: 60/329,113
PRIOR APPLICATION NUMBER: 60/329,113
PRIOR APPLICATION NUMBER: 60/329,113
PRIOR APPLICATION NUMBER: 60/360,489
PRIOR APPLICATION NUMBER: 60/360,489
NUMBER OF SEQ ID NOS: 759
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LIBNGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.4%; Score 15.4; DB 1; Length 18; 94.1%; Pred. No. 5.5e+02;
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                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SUFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92010.426C2
TELEPONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 983:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: MUCLic acid
STRANDEDNESS: single
                                                                                                   STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 716, Application US/10321039 Publication No. US20040014067A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2335 GTGTGTGTGTGTGT 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 Grererarerererere
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Matches 16; Conserva
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APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Ugenan, Nassim
APPLICANT: Ugenan, Nassim
APPLICANT: Ugenan, Nassim
APPLICANT: Ugenan, Nassim
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sinA)
FILE REPERENCE: 400/134 (02-142-H)
CURRENT PAPLICATION NUMBER: US 60/350,22
PRIOR APPLICATION NUMBER: DG 60/350,22
PRIOR PELING DATE: 2002-02-20
PRIOR PELING DATE: 2002-03-11
PRIOR PELING DATE: 2002-06-06
PRIOR PELING DATE: 2002-06-06
PRIOR PELING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/399,348
PRIOR FILING DATE: 2002-07-03
PRIOR PELING DATE: 2002-07-03
PRIOR PELING DATE: 2002-06-06
PRIOR PELING DATE: 2002-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 91, Application US/08953047

Publication No. US20030087854A1

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

CURRENT APPLICATION NUMBER: US/09/953,047

CURRENT FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 95

SEQ ID NO 91

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 256
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                                                                                                                                                                                                                                       Sequence 120, Application US/10683990 publication No. US20040198682A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2893 GGGGCACAGGAGGCAG 2909
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn version 3.2
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Matches 16; Conserv
                                                                                                                                                                    RESULT 723
US-10-683-990-120
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| Publication Work US2004019862A1
| Sequence 23, Application US/10683990
| Publication Work US2004019862A1
| SEREMAL INFORMATION:
| APPLICANT: Sirra Therapeutics
| APPLICANT: Grain Therapeutics
| APPLICANT: USCANIGNER, Wasela
| APPLICANT: USCANIGNER, WAS INCEFERRED USING MUCHEC ACID (INNA)
| TITLE OF INVENTION: RAM Interference Mediated Inhibition of Placental Growth Factor ITILE OF INVENTION: GRAE Expression Using Short Interfering Nucleic Acid (sina)
| TITLE OF INVENTION: RAM INCERS: 1070-10-10
| PRIOR PRILING DATE: 2003-10-10
| PRIOR APPLICATION NUMBER: US 60/358,580
| PRIOR PLING DATE: 2002-03-10
| PRIOR PLING DATE: 2002-04-29
| PRIOR APPLICATION NUMBER: US 60/399,348
| PRIOR APPLICATION NUMBER: US 60/399,348
| PRIOR APPLICATION NUMBER: US 60/406,784
| PRIOR APPLICATION NUMBER: US 60/406,784
| PRIOR APPLICATION NUMBER: US 60/406,293
| PRIOR PRIING DATE: 2002-09-09
| PRIOR PLING DATE: 2002-09-09
| PRIOR PL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/sinA sense US-10-683-990-23
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0.4%; Score 15.4; DB 1;
Best Local Similarity 94.1%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 1;
                                                                      PRIOR APPLICATION NUMBER: 60/445,968
PRIOR FILING DATE: 2003-02-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 19
CURRENT APPLICATION NUMBER: US/10/773,951
CURRENT FILING DATE: 2004-02-06
                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: reverse primer US-10-773-951-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1747 GTGAAGTGGATGGCGCC 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 GTGAAGTGGATGGCACC 2
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-683-990-23/c
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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TYPE: DNA

2893 GGGGCACAGGAGGCAG 2909

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Gaps
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                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Wint Wasyuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.4; DB 1; Length 20;
Pred. No. 6.1e+02;
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOURE: IBM PC compatible
COMPOURE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,455
FILING DATE: 2-UN-1995
CLASSIFICATION NUMBER: US 08/368,704
PILING DATE: 4-JAN-1995
CLASSIFICATION NUMBER: US 08/368,704
PILING DATE: 4-JAN-1995
CLASSIFICATION NUMBER: US 08/258,287
FILING DATE: 10-JUN-1994
CLASSIFICATION NUMBER: US 08/080,850
FILING DATE: 10-JUN-1994
CLASSIFICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INPORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 0609.3920003
TELECOMMUNICATION NUMBER: 0609.3920003
TELECOMMUNICATION NUMBER: 0609.3920003
    ;
                                                                                                                                                                                                                                                                                                                                STREET: 1100 New York Avenue, Goldstein & Fox STREET: 1100 New York Avenue, Suite 600 CITY: Washington STATE: D.C. COUNTRY.
  0; Mismatches
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                                                                                                                                                                                                      Sequence 89, Application US/08459455
Publication No. US20030124105A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1353 GGAGATGATGAAGATGA 1369
                                                 3465 TATATATCTATATAT 3481
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TELEFAX: 48636 SSK
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 94.1%;
Matches 16; Conservative
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    Matches 16; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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publication No. U220040116366A1

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Brett P. Monia

TITLE OF INVENTION: ANTIENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT FILE REFERENCE: ISPH-0746

TITLE OF INVENTION: ANTIENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT FILE REFERENCE: ISPH-0746

CURRENT APPLICATION NUMBER: US/10/467,008

CURRENT FILING DATE: 2002-01-31

PRIOR PILING DATE: 2002-01-31

PRIOR PILING DATE: 2002-01-31

PRIOR FILING DATE: 2001-02-09

WHORE POS EQ ID NOS: 135

BROTH: 20

LENGTH: 20

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                       Sequence 91, Application US/10630401
Publication No. US20040048824A1
EMENRAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH PACTOR RECEPTOR 3 EXPRE FILE REFERENCE: RTS-0157
CURRENT APPLICATION NUMBER: US/10/630,401
CURRENT APPLICATION NUMBER: US/09/953,047
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 95
SEQ ID NO 91
LENGTH: 20
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                                                                                                                                                                 1; Indels
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Pred. No. 6.1e+02;
                                                                                                                  Score 15.4; DB 1;
Pred. No. 6.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Antisense Oligonucleotide US-10-630-401-91
                                       ; OTHER INFORMATION: Antisense Oligonucleotide US-09-953-047-91
                                                                                                                                                                 0; Mismatches
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                                                                                                                    Query Match 0.4%;
Best Local Similarity 94.1%;
Matches 16; Conservative
       ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-467-008-110
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-10-630-401-91
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| JUNEARAN INTEGRATION | JUNE 
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APPLICANT: Behr, Regine
APPLICANT: Behr, Regine
APPLICANT: William
APPLICANT: William
APPLICANT: Tang, Maria
APPLICANT: Sternberg, David
APPLICANT: Sternberg, David
APPLICANT: Sternberg, David
APPLICANT: Sternberg, David
TITLE OF INVENTION: Methods for Producing Hyaluronan In a Recombinant Host Cell
FILE REFERENCE: 10241.200-US
CURRENT FILING DATE: 2002-12-20
PRIOR PILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15.
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Pred. No. 6.1e+02;
0; Mismatches 1;
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; Publication No. US20030185829A1
; GENERAL INFORMATION:
                                                                                                              Sequence 15, Application US/10326185
Publication No. US20030175902A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/10326185; Publication No. US20030175902A1; GENERAL INFORMATION:
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; ORGANISM: Bacillus subtilis
US-10-326-185-15
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7 ORGANISM: Bacillus subtilis
US-10-326-185-18
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Best Local Similarity 94.1
Matches 16; Conservative
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### APPLICANT: Grosse et al
TITLE OF INVENTION: No. US20030190715Alel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 14062-15.

CURRENT APPLICATION NUMBER: US/09/976,782

CURRENT FILING DATE: 2001-10-12

PRIOR PLILOR DATE: 2000-10-12

PRIOR PLILOR DATE: 2000-10-16

PRIOR PLING DATE: 2001-10-16

PRIOR PLING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: 60/240,648

PRIOR PLING DATE: 2000-10-16

PRIOR PLING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: 60/240,648

PRIOR APPLICATION NUMBER: 60/240,648

PRIOR PLING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: 60/240,648

PRIOR PLING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: 90-10-16

PRIOR PRIOR APPLICATION NUMBER: 90-
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US-09-976-782-72
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-091-625-51
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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FILE REFERENCE: ISIS-4503
CURRENT APPLICATION NUMBER: US/10/388,263
CURRENT FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 947
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 421
LENGTH: 20
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                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Matches 16; Conserv
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APPLICANT: Brooks, Douglas G.
APPLICANT: Obrahi, Cara.
APPLICANT: Watt, Jacqueline R.
APPLICANT: Worters, Timothy A.
TITLE OF INVENTION: IDENTIFICATION BY OLIGONUCLEOTIDES AND
TITLE OF INVENTION: GENERATION BY OLIGONUCLEOTIDES FOR GENE MODULATION
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CURRENT PAPLICATION NUMBER: US/10/461,668
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/10/091,625
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 51
LENGTH: 20
                        APPLICANT: Shepard, Peter J.
TITLE OF INVENTION: JAGGED 2 INHIBITORS FOR INDUCING APOPTOSIS
TITLE REPERENCE: ISPH-0660
CURRENT APPLICATION NUMBER US/10/096,399A
CURRENT FILLING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin version 3.1
SEQ ID NO 51
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                               Length 20;
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0.4%; Score 15.4; DB 1;
Best Local Similarity 94.1%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Antisense Oligonucleotide
US-10-461-668-51
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Publication No. US20030228597A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51, Application US/10461668 Publication No. US20030207839A1 GENERAL INFORMATION:
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Freier, Susan M.
Sasmor, Henri M.
Brooks, Douglas G.
Ohashi, Cara
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ORGANISM: Artificial Sequence
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               APPLICANT: Koller, Erich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-388-263-421/c
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RESULT 736
US-10-199-199-98/C
US-10-199-199-98/C
Sequence 98, Application US/10199199
Sequence 98, Application US/004004047A1
Sequence 10 No. US20040014047A1
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. Dobie
TITLE OF INVENTION: ANTIERNSE MODULATION OF LIM DOMAIN KINASE I EXPRESSION
TITLE OF INVENTION: ANTIERNSE US/10/199,199
CURRENT FILING DATE: 2022-07-18
NUMBER OF SEQ ID NOS: 148
SEQ ID NO 98
LENGTH: 20
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Publication No. US20040014047A1
Publication No. US20040014047A1
Publication No. US20040014047A1
APPLICANT: Lex M. Cowsert
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIM DOMAIN KINASE 1 EXPRESSION FILE REFERENCE: RTS-0375
CURRENT APPLICATION NUMBER: US/10/199,199
CURRENT PILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 148
SEQ ID NO 21
LENGTH: 20
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0.4%; Score 15.4; DB 1;
Best Local Similarity 94.1%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 1;
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0.4%; Score 15.4; DB 1;
Best Local Similarity 94.1%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 1;
; OTHER INFORMATION: Antisense Oligonucleotide US-10-388-263-421
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Publication No. US20040023383A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SUBAN BABADC
APPLICANT: SUBAN M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF RESISTIN EXPRESSION
FILE REFERENCE: RTS-0396
CURRENT APPLICATION UNUMBER: US/10/210,833
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 149
LENGTH: 20
                                                                                                                                                                                                                                                       APPLICANT: Sugan M. Freier
APPLICANT: Sugan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF RESISTIN EXPRESSION
FITLE REFERENCE: RTS-0196
CURRENT APPLICATION NUMBER: US/10/210,833
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 165
LENGTH: 20
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Pred. No. 6.1e+02;
0; Mismatches 1; Indels
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Publication No. US20040101856A1
SEGRERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: Reneth W. Dobie
TITLE OF INVENTION: MODULATION OF MAD2-LIKE 1 EXPRESSION
FILE REFERENCE: RTS-0372
CURRENT APPLICATION NUMBER: US/10/304,109
CURRENT FILING DATE: 2002-11-23
NUMBER OF SEQ ID NOS: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Antisense Oligonucleotide US-10-210-833-50
                                                                                                                                                               Sequence 50, Application US/10210833 Publication No. US20040023383A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
   19 TACCTGGAGATGGGAGC
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ORGANISM: H. sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/329,414
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-2
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-29
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; OTHER INFORMATION: Description of Artifical Sequence: Primer/Probe
US-10-262-445-72
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CURRENT APPLICATION NUMBER: US/10/262,445
CURRENT FILING DATE: 2002-10-01
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PRIOR APPLICATION NUMBER: 60/327,454
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/327,917
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Patturajan, Mera
Rieger, Daniel
Spytek, Kimberly
Taupier, Tr., Raymond J.
Zerhueen, Bryan
Zhong, Haihong
                                                                                                                                                                                                                           Sequence 72, Application US/10262445
Publication No. US20040014058A1
                                                                                                                                                                                                                                                                                                                APPLICANT: Alsobrook II, John
APPLICANT: Burgess, Catherine
APPLICANT: Catterton, Elina
APPLICANT: Chant, John
APPLICANT: Chaudhuri, Amitabha
APPLICANT: Edinger, Shlomit
APPLICANT: Giot, Loic
2382 TCTTGCCTCCAGGTGCA 2398
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ORGANISM: Artificial Sequence
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Guo, Xiaojia
Kekuda, Ramesh
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Best Local Similarity 94.1
Matches 16; Conservative
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2734 TACCTGAAGATGGGAGC 2750

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Length 20;
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              Score 15.4; DB 1;
Pred. No. 6.1e+02;
0; Mismatches 1;
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                Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 94.13
Matches 16; Conservative
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US-10-671-395-1333/c
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; Sequence 1187, Application US/10671395
; Sequence 1187, Application US/10671395
; Bublication No. US20040132063A1
; GENERAL INFORMATION:
    APPLICANT: Pharmacia Corp.
; APPLICANT: Glerse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR PILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE PALENTIN Version 3.2
; SEQ ID NO 1187
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1171, Application US/10671395

5 Sequence 1171, Application US/10671395

5 Publication No. US20040132063A1

5 GENERAL INFORMATION:

5 APPLICANT: Pharmacia Corp.

7 APPLICANT: Gierse, James K

7 TILLE OF INVENTION: ARTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

7 TILLE OF INVENTION: ARTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN BZ SYNTHASE

7 TILLE OF INVENTION: ARTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN BZ SYNTHASE

7 TILLE OF INVENTION: ASTRESSION

7 FILE REFERENCE: 1179/1/US

7 CURRENT APPLICATION NUMBER: US/10/671,395

7 CURRENT FILING DATE: 2003-09-25

7 NUMBER OF SEQ ID NOS: 1809

7 SEQ ID NO 1171

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                                                                                                               ) OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-109-45
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US-10-671-395-1187
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                   LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 16; Conservative
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US-10-671-395-1171/c
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SEQ ID NO 45
LENGTH: 20
                                                                                                                                                                                      Query Match
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                                                                                              FEATURE:
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Sequence 1204, Application US/10671395
; Bublication No. US20040132063A1
; Bublication No. US20040132063A1
; GENBRAL INFORMATION:
APPLICANT: Giere, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PALENTIN VERSION 3.2
; SEQ ID NO 1204
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Sequence 17, Application US/10465347

Sequence 17, Application US/10465347

Sequence 17, Application US/10465347

Sequence 17, Application US/104949A1

GENERAL INFORMATION:
APPLICANT: Fazio, Vito M.
TITLE OF INVENTION: DAM VACCINES EXPRESSING HYPERVARIABLE VH-CDR3 IDIOTYPIC DETERMIN/
FILE REPERBNCE: 02901/0000028-USO
CURRENT APPLICATION NUMBER: US/10/466,347

CURRENT APPLICATION NUMBER: PCT/IT01/00014

FRIOR APPLICATION NUMBER: PCT/IT01/00014

FRIOR APPLICANTON NUMBER: PCT/IT01/00014

FRIOR APPLICANTON NUMBER: DCT/IT01/00014

SEQ ID NOS: 17

LENGTH: 21
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Publication No. US20040161768A1
GENERAL INFORMATION:
APPLICANT: BRINKAANN, ULRICH
APPLICANT: MORNHINWEG, ESTHER
TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
TITLE OF INVENTION: RESISTANCE-ASSOCIATED PROTEIN 1 (MRP-1) AND THEIR USE IN
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 21;
                                                                           Sequence 26, Application US/10151320

Publication No. US20030092114A1

GENERAL INCRMATION:

APPLICANT: Luche, Ralf M.

TITLE OF INVENTION: DSP-18 DUAL-SPECIFICITY PHOSPHATASE

FILE REFERENCE: 201225.436

CURRENT APPLICATION NUMBER: US/10/151,320

CURRENT FILING DATE: 2002-05-16

NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Oligonucleotide primer used for PCR US-10-151-320-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.4%; Score 15.4; DB 1; Best Local Similarity 94.1%; Pred. No. 6.5e+02; Matches 16; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-627-253A-351
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                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 748
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                                                                                                                                                                                                                       APPLICANT: Pharmacia Corp.
APPLICANT: Giere, James K
TITLE OF INVENTION: ANTIESENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT PILING DATE: 2003-09-25
PRIOR PILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SEQ ID NO 1595
LENGTH: 20
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Publication No. US20020146798A1

SEQUENCE LIRPORMATION:

APPLICANT: CADUS PHARMACUTICAL CORPORATION

TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES

TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES

TITLE OF INVENTION: AND USES THEREFOR

FILE REFERENCE: CPI-095CPC

CURRENT APPLICATION NUMBER: US/10/000,864

CURRENT PILING DATE: 2001-10-31

EARLIER PILING DATE: 1999-03-15

EARLIER PILING DATE: 1999-03-15

EARLIER PILING DATE: 1999-03-16

EARLIER PILING DATE: 1999-03-16

EARLIER PILING DATE: 1999-03-16

EARLIER PILING DATE: 1999-03-16

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.4%; Score 15.4; DB 1; Length 21; ilarity 94.1%; Pred. No. 6.5e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Human PGE2 antisense US-10-671-395-1595
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                                                                                                                                     Sequence 1595, Application US/10671395
Publication No. US20040132063A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2334 CGTGTGTGTGTGTGT 2350
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ORGANISM: Artificial Sequence
   CGTGTGTGTATGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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Best Local Similarity
                                                                                                                   US-10-671-395-1595/c
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Gaps
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patent No. US20020137708A1

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowsert
ILE REPERBNCE: ISPH-0585
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/918,186A
CURRENT FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 09/496,694
PRIOR PILING DATE: 1999-04-05
PRIOR PILING DATE: 1999-04-05
PRIOR PILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 250
SEQ ID NO 235
LENGTH: 20
                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
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Sequence 235, Application US/20030211607A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Britzabeth J. Ackermann
APPLICANT: Lex M. Cowsert
APPLICATION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: ISPH-0650
CURRENT APPLICATION NUMBER: US/10/181,316
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                                                                                                                                                                                                                                                                                                                                                                                       Length 30;
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CURRENT APPLICATION NUMBER: US/09/874,991C
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                        CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION WUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 30
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                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: BRINKMANN, ULRICH
APPLICANT: BRINKMANN, ULRICH
APPLICANT: HOFFWEYER, SVEN
APPLICANT: HOFFWEYER, SVEN
TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
FILE REFERENCE: VOS-42 CON
CURRENT FILING DATE: 2003-07-24
PRIOR FILING DATE: 2003-07-24
PRIOR PELICATION NUMBER: PCT/EPD2/00796
PRIOR PELICATION NUMBER: PCT/EPD2/00796
PRIOR PILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 406
SOFTWARE: PATENTIN VORTION 3.2
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
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Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINNAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.4%; Score 15.4; DB 1; Length 21; 84.2%; Pred. No. 6.5e+02; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               0.4%; Score 15.4; DB 1; Length 21; 84.2%; Pred. No. 6.5e+02; tive 1; Mismatches 2; Indels
  FILE REFERENCE: VOS-42 CON
CURRENT APPLICATION NUMBER: US/10/627,253A
CURRENT FILING DATE: 2003-07-24
FRIOR PRIOR PAPLICATION NUMBER: PCT/RE02/00796
FRIOR FILING DATE: 2002-01-25
FRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 406
SOFTWARE: Patentin version 3.2
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; sequence 352, Application US/10627253A
; Publication No. US20040161768A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGGTGGCACRGTGCTGGTG 20
                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 750
US-10-627-253A-352/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Pred. No. 6.6e+02;
0; Mismatches 3; Indels
                                       APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 209, Application US/09752983
Patent No. US20010016575A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS:
ADDRESSES: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PC
                  : Loren J. Miraglia, Pamela Nero, Mark J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                    ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFIMACE: WOLDERFECT 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,983
FILING DATE: 02-Jan-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/280,805
FILING DATE: <UNANDATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0346
TELECOMMUNICATION:
TELEPHONE: 609-810-1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDERPECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1346 CTGAGATGGAGATGATGAAG 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 CTCAGATGAAGATGATGAGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 609-810-1454
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTI
                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 08053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Marlton
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-752-983-209/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-752-983-147
            APPLICANT
                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JAPELICANT: KURANIE, RYUICHIRO
JAPELICANT: KURANIE, RYUICHIRO
JAPELICANT: KANAGAMA, TAKAHIRO
JAPELICANT: KANAGAMA, TAKAHIRO
JAPELICANT: KANAGAMA, TAKATIAKA
JAPELICANT: YANADA, KAZUTAKA
JAPELICANT: YOKOMAKU, TOYOKAZU
JAPELICANT: YOKOMAKU, TOYOKAZU
JAPELICANT: YOKOMAKU, TOYOKAZU
JAPELICANT: KOYAMA, OSAMU
JAPELICANT: FUNENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
JITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
JITLE OF INVENTION: THE METHOD
JELING DATE: 199953USOXDIV
CURRENT APPLICATION NUMBER: US 09/556,127
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: UP 1999-111601
PRIOR PELLING DATE: 1999-04-20
JENIOR APPLICATION NUMBER: 1999-04-20
JENIOR APPLICATION NUMBER: 2000-04-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.4%; Score 15.2; DB 1; Length 20;
85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      FRATURE:

COTHER INFORMATION: Antisense Oligonucleotide
US-10-181-316-235
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: PCT/US01/02939
PRIOR FILING DATE: 2001-0.30
PRIOR PILING DATE: 2000-0.20
PRIOR PILING DATE: 2000-0.02
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR PILING DATE: 1999-04-05
PRIOR FILING DATE: 1998-04-05
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 249
LENGTH: 20
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Patent No. US20010016575A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3458 AAGTTTATATATATCTATAT 3477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3473 TATATATATATTTGAG 3492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/09725265
Publication No. US20010000175A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATATATATTTTTTGGG 20
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                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.0%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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US-09-752-983-147/c
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APPLICANT: Jacqueline Wyatt
APPLICANT: Jacqueline Wyatt
APPLICANT: Bret P. Monia
APPLICANT: Bret P. Monia
APPLICANT: Rebert McKay
TITLE OF INVANTON: MCHAIN
TITLE OF INVANTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
TITLE OF INVANTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
TITLE OF INVANTION: NUMBER: 18/09/854,883
CURRENT FILING DATE: 2000-05-14
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR APPLICATION NUMBER: US 09/487,368
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 389
SEQ ID NO 305

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.4%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 15.2; DB 1; Length 20;
ilarity 85.0%; Pred. No. 6.6e+02;
Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Antisense Oligonuclectide US-09-854-883-305
                                                                                                                              NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: 1SPH-0346
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-810-1515
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH 20 base pairs
LENGTH 20 base pairs
TERNANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 305, Application US/09854883 Patent No. US20020055479A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3462 TTATATATATCTATATAT 3481
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                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/280,805
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 TCATGGAAAGCGTGCCC 435
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ORGANISM: Artificial Sequence
02-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
NATI-SENSE: Yes
US-09-752-983-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT: Chris Somerville

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Sequence 23, Application US/09891517

Sequence 23, Application US/09891517

Patent No. US20020106653A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KANAGARA, TAKAHIRO
APPLICANT: KANAGARA, TAKAHIRO
APPLICANT: YORIMURA, MASAKI
APPLICANT: YORIMURA, YORIMURA
APPLICANT: YOROMAKU, TOYOKARAI
APPLICANT: YOROMAKU, TOYOKARAI
APPLICANT: YOROMAKU, TOYOKARAI
APPLICANT: YOROMAKU, TOYOKARAI
APPLICANT: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
TITLE OF INVENTION: WETHOD
FILE REFERENCE: 210352US-1994-163-0-X
CURRENT APPLICATION NUMBER: US/09/891,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                           TITLE OF INVENTION: Production of Hydroxylated Fatty Acids in
Genetically Modified Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/530,862B
FILING DATE: 06-Feb-1996
APPLICATION NUMBER: PCT/US95/11855
FILING DATE: September 25, 1995
APPLICATION NUMBER: US 08/530,862
FILING DATE: September 20, 1995
APPLICATION NUMBER: US 08/320,982
FILING DATE: October 11, 1994
APPLICATION NUMBER: US 08/314,596
FILING DATE: September 26, 1994
INFORMATION FOR SEQ 1D NO: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: IBM PC-compatible
COMPATING SYSTEM: MS-DOS
SOFTWARE: MS WOORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
CLASSIPICATION:
CL
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                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSER: Pillsbury Winthrop,
STREET: 1600 Tysons Boulevard
CITY: McLean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP2000-193133
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: JP2000-236115
PRIOR FILING DATE: 2000-08-03
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Frank van de Loo
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TOPOLOGY: linear
JULE TYPE: CDNA
                                                                                                                                                NUMBER OF SEQUENCES: 15
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: Bodnar, Jackie S.
APPLICANT: Castellani, Lawrence W.
APPLICANT: Chatterjee, Aurobindo
APPLICANT: Chatterjee, Aurobindo
APPLICANT: Lusis, Aldons J.
APPLICANT: Ohmen, Jeff
APPLICANT: Tafuri, Sherrie
APPLICANT: Tafuri, Sherrie
APPLICANT: Tafuri, Sherrie
APPLICANT: Wu, Chenyan
TITLE ROF INVENTION: Gene and Sequence Variation Associated with Cancer;
FILE REFERENCE: 02810.0014.NPUSO2
CURRENT APPLICATION NUMBER: US/09/949,427
CURRENT FILING DATE: 2000.09-07
PRIOR PILING DATE: 2000.09-08
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            TITLE OF INVENTION: Genetically Modified Plants
                                                                                                                        ADDRESSEE: PILLSBURY MADISON & SUTRO, LLP
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/PC-DOS
SOOFWAREN: Word Perfect 5.1
CURRENT APPLICATION NUMBER: US/09/885,189
FILING DATE: 21-June-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/597,313D
FILING DATE: Pebruary 6, 1996
FILING DATE: Pebruary 6, 1996
FILING DATE: September 20, 1995
FILING DATE: OCCODER 11, 1994
FILING DATE: OCCODER 11, 1994
FILING DATE: OCCODER 11, 1994
FILING DATE: SEPTEMBER: 08/310,982
FILING DATE: SEPTEMBER: 08/310,982
FILING DATE: SEPTEMBER: 08/310,982
FILING DATE: SEPTEMBER: 08/314,596
FILING DATE: OUCCODER DATE: 00/313: 00/314,596
FILING DATE: 00/314,596
FILING
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Publication No. US20030054418A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 252
LENGTH: 20
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STRANDEDNESS: single
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US-09-885-189-13
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APPLICANT: KURANE, RYUICHIRO
APPLICANT: KURANE, YAKHIRO
APPLICANT: KAMAGATA, YOLGHI
APPLICANT: TORIMURA, SHINYA
APPLICANT: TORIMURA, SHINYA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOWAKU, TOYOKAZU
TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
TITLE OF INVENTION: MCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
TITLE OF INVENTION: METHOD
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APPLICANT: Pierre BROUN
APPLICANT: Prank VAN DE LOO
TITLE OF INVENTION: Production of Hydroxylated Fatty Acids in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indel8
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PRIOR APPLICATION NUMBER: JP2000-193133
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: JP2000-236115
PRIOR APPLICATION NUMBER: JP2000-236115
PRIOR FILING DATE: 2000-08-26
NUMBER: OF SEQ ID NOS: 108
SEQ ID NO 34
LENGTH: 20
PRIOR APPLICATION NUMBER: JP2000-292483
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/09891517
Patent No. US20020106653A1
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; OTHER INFORMATION: Synthetic DNA
US-09-891-517-23
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Best Local Similarity 85.03
Matches 17; Conservative
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US-05-953-318-72/c

JOS-05-953-318-72/c

Sequence 72, Application US/09953318

Publication No. US20030105036A1

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Andrew T. Watt

TITLE OF INVENTION: ARRESSION

TITLE OF INVENTION: ARRESSION

TITLE REPERENCE: TTS-0232

CURRENT APPLICATION NUMBER: US/09/953,318

CURRENT PILING DATE: 2001-09-13

NUMBER OF SEQ ID NOS: 154

SEQ ID NO 72

LENGTH: 20
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US-09-919-197-76/c
US-09-919-197-76/c
Sequence 76, Application US/09919197
; Sequence 76, Application No. US20030083484A1
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
; FILE REFERENCE: 15PH-0593
; CURRENT APPLICATION NUMBER: US/09/919,197
; CURRENT PILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 20
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Query Match
0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
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Local Similarity 85.0%; Pred. No. 6.6e+02;
Los 17; Conservative 0; Mismatches 3;
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OTHER INFORMATION: Antisense Oligonucleotide US-09-953-318-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Antisense Oligonucleotide US-09-919-197-76
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                                                                                                  1945 TACATGATCATGCGGGAGTG 1964
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; Sequence 74, Application US/09953318
; Publication No. US20030105036A1
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ORGANISM: Artificial Sequence
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US-09-954-556-98/c
US-09-954-556-98/c
Sequence 98, Application US/09954556
Publication No. US20030078219A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Breat P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRESTITE APPLICANTON NUMBER: US/09/954,556
CURRENT APPLICATION NUMBER: US/09/954,556
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 98
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bodnar, Jackie S.
APPLICANT: Castellani, Lawrence W.
APPLICANT: Castellani, Lawrence W.
APPLICANT: Castellani, Lawrence W.
APPLICANT: Chatterjee, Aurobindo
APPLICANT: de Jong, Pieter
APPLICANT: Dusis, Aldons J.
APPLICANT: Noss, David
APPLICANT: Ross, David
APPLICANT: Ross, David
APPLICANT: Wu, Chenyan
TITLE OF INVENTION: Gene and Sequence Variation Associated with Lipid Disorder
FILE REFERENCE: 02810.0014.NPUSO;
CURRENT APPLICATION NUMBER: US/09/949,428
CURRENT FILING DATE: 2000-09-08
CURRENT PAPLICATION NUMBER: 06/231,322
PRIOR APPLICATION NUMBER: 2000-09-08
NUMBER OF SEQ ID NOS: 405
SOFTWARE: Patentin version 3.1
SEQ ID NO 252
LENGTH: 20
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                                                                                                         Length 20;
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0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-428-252
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Publication No. US20030064372A1
GENERAL INFORMATION:
                                    ; OTHER INFORMATION: Synthetic Primer US-09-949-427-252
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                 FEATURE:
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llarity 85.0%; Pred. No. 6.6e+02;
Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
          APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
FILE REFERENCE: ISPH-0617
CURRENT APPLICATION NUMBER: US/10/001,844
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 33
LENGTH: 20
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APPLICANT: Alexander H. Borchers
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
FILE REFERENCE: RTS-0345
CURRENT APPLICATION NUMBER: US/10/007,010
CURRENT FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.4%; Score 15.2; DB 1; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-229-346-34/C
US-10-229-346-34/C
Sequence 34, Application US/10229346
Publication No. US20030120054A1
GENERAL INFORMATION:
APPLICANT: Chen, Eric
APPLICANT: Chen, Eric
APPLICANT: Chen, Eric
TILE REFERENCE: 60065A
CURRENT APPLICATION WUMBER: US/10/229,346
CURRENT APPLICATION NUMBER: 60/316,421
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 38
SOCIED NO 34
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Antisense Oligonucleotide US-10-001-844-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2004 GCTGGTGGAGGACCTGGACC 2023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 GCTGGTGAAGGACCTGAGCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 crrcarecaecaecrecaec 1
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OTHER INFORMATION: CMS16 Primer
                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 17; Conserv
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                  FEATURE:
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FUBLICANT: KURANE, RYUICHIRO

APPLICANT: KANAGANA, TAKHIRO

APPLICANT: KANAGANA, TAKHIRO

APPLICANT: KANAGANA, VOICHI

APPLICANT: KANAGANA, VOICHI

APPLICANT: KOYAMA, OSAMU

TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI

TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI

TITLE OF INVENTION: THE METHOD

TITLE OF INVENTION: THE METHOD

TITLE OF INVENTION: THE METHOD

FILE REFERENCE: 199953USOXDIV

CURRENT APPLICATION NUMBER: US/09/725,265

PRIOR FILING DATE: 2000-11-29

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 10999-04-20

PRIOR FILING DATE: 10999-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20
     APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-023
CURRENT APPLICATION NUMBER: US/09/953,318
CURRENT FILING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 154
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.4%; Score 15.2; DB 1; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Antisense Oligonucleotide US-09-953-318-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1610 AGTGCATCCACAGGGACCTG 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3473 TATATATATATTTTGAG 3492
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Publication No. US20030082592A1
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; Sequence 33, Application US/10001844
; Publication No. US20030105041A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 rarararararrrrrrggg 20
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                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 20
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                  FEATURE:
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Sequence 147, Application US/10005344 Publication No. US20030203862A1 GENERAL INFORMATION:
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TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 GCTCCATCCTCGGGAGATGA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Loren J. Miraglia APPLICANT: Pamela Nero
                STATE: Virginia
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-10-005-344-147/c
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STREET: 1100 No. US20030181660Alth Glebe Road, Eighth Floor
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                        Query Match 0.4%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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Kawaguchi, Yoshiniko
Merriman, Tony R
Merriman, Tony R
Merzker, Michael L
TITLE OF INVENTION: NO. US20030181660A1el LDL-Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of p38 Mitogen
TITLE OF INVENTION: Activated Protein Kinase Expression
TITLE OF INVENTION: Activated Protein Kinase Expression
TITLE OF INVENTION: Activated Protein Kinase Expression
TITLE OF INVENTION: 1SPH-0468
CURRENT APPLICATION NUMBER: 09/640,101
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 107
SEPURARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 20
                                                                                 ; OTHER INFORMATION: AntiBense Oligonucleotide US-10-007-010-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-238-442-22
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Publication No. US20030181660A1
GENERAL INFORMATION:
APPLICANT: Todd, John A
Hess, John W
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22, Application US/10238442; Publication No. US20030176383A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caskey, Charles T
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Gerhold, David
Hammond, Holly
Hey, Patricia
                     TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Matches 17; Conserv
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US-10-331-907-75/c
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LENGTH: 20
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                                                                       FEATURE:
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Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/331,907
FILING DATE: 31-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                    APPLICATION NUMBER: US/09/402,923A
FILING DATE: 14-Feb-2001
APPLICATION NUMBER: ECT/GB98/01102
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: B.J.Sadoff
                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ.ID NO: 75:
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Publication No. US20030204076A1

Publication No. US20030204076A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT
TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT
TITLE OF INVENTION: BXPRESSION
TITLE OF INVENTION WIMBER: US/10/446,373
CURRENT FILING DATE: 2003-05-28
PRIOR PRLING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 74
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Sequence 60, Application US/10380931

Publication No. US20030215944A1

GENERAL INFORMATION:

APPLICANT: ISLS Pharmaceuticals, Inc.

APPLICANT: Grank Bennett

APPLICANT: Jacqueline Wyatt

APPLICANT: Jacqueline Wyatt

APPLICANT: Basan M. Freier

ITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION

FILE REFERENCE: RTSP-0187

CURRENT APPLICATION WUMBER: US/10/380, 931

CURRENT FILING DATE: 2003-03-18

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 182

LENGTH: 20
                                                                          Gaps
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                         Length 20;
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                                                                       Indels
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                    Score 15.2; DB 1;
Pred. No. 6.6e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Antisense Oligonucleotide US-10-446-373-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Antisense Oligonucleotide US-10-380-931-60
                                                                                                                        1573 CAGGTGGCCCGGGGCATGGA 1592
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                       0.4%;
ilarity 85.0%;
Conservative 0
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                       Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                       US-10-446-373-74/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Andrew T. Water TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT FILE OF INVENTION: EXPRESSION FILE OF INVENTION: EXPRESSION NUMBER: US/10/446,373
CURRENT APPLICATION NUMBER: US/09/953,318
PRIOR FILING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 154
LENGTH: 20
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FILE REFERENCE: ISPH-0622
CURRENT APPLICATION NUMBER: US/10/005,344
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 09/048,810
FRIOR APPLICATION NUMBER: US 09/280,805
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 379
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 209
LENGTH: 20
                                                                     Query Match 0.4%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.4%; Score 15.2; DB 1; Length 20;
85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
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OTHER INFORMATION: Antisense Oligonucleotide
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                                                                                                                                                                                                                                                                                                                                       Sequence 209, Application US/10005344
Publication No. US20030203862A1
GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia
APPLICANT: Pamela Nero
                                                                                                                                                                      1346 CTGAGATGGAGATGATGAAG 1365
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US-10-446-373-72/c
; Sequence 72, Application US/10446373
; Publication No: US2030204076A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
                                                                                                                                                                                                                    20 crcacarcaacarcarcacc 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pamela Nero
APPLICANT: Mark J. Graham
APPLICANT: Brett P. Monia
APPLICANT: Brich Koller
APPLICANT: Ming'i Chiang
APPLICANT: Mano Manoharan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 85.0
Matches 17; Conservative
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     ; OTHER INFORMA
US-10-005-344-147
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RESULT 783
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US-10-160-497-22/c
US-10-160-497-22/c
Sequence 22, Application US/10160497
Publication No. US20030224513A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Erich Koller
APPLICANT: Erich Koller
FILE REFERENCE: RTS-036
CURRENT APPLICATION NUMBER: US/10/160,497
CURRENT APPLICATION NUMBER: US/10/160,497
NUMBER OF SEQ ID NOS: 145
SEQ ID NO 22
LENGTH: 20
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Sequence 305, Application US/10360510
; Sequence 305, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
APPLICANT: Lax M. Cowsert
APPLICANT: Susan M. Freier
APPLICANT: Brett P. Monia
APPLICANT: Robert P. Monia
APPLICANT: Robert M. Butler
APPLICANT: Robert M. Butler
APPLICANT: Robert M. Butler
APPLICANT: Robert MCKAY
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
FILE REFERENCE: ISPH-0576
CURRENT APPLICATION NUMBER: US/10/360,510
FURRENT FILING DATE: 2001-05-14
FRIOR FILING DATE: 2001-05-14
FRIOR FILING DATE: 2000-07-31
FRIOR FILING DATE: 2000-07-31
FRIOR PRICED DATE: 2000-07-31
FRIOR PLING DATE: 2000-07-31
FRIOR FILING DATE: 2000-07-31
FRIOR PLING DATE: 2000-07-31
FRIOR FILING DATE: 2000-07-31
FRIOR PLING DATE: 2000-07-31
FRIOR APPLICATION NUMBER: US 09/487,368
FRIOR PLING DATE: 2000-07-31
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0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-305
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RESULT 781 US-10-348-750-22/c

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Sequence 15, Application US/10372909
; Sequence 15, Application US/10372909
; Publication No. US20030237109A1
; Publication No. US20030237109A1
; Publication No. US20030237109A1
; APPLICANT: KOTODA, NOBUHIRO
; APPLICANT: SOBJIMA, UUNICHI
; TITLE OF INVENTION: FLOWER-BUD FORMATION SUPPRESSOR GENE AND EARLY FLOWERING PLANT
; TITLE OF INVENTION: FLOWER-BUD FORMATION SUPPRESSOR GENE AND EARLY FLOWERING PLANT
; TITLE OF INVENTION: FLOWER-BUD FORMATION SUPPRESSOR GENE AND EARLY FLOWERING PLANT
; TITLE OF INVENTION: FLOWER-BUD 2002-18029
; CURRENT FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 15
; LENGTH: 20
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Sequence 74, Application US/10210290

Sequence 74, Application US/10210290

Sequence 74, Application US/10210290

GENERAL INFORMATION:
APPLICANT: Ming-Yi Chiang

APPLICANT: Eric G. Marcusson

APPLICANT: Eric G. Marcusson

TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION

FILE REFERENCE: RIS-0367
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; Sequence 22, Application US/10348750; Publication No. US20030225019A1; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
APPLICANT: Erich Koller
; TILL OF INVENTION: NOTCHI INHIBITORS FOR INDUCING APOPTOSIS; FILE REFERENCE: ISPH-0729
; CURRENT APPLICATION NUMBER: US/10/348,750
; CURRENT APPLICATION NUMBER: 10/160,497
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 146
; SEQ ID NO 22
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Best Local Similarity 85.0%
Matches 17; Conservative
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TYPE: DNA ORGANISM: Artificial
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Publication No. US20040023378A1

GENERAL INFORMATION:
APPLICANT: Mingle File G. Marcusson
APPLICANT: Kenneth W. Dobie
TILLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
CURRENT APPLICATION NUMBER: US/10/210,290
CURRENT APPLICATION NUMBER: US/10/210,290
CURRENT APPLICATION DOS: 134
SEQ ID NO 128
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US-10-380-124-39/c

Sequence 39, Application US/10380124

Publication No. US20040053874A1

GENERAL INFORMATION:

APPLICANT: Bais Pharmaceuticals, Inc.

APPLICANT: Brett P. Monia

APPLICANT: Brett P. Monia

TITLE OF INVESTION: ANTIGENSE MODULATION OF CLUSTERIN EXPRESSION

FILE REPERENCE: RTS-0156

CURRENT APPLICATION NUMBER: US/10/380,124

CURRENT FILING DATE: 2003-03-10

SEQ ID NOS: 90

LENGTH: 20
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-290-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-39
CURRENT APPLICATION NUMBER: US/10/210,290 CURRENT FILING DATE: 2002-07-31 NUMBER OF SEQ ID NOS: 134 SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                     1610 AGTGCATCCACAGGGACCTG 1629
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                                                                                 LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 85.0
Matches 17; Conservative
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Publication No. US20040077099A1

GENERAL INFORMATION:
APPLICANT: Argome National Laboratory
APPLICANT: Argome National Laboratory
APPLICANT: Argome National Laboratory
APPLICANT: Alexander
APPLICANT: Alexander
APPLICANT: Alexander
APPLICANT: Alexander
APPLICANT: ALOSTITIONING
FILE OF INVENTION: BOOSTITONING
FILE REFERENCE: ANL-IN-01-052
CURRENT APPLICATION NUMBER: US/10/619,284A
CURRENT PLING DATE: 2003-07-14
FRIOR APPLICATION NUMBER: US/10/139842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3473 TATATATATATTTGAG 3492
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489 GCAGACGTACACGCTGGACG 508
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                                                                                                                      20 GCAGACGCACATGCTGGATG 1
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0; Mismatches
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Best Local Similarity 85.0%;
Matches 17; Conservative
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US-10-274-085-145
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## APPLICANT: Argenne National Laboratory
## APPLICANT: Argenne National Laboratory
## APPLICANT: Argenne Nation Alexander
## APPLICANT: Argenne Nation Alexander
## APPLICANT: Argenne Nation Alexander
## TITLE OF INVENTION: BIOCHIP READER WITH ENHANCED ILLUMINATION AND BIOARRAY
## TITLE OF INVENTION: BOSTIONING
## TITLE OF INVENTION: BOSTIONING
## TITLE OF INVENTION: BOSTIONING
## TITLE OF INVENTION: DATE: 2003-07-14
## CURRENT APPLICATION NUMBER: US/10/619,284A
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| Sequence 33, Application No. US2004007570A1
| GENERAL INFORMATION:
| APPLICANT: Suean M. Freier
| APPLICANT: Kenneth W. Dobie |
| TITLE OF INVENTION: ANTISENSE MODULATION OF FAITY ACID SYNTHASE EXPRESSION TITLE OF INVENTION NUMBER: US/10/274,085
| CURRENT APPLICANION NUMBER: US/10/274,085
| CURRENT PILING DATE: 2002-10-17
| NUMBER OF SEQ ID NOS: 225
| SEQ ID NO 33
| LENGTH: 20
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Score 15.2; DB 1; Length 20;
Pred. No. 6.6e+02;
0; Mismatches 3; Indels
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0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismarches
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 74, Application US/10619284A Publication No. US20040077099A1 GENERAL INFORMATION:
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                                                                                                                                                            1350 GATGGAGATGATGAAGATGA 1369
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ORGANISM: Artificial Sequence
              Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial
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Publication No. US20040077570A1
GENERAL INFORMATION:
APPLICANT: Sunan W. Freier
APPLICANT: Kenneth W. Dobie
APPLICANT: Kenneth W. Dobie
APPLICANT: Sanjay Bhanot
ITHE OF INVENTION: ANTISENSE MODULATION OF FATTY ACID SYNTHASE EXPRESSION
FILE REFERENCE: ISPH-0714
CURRENT APPLICATION NUMBER: US/10/274,085
CURRENT FILING DATE: 2002-10-17
SEQ ID NO 172
Sequence 64, Application US/10274085
Publication No. US20040077570A1
GENERAL INFORMATION:
APPLICANT: Sunan M. Fraier
APPLICANT: Renneth W. Dobie
TITLE OF INVENTION ANTISENSE MODULATION OF FATTY ACID SYNTHASE EXPRESSION
TITLE OF INVENTION ANTISENSE WOULATION OF FATTY ACID SYNTHASE EXPRESSION
CURRENT APPLICATION NUMBER: US/10/274,085
CURRENT PILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 225
ILENGTH: 20
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US-10-274-085-145
Sequence 145, Application US/10274085
Publication No. US20040077570A1
GENERAL INFORMATION:
APPLICANT: Sunan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF FATTY ACID SYNTHASE EXPRESSION
FILE REFERENCE: ISPH-0714
CURRENT APPLICATION NUMBER: US/10/274,085
CURRENT APLICATION NUMBER: 2002-10-17
SEQ ID NOS: 225
SEQ ID NO 145
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Pred. No. 6.6e+02;
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0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
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US-10-300-642-65
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LENGTH: 20
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; Sequence 128, Application US/10210802
; GENERAL INFORMATION:
   APPLICANT: Ming-Yi Chiang
   APPLICANT: Ming-Yi Chiang
   APPLICANT: Kemeth W. Dobie
   TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
   FILE REFERENCE: FIS-036
   CURRENT APPLICATION NUMBER: US/10/210,802
   CURRENT FILING DATE: 2002-07-31
   NUMBER OF SEQ ID NOS: 134
   ENGIN: 20

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Publication No. US20040087523A1
Publication No. US20040087523A1
GENERAL INFORMATION:
APPLICANT: Minds Yi Chiang
APPLICANT: Menneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION FILE REPERENCE: RTS-037
CURRENT APPLICATION NUMBER: US/10/210,802
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 74
LENGTH: 20
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                                                                                                              Query Match
0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Antisense Oligonucleotide US-10-210-802-74
                                                                                                                                                                                                       1891 CTGCTGAAGGAGGCCACCG 1910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                         TYPE: DNA
CORGANISM: H. sapiens
US-10-274-085-172
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US-10-210-802-128/c
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                                                                                                                                                                                                                                                                                                                RESULT 793
US-10-210-802-74
LENGTH: 20
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RESULT 795 US-10-300-642-33/c

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Sequence 33, Application US/10300642
Publication No. US20040096836A1
GENERAL INFORMATION
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Eveier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE 13 EXPRESSION
FILE REFERENCE: HTS-0045
CURRENT APPLICATION NUMBER: US/10/300,642
CURRENT FILING DATE: 2002-11-19
NUMBER OF SEQ ID NOS: 78
SEQ ID NO 33
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PEDLICANT: Kenneth W. Dobie

TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE 13 EXPRESSION
FILE REFERENCE: HTS-0045
CURRENT APPLICATION NUMBER: US/10/300,642
CURRENT FILING DATE: 2002-11-19
NUMBER OF SEQ ID NOS: 78
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; Sequence 88, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 0.1393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR APPLICATION NUMBER: 60/419,268
; RIUNG DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SEQ ID NO 88
; LENGTH: 20
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85.0%; Pred. No. 6.6e+02;
ative 0; Mismatches 3;
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Pred. No. 6.6e+02;
0; Mismatches 3;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-300-642-33
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Best Local Similarity 85.03
Matches 17; Conservative
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Best Local Similarity 85.03
Matches 17; Conservative
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ORGANISM: H. sapiens
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RESULT 802
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TITLE OF INVENTION: MODULATION OF ENDOTHELIAL LIPASE EXPRESSION
FILE REFERENCE: RTS-0447
CURRENT APPLICATION NUMBER: US/10/319,915
CURRENT FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 279
SEQ ID NO 120
LENGTH: 20
                                                                                                                                                                                                                                                                                                                   US-10-688-706-102

| Sequence 102, Application US/10688706
| Sequence 102, Application US/10688706
| Publication No. US20040102412A1
| GABERAL INFORMATION:
| APPLICANT: Pharmacia Corp.
| APPLICANT: Broschat, Kay
| TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
| FILE REFERENCE: 01393/1
| CURRENT APPLICATION NUMBER: US/10/688,706
| CURRENT FILING DATE: 2003-10-17
| PRIOR APPLICATION NUMBER: 60/419,268
| PRIOR APPLICATION NUMBER: 60/419,268
| RIGHT FILING DATE: 2002-10-17
| NUMBER OF SEQ ID NOS: 3071
| SEQ ID NO 102
| LENGTH: 20
                                                                                                             Length 20;
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0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                         3; Indels
                                                                                                        Query Match

0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
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                  FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: human GFAT antisense US-10-688-706-102
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US-10-319-915-120/c
; Sequence 120, Application US/10319915
; Publication No. US20040115653A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3237 TAGTIGGAGGIGATICCAGT 3256
                                                                                                                                                                                                   3238 AGTTGGAGGTGATTCCAGTG 3257
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Best Local Similarity 85.09
Matches 17; Conservative
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ORGANISM: artificial
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## Sequence 174, Application US/10671395
## Sequence 174, Application US/10671395
## Sequence 174, Application No. US20040132063A1
## GENERAL INFORMATION:
## SPELICANT: Pharmacia Corp.
## APPLICANT: Gierse, James K
## TITLE OF INVENTION: EXPRESSION
## TITLE OF INVENTION: EXPRESSION
## FILLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
## TITLE OF INVENTION: EXPRESSION
## FILLE OF INVENTION OWNER: 60/413,549
## PRIOR APPLICATION NUMBER: 60/413,549
## PRIOR PILLING DATE: 2002-09-25
## NUMBER OF SEC ID NOS: 1809
## SEC ID NO 174
## ILLEGATH: 20
## I
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; Publication No. US20040132063A1
; General Information:
; APPLICANT: Dierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
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         Sequence 247, Application US/10319915
Publication No. US20040115653A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF ENDOTHELIAL LIPASE EXPRESSION
FILE REFERENCE: RTS-0447
CURRENT APPLICATION NUMBER: US/10/319,915
CURRENT FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 279
SEQ ID NO 247
LIENGTH: 20
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Pred. No. 6.6e+02;
0; Mismatches 3; Indels
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Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3;
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US-10-671-395-174
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Best Local Similarity 85.0%;
Matches 17; Conservative (
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US-10-319-915-247
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Gaps

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Length 20;

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Sequence 1312, Application US/10671395

Fublication No. US20040132063A1

Fublication No. US20040132063A1

FUBLICANT: Pharmacia Corp.

APPLICANT: Pharmacia Corp.

APPLICANT: Gierse, James K

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: 1179/1/US

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT APPLICATION NUMBER: 02/10/671,395

FROR APPLICATION NUMBER: 02/10/671

FROR APPLICATION NUMBER: 06/413,549

FROR FILING DATE: 2002-09-25

FRICK APPLICATION DATE: 2002-09-25
                                                                                                                              Score 15.2; DB 1;
Pred. No. 6.6e+02;
0; Mismatches 3;
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                            ; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1279
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US-10-671-395-1312
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Sequence 1350, Application US/10671395; Publication No. US20040132063A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                               2002 CAGCTGGTGGAGGACCTGGA 2021
                                                                                                                                                                                                                                                                                    20 CAGTGGGTGGAGGACCGGGA 1
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                                                                                                                              Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative (
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SOFWARE: Patentin version 3.2
SEQ ID NO 1312
LENCTH: 20
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SOFTWARE: Patentin version 3.2
SEQ ID NO 1350
LENGTH: 20
     ORGANISM: artificial
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APPLICANT: Pharmacia Corp.

APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTENSENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/6/71,395
CURRENT FILING DATE: 2003-09-25
PRIOR PILING DATE: 2003-09-25
PRIOR PILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 1279
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APPLICANT: Pharmacia Corp.

APPLICANT: Giere, James K
TITLE OF INVENTION: ANTERNSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NOWBER: US/10/671,395
CURRENT APPLICATION NUMBER: 60/413,549
PRIOR PILING DATE: 2002-09-25
PRIOR PILING DATE: 2002-09-25
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Pred. No. 6.
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US-10-671-395-1138
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US-10-671-395-1175
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Publication No. US20040132063A1
GENERAL INFORMATION:
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Publication No. US20040132063A1
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
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                                               NUMBER OF SEQ ID NOS: 1809
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1138
LENGTH: 20
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SOFWARE: Patentin version 3.2
SEQ ID NO 1175
LENGTH: 20
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Best Local Similarity 85.0%;
Matches 17; Conservative (
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Gaps

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Length 20; 3; Indels

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APPLICANT: PLAIMACIA COLP.
APPLICANT: PLAIMACIA COLP.
APPLICANT: Gierse, James K
ATTLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT PELLING DATE: 2003-09-25
PRIOR PILLING DATE: 2002-09-25
PRIOR FILLING DATE: 2002-09-25
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85.0%; Pred. No. 6.6e+02;
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Best Local Similarity
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Sequence 1423, Application US/10671395

Sequence 1423, Application US/10671395

Publication No. US20040132063A1

GENERAL INFORMATION:

APPLICANT: Pharmacia Corp.

APPLICANT: Gierse, James K

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE;

TITLE OF INVENTION: ANTISENSE NOULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE;

TITLE OF INVENTION: 1179/1/US

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT FILING DATE: 2003-09-25

PRIOR FILING DATE: 2002-09-25

NUMBER OF SEQ ID NOS: 1809

SOUTHWARE: PATENTIN VERSION 3.2

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1423
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US-10-671-395-1431
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APPLICANT: Giere, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/US
CURRENT FILING DATE: 2003-09-25
CURRENT PLING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SSOFTWARE: Patentin version 3.2
SSQ ID NO 1399
LENGTH: 20
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Publication No. US20040132063A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Giera, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE FOF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT PILING DATE: 2003-09-25
PRIOR PILING DATE: 2002-09-25
PRIOR FILING DATE: 2002-09-25
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3; Indels
   0; Mismatches
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US-10-671-395-1399
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Publication No. US20040132063A1
GENERAL INFORMATION:
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SOFWRARE: Patentin version 3.2
SEQ ID NO 1406
LENGTH: 20
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   Matches 17; Conservative
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ORGANISM: artificial
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Best Local Similarity
Matches 17; Conserv
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NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
SEQ ID NO 1627
LENGTH: 20
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                                                                                            TYPE: DNA
ORGANISM: artificial
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APPLICANT: Pharmacia Corp.
APPLICANT: Giere, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT APPLICATION NUMBER: 60/413,549
PRIOR PILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SEQ ID NOS: 1809
SEQ ID NO 1566
LENGTH: 20
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE TITLE OF INVENTION: EXPRESSION PILE REFERENCE: 1179/1/US CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT APPLICATION NUMBER: 60/413,549
PRIOR PILING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: PATENTING DATE: 2002-09-25
LENGTH: 20
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Publication No. US20040132063A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Glerse, James K
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/US
CURRENT APPLICATION UNMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
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Pred. No. 6.6e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1566
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; Sequence 1566, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: artificial
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Sequence 1628, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: EXPRESSION
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT APPLICATION NUMBER: G0/413,549
; PRIOR APPLICATION NUMBER: G0/413,549
; RIGH RILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SEQ ID NO 1628
; LENGTH: 20
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Sequence 1640, Application US/10671395

Publication No. US20040132063A1

GENERAL INFORMATION:

APPLICANT: Pharmacias Corp.

APPLICANT: Glarge Corp.

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE;

TITLE OF INVENTION: ANTISENSE NOULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE;

TITLE OF INVENTION: ANTISENSE US/10/671,395

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT FILING DATE: 2003-09-25

PRIOR FILING DATE: 2002-09-25

NUMBER OF SEQ ID NOS: 1809

SOGTWARKE: Patentin version 3.2

LENGTH: 20
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                                                                                     Query Match 0.4%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
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, OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1627
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US-10-671-395-1670/c

J Sequence 1670, Application US/10671395

J Sequence 1670, Application US/10671395

J Sequence 1670, US20040132063A1

GENERAL INFORMATION:

J APPLICANT: Pharmacia Corp.

J TITLE OF INVENTION: EXPRESSION

J TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: 1179/1/US

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT PILICA DATE: 2003-09-25

PRIOR APPLICATION NUMBER: 60/413,549

PRIOR PLICATION NUMBER: 60/413,549

PRIOR FILING DATE: 2002-09-25

NUMBER OF SEQ ID NOS: 1809

SOFTWARE: Patentin version 3.2

SEQ ID NO 1670

LENGTH: 20
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; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Glerse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT PILING DATE: 2003-09-25
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1685

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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1670
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2319 GTGTGTGTGTGTGCGTGT 2338
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Matches 17; Conservative
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ORGANISM: artificial
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US-10-671-395-1685/c
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US-10-654-102-126/c
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; Sequence 1665, Application US/10671395
; Sequence 1665, Application No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/L/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2002-09-25
; PRIOR PAPLICATION NUMBER: 60/413,549
PRIOR PLING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1665
                                                                                                                                                                                                                                                                                              Sequence 1641, Application US/10671395
; Sequence 1641, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
    APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
    TITLE OF INVENTION: BYPRESSION
; TITLE OF INVENTION: BYPRESSION
; FILE REPERBUCE: 11791/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR PILIAG DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SCFUMBER OF SEQ ID NOS: 1809
; SEQ ID NO 1641
LENGTH: 20
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                                                               Query Match

0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
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; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1641
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; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1640
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Best Local Similarity 85.0
Matches 17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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US-10-671-395-1641/c
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US-10-671-395-1665/c
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US-09-771-730-103
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APPLICANT: Popoff, Ian
APPLICANT: Wong, Wai Shiu Fred
APPLICANT: Wong, Wai Shiu Fred
TITLE OF INVENTION: Antisense Oligonuclectide Modulation of p38 Mitogen
TITLE OF INVENTION: Activated Protein Kinase Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic J. OTHER INFORMATION: Primer US-10-654-102-126
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85.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 3; Indels
                                                                                      APPLICANT: KOJIMA, HIDETO
TITLE OF INVENTION: INDUCTION OF PANCREATIC ISLET FORMATION
FILE REFERENCE: PO2409091
CURRENT APPLICATION NUMBER: US/10/654,102
CURRENT FILING DATE: 2003-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 126
LENGTH: 20
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CURRENT APPLICATION NUMBER: US/10/641,455A
CURRENT FILING DATE: 2003-08-15
PRIOR APPLICATION NUMBER: US 10/238,442
PRIOR PILING DATE: 2002-09-09
PRIOR PILING DATE: 2000-08-15
PRIOR PILING DATE: 2000-08-15
PRIOR PILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 266
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 20
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Sequence 126, Application US/10654102
Publication No. US20040132679A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1609 AAGTGCATCCACAGGGACCT 1628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2321 GTGTGTGTGTGTGTGTGT 2340
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                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 17; Conservative
                                                                       APPLICANT: CHAN, LAWRENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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RESULT 822 US-10-835-208-76/c ; Sequence 76, Application US/10835208

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APPLICANT: Syngenta Participations AG
TITLE OF INVENTION: Modified Cry3A Toxins and Nucleic Acid Sequences Coding Therefor
FILE REFERENCE: 60065/PCT
CURRENT APPLICATION NUMBER: US/10/487,846
CURRENT FILING DATE: 2004-02-25
PRIOR PRILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 34
SOFTWARE OF SEQ ID NOS: 34
SOFTWARE OF SEQ ID NOS: 34
SOFTWARE OF SEQ ID NOS: 34
GENERAL INFORMATION:
APPLICANT: Rosanne M. Crooke
APPLICANT: Mark J. Graham
TITLE OF INVENTION: ANTIEENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
FILE REFERENCE: ISPH-0593
CURRENT APPLICATION NUMBER: US/10/835,208
CURRENT FILING DATE: 2004-04-29
PRIOR PEPLICATION NUMBER: US/09/919,197
PRIOR FILING DATE: 2001-07-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.4%; Score 15.2; DB 1; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.4%; Score 15.2; DB 1; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Antisense Oligonucleotide US-10-835-208-76
                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 89
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 76
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2396 GCAGAGGTACCCTGGGTGTC 2415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/10487846 Publication No. US20040199939A1 GENERAL INFORMATION:
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MacDougall, John R.
Spytek, Kimberly Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature; LOCATION: (1)...(20)
COTHER INFORMATION: CMS16 Primer
US-10-487-846-34
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                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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APPLICANT:
APPLICANT:
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Gaps
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APPLICANT: Majumder, Vishna

APPLICANT: Mainta, Vishna

APPLICANT: Mease, Peter S

APPLICANT: Reacelll, Luca

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REFRENCE: 15966-697

CURRENT APPLICATION NUMBER: US/09/800,198

CURRENT APPLICATION NUMBER: 60/186,596

PRIOR APPLICATION NUMBER: 60/186,596

PRIOR APPLICATION NUMBER: 60/186,596

PRIOR PRILING DATE: 2000-03-03

NUMBER OF SEQ ID NOS: 98

SOFTWARE PATENTIN Ver. 2.1

SEQ ID NO 33

LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                     Gapa
                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence:Ag427 Probe US-09-808-602-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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APPLICANT: Echt, Craig. S
APPLICANT: Nelson, C. Dana
TITLE OF INVENTION: MICROSATELITE DNA MARKERS AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 4481/1E188US1
                                                                                                                                                                                                                                                                               Query Match

0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.9e+02;
Matches 17; Conservative 0; Mismatches 3;
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CURRENT APPLICATION NUMBER: US/09/232,785
; CURRENT FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 09/232,884
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 390
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Sequence 390, Application US/09232785; Publication No. US20030049612A1; GENERAL INFORMATION:
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                                                                                            TYPE: DNA OKGANISM: Artificial Sequence FEATURE:
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 35
LENGTH: 21
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Best Local Similarity 85.0
Matches 17; Conservative
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ORGANISM: Pinus taeda L.
US-09-232-785-390
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APPLICANT: Vernation:
APPLICANT: Fernations, Elina
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Harman, John L
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Macsa, Peter S
APPLICANT: Maccougall, John
TITLE OF INVENTION: No. US2002155115Alel Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
CURRENT FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2000-03-05
PRIOR FILING DATE: 2000-03-05
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
F: Vernet, Corine A. M. INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: NOV 12 Probe COTHER INFORMATION: Primer Sequence US-09-771-730-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 15.2; DB 1; Length 21; 85.0%; Pred. No. 6.9e+02; tive 0; Mismatches 3; Indels
                                                           CURRENT APPLICATION NUMBER: US/09/771,730
CURRENT PILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US/09/771,730
CURRENT FILING DATE: 2000-01-27
PRIOR PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/178,406
PRIOR PILING DATE: 2000-01-27
PRIOR PILING DATE: 2000-01-27
PRIOR PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/180,634
PRIOR PILING DATE: 2000-07-27
PRIOR PILING DATE: 2000-07-27
PRIOR PILING DATE: 2000-07-28
PRIOR PILING DATE: 2000-07-28
PRIOR PILING DATE: 2000-07-28
PRIOR PELING DATE: 2000-07-28
PRIOR PILING DATE: 2000-07-28
PRIOR PILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/221,943
PRIOR PILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/221,943
PRIOR PILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/257,599
PRIOR APPLICATION NUMBER: 60/250,516
PRIOR PILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/250,516
PRIOR PILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/250,516
PRIOR PILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/250,516
PRIOR PILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 60/250,516
PRIOR PILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/250,516
PRIOR APPLICATION NUMBER: 60/250,516
PRIOR PILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/250,516
PRIOR PILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 148
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ORGANISM: Artificial Sequence
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Matches 17; Conservative
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APPLICANT: "yatt, Jacqueline R.
APPLICANT: Borchers, Alexander
APPLICANT: Uickers, Timothy A.
TITLE OF INVENTION: UDBNTIFICATION OF GENETIC TARGETS FOR
TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES AND
TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
FILE REFERENCE: ISIS-4503
CURRENT APPLICATION NUMBER: US/10/388,263
CURRENT PILION DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 947
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 203
LENGTH: 21
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| Fublication No. US20030228302A1
| GENERAL INFORMATION:
| TLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS FILE REFERENCE: 1551-2001-001
| CURRENT APPLICATION UNMBER: US/10/418,182
| CURRENT FILING DATE: 2003-04-16
| PRIOR APPLICATION NUMBER: 60/373,558
| PRIOR APPLICATION NUMBER: 60/373,558
| PRIOR APPLICATION WINDER: 60/373,558
| PRIOR FILING DATE: 2002-04-17
| NUMBER OF SEQ ID NOS: 423
| SEQ ID NO 112
| LENGTH: 21
                                                                                                                                            Query Match 0.4%; Score 15.2; DB 1; Length 21; Best Local Similarity 85.0%; Pred. No. 6.9e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 85.0%; Pred. No. 6.9e+02;
Matches 17; Conservative 0; Mismatches 3;
                       ; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Allele DQB1*06011
US-10-253-967-36
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Publication No. US20030228597A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                      231 CTGGACACGGCCCGAGCGGA 250
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Sasmor, Henri M.
Brooks, Douglas G.
Ohashi, Cara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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APPLICANT: Baker, Brenda F.
APPLICANT: McNeil, John
ORGANISM: Homo sapiens
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LOCATION: (16) ...(16)
OTHER INFORMATION: Glen research spacer 9 (cat # 10-1909-90) between c 15 and c 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/10142566

Publication No. US20030119016A1

GENERAL INFORMATION:
APPLICANT: Riley, Timothy A.
APPLICANT: Brown, Bob D.
APPLICANT: Arnold, Lyle J.
APPLICANT: Arnold, Lyle J.
TITLE OF INVENTION: ANTIERNSE OLIGONUCLEOTIDES WITH INCREASED RNASE SENSITIVITY
FILE REFERENCE: OASBIO.003DV1
CURRENT APPLICATION NUMBER: US/10/142,566
PRIOR FILING DATE: 2002-08-06
PRIOR FILING DATE: 1996-08-18
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
                                                               OTHER INFORMATION: Description of Artificial Sequence:Ag427 Probe CTHER INFORMATION: Primer US-09-800-198-33
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                                                                                                                                                                      0.4%; Score 15.2; DB 1; Length 21;
85.0%; Pred. No. 6.9e+02;
tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (21)...(21)
; OTHER INFORMATION: propyl linker attached to t 21
US-10-142-566-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: synthetic oligonucleotide
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TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                 Best Local Similarity 85.0
Matches 17; Conservative
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US-10-142-566-49
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LENGTH: 21
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US-10-380-195A-44/c

Sequence 44, Application US/10380195A

Publication No. US20040072776A1

Sequence 44, Application US/10380195A

Publicant US20040072776A1

APPLICANT: Gleave, Martin

APPLICANT: Niyama, Satoshi

APPLICANT: Nelson, Colleen

TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBB)-2

TITLE OF INVENTION: Antisense US (10/380,195A)

TITLE OF INVENTION: Oligodeoxynucleotides for Prostate and Endocrine Tumor Therapy

FILE REFERENCE: UBC.P-023

TITLE OF INVENTION: UNMBER: PCT/US01/28748

FRIOR APPLICATION NUMBER: PCT/US01/28748

PRIOR APPLICATION NUMBER: US 60/232,641

PRIOR APPLICATION NUMBER: US 60/232,641
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             PRIOR PELICATION NUMBER: 60/310, 291
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2002-03-05
PRIOR PLICATION NUMBER: 60/310, 951
PRIOR PLING DATE: 2002-03-05
PRIOR PLING DATE: 2002-08-08
PRIOR PLING DATE: 2002-08-08
PRIOR PLING DATE: 2002-03-05
PRIOR PLING DATE: 2001-08-08
PRIOR PLING DATE: 2001-08-09
PRIOR PLING DATE: 2001-08-09
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-13
PRIOR PLING DATE: 2001-08-14
PRIOR PLING DATE: 2001-08-14
PRIOR PLING DATE: 2001-08-17
PRIOR PLING DATE: 2010-08-17
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0.4%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 6.9e+02;
Matches 17; Conservative 0; Mismatches 3;
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US-10-380-195A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3669 CATGGCTCAGGGTGGTCTCT 3688
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ORGANISM: Artificial Sequence
2001-08-02
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APPLICANT: Taupier, Raymond J., Jr.
APPLICANT: Taupier, Stacie
APPLICANT: Caeman, Stacie
APPLICANT: Rothenberg, Mark E.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Boldog, Ferenc L.
TITLE OF INVENTION: THE SAME
FILE OF INVENTION: THE SAME
FILE REFERENCE: 21402-416D
CURRENT APPLICATION NUMBER: US/10/210,281
PRIOR APPLICATION NUMBER: 60/309,501
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WESUL 92.4

Sequence 82, Application US/10377079

Sequence 82, Application US/10377079

Publication No. US2030323395A1

GENERAL INFORMATION:

APPLICANT: Huang, Shi

TITLE OF INVENTION: Antibodies and Methods

TITLE OF INVENTION: Antibodies and Methods

FILE REFRENCE: P-LJ 3611

CURRENT TILING DATE: 2003-02-28

NUMBER OF SEQ ID NOS: 93

NUMBER OF SEQ ID NOS: 93

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 82

LENGTH: 21
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0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 6.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                      Query Match 0.4%; Score 15.2; DB 1; Length 21; Best Local Similarity 85.0%; Pred. No. 6.9e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                         860 AGCTGGTGGAGGCTGACGAG 879
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APPLICANT: Zerhusen, Bryan D.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Padigaru, Muralidhara
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                    20 AGCTGGTGGATGCAGAGGAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GAAGACAATCAACAGGGGC 2
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                             OTHER INFORMATION: PCR Primer US-10-388-263-203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patturajan, Meera
Miller, Charles E.
Ji, Weizhen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-377-079-82
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APPLICANT:
APPLICANT:
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FEATURE:
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TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN TITLE OF INVENTION: KINASE FILE REPERBERGE: AM10101.

CURRENT APPLICATION NUMBER: 60/429,381

PRIOR PERIOR PILING DATE: 2003-11-07

NUMBER OF SEQ ID NOS: 306

SEQ ID NOS: 306

SEQ ID NO 161

LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 289, Application US/10702496

Publication No. US20040121383A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wyeth

TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN

TITLE OF INVENTION: KINASE

TITLE OF INVENTION: KINASE

FILE REFERENCE: AMIO1071

CURRENT APPLICATION NUMBER: US/10/702,496

CURRENT APPLICATION NUMBER: 60/429,381

PRIOR APPLICATION NUMBER: 60/429,381

PRIOR PRICING DATE: 2003-11-27

NUMBER OF SEQ ID NOS: 306

SOFTWARE: Patentin version 3.2

SEQ ID NO 289

LENGTH: 21
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Publication No. US20040142896A1
GENERAL INFORMATION:
APPLICANT: Wang, Jui, H
APPLICANT: Wang, Jui, H
TITLE OF INVENTION: High Efficacy Antisense RI alpha PKA Poly-DNP Oligoribonucleotide
FILE REFERENCE: 11520.0338
CURRENT APPLICATION NUMBER: US/10/728,491
CURRENT APPLICATION NUMBER: US 60/431,694
PRIOR APPLICATION NUMBER: US 60/431,694
PRIOR FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 27
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Pred. No. 6.9e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                        Length 21;
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Pred. No. 6.9e+02;
4; Mismatches 3;
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Best Local Similarity 65.0'
Matches 13; Conservative
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Best Local Similarity 85.v.
These 17; Conservative
                                                                                                                                                                                                                                                              ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-702-496-161
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US-10-702-496-289
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                                                                                    US-10-432-364-35/c

US-10-432-364-35/c

Sequence 35, Application US/10432364

Publication No. US20040091996A1

Publication No. US20040091996A1

APPLICANT: VIRGENE BIOTECHNOLOGY LIMITED

TITLE OF INVENTION: A VIRUS WHICH CAN EXPRESS TUMOR ANGIOSTATIN FACTOR WITH HIGH EFFI

TITLE OF INVENTION: SPECIFIC TUMOR CELLS AND THE USE OF IT

TITLE OF INVENTION: A VIRUS WHICH CAN EXPRESS TUMOR ANGIOSTATIN FACTOR WITH HIGH EFFI

CURRENT APPLICATION NUMBER: US/10/432,364

CURRENT FILING DATE: 2003-11-06

NUMBER OF SEQ ID NOS: 36

SOOFWARE: Patentin version 3.1

SEQ ID NO 3:

LENGTH: 21
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APPLICANT: Wu, Leeying
TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
TITLE OF INVENTION: KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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US-10-432-364-35
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CURRENT APPLICATION NUMBER: US/10/702,496
CURRENT FILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: 60/429,381
PRIOR FILING DATE: 2002-11-27
NUMBER OF SEQ ID NOS: 306
SOFTWARE: Patentin version 3.2
SOFTWARE: 21
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US-10-702-496-154
; Sequence 154, Application US/10702496
; Publication No. US20040121383A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
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o. US20040121383A1
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           20 CCATCCGGGGGGACCCCGAG 1
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Best Local Similarity 85.0
Matches 17; Conservative
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Publication No. US20040121

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Liu, Wei

APPLICANT: Wu, Leeying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
US-10-702-496-154
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                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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Sequence 17100, Application US/10786720
; SEQUENCE OF USERVATION: APPLICANT: Weth
; APPLICANT: Weth
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
; TITLE OF INVENTION: DISEASES
; TITLE OF INVENTION: DISEASES
; TITLE OF INVENTION: USFERENCE: 031896-023000 (AMI01331L)
; CURRENT APPLICATION NUMBER: US/10/786,720
; CURRENT PILING DATE: 2004-02-26
                         Sequence 11538 Application US/10786720
Sequence 11538 Application US/10786720
Publication No. US20040191818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Liu, Wei
APPLICANT: US/10/786,720
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT PILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 11538
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: RNAi-antisense strand US-10-786-720-11538
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Fublication No. US20040191818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: O'TOOLe, Margot
APPLICANT: Liu, Wei
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT PILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 11203
LENGTH: 21
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                                                                                 Query Match 0.4%; Score 15.2; DB 1; Length 21; Best Local Similarity 85.0%; Pred. No. 6.9e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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85.0%; Pred. No. 6.9e+02;
iive 0; Mismatches 3; Indels
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US-10-786-720-11219/C
Sequence 11219, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION;
; APPLICANT: Wyeth
; APPLICANT: Wyeth
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR;
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 031896-023000 (AM101331L)
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 21135
; SOFTWARE: Patentin version 3.2
; ENGTH: 21
  ; FEATURE:
; OTHER INFORMATION: 5-base mismatched strand
US-10-728-491-9
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Best Local Similarity 85.0
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-10-786-720-11203
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Matches 17; Conserv
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FEATURE:
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Sequence 17110, Application US/10786720
Publication No. US20040191818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Weth
APPLICANT: Liu, Wei
APPLICANT: US/10/786,720
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT PILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOUTHARE: Parentin version 3.2
SEQ ID NO 17110
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Publication No. US20040191818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Liu, Wei
APPLICANT: Liu, We
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APPLICANT: O'Toole, Margot
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
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40.0%; Pred. No. 6.9e+02;
tive 9; Mismatches 3;
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. Sequence 18288, Application US/10786720

; Publication No. US20040191818A1

; GENERAL INFORMATION:
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; ORGANISM: RNAi-antisense strand
US-10-786-720-18285
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Best Local Similarity 40.0
Matches 8; Conservative
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US-10-786-720-17110
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LENGTH: 21
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Publication No. US20040191818A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: USEASSES

FILE REFERENCE: 031896-023000 (AM101331L)

CURRENT APPLICATION NUMBER: US/10/786,720

CURRENT FILING DATE: 2004-02-26

NUMBER OF SEQ ID NOS: 21135

SOFTWARE: PatentIn version 3.2

SEQ ID NO 17103
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Suguence 17106, Application US/10786720
Sublication No. US20040191818A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOGTWARE: Patentin version 3.2
SEQ ID NO 17106
LENGTH: 21
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40.0%; Pred. No. 6.9e+02;
tive 9; Mismatches 3; Indels
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CRGANISM: RNAi-antisense strand
US-10-786-720-17100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-786-720-17103
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; ORGANISM: RNAi-antisense strand
US-10-786-720-17106
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 17100
LENGTH: 21
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Best Local Similarity 40.0
Matches 8; Conservative
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; Sequence 16, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REPRENCE: 02811-018
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT PILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; RIOR FILING DATE: 2000-08-29
; RIOR FILING DATE: PATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
                                                          Gaps
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBACE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SEGTWARE: PatentIn Ver. 2.0
LENGTH: 38
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85.0%; Pred. No. 6.9e+02;
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100.0%; Pred. No. 5.1e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                        Sequence 10176, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
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                                                                                                                                                               20 TATGTGTGTGTCTGCTTGTG 1
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                             Best Local Similarity 85.0%
Matches 17; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 63.9
Matches 23; Conservative
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CORGANISM: Homo sapiens
US-09-764-891-10176
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US-09-263-959-543/c
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i Sequence 18295, Application US/10786720

i Sequence 18295, Application US/10786720

i Publication No. US20040191818A1

i APPLICANT: Wyeth

APPLICANT: Liu, Wei

I TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE

I TITLE OF INVENTION: DISEASES

TITLE OF INVENTION: DISEASES

I TITLE OF INVENTION: DISEASES

CURRENT APPLICATION NUMBER: US/10/786,720

CURRENT APPLICATION NUMBER: US/10/786,720

CURRENT APPLICATION NUMBER: US/10/786,720

CURRENT PILING DATE: 2004-02-26

NUMBER OF SEQ ID NOS: 21135

SEQ ID NO 18295

LENGTH: 21
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US-10-786-720-18291
| Sequence 18291, Application US/10786720
| Publication No. US20040191818A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Wyeth
| APPLICANT: Wyeth
| APPLICANT: Win weith | Weith 
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Pred. No. 6.9e+02;
9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 15.2; DB 1; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.2; DB 1;
Pred. No. 6.9e+02;
9; Mismatches 3;
                                      TITLE OF INVENTION: DISEASES
FILE REPERBUCE: 031896-023000 (AMI01331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 18288
LENGTH: 21
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| GUGUCUGCUUGUGUGUCUGU 20
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; ORGANISM: RNAi-antisense strand
US-10-786-720-18291
                                                                                                                                                                                                                                                                                                 TYPE: RNA · ORGANISM: RNAi-antisense strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.4%;
                                                                                                                                                                                                                                                                                                                                                                                                               0.4%;
Local Similarity 40.0%;
les 8; Conservative 5
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Best Local Similarity 40.0
Matches 8; Conservative
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US-10-138-674-6070
US-10-138-674-6070
US-10-138-674-6070
Sequence 6070, Application US/10138674
Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSviggen, Jam
APPLICANT: Stinchcomb, Dan
APPLICANT: Scobedo, Jaime
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refire Reference: MBHB00-876-N (400/049)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 222, Application US/10085906

Sequence 222, Application WS/10085906

Publication No. US20030054371A1

GENERAL INFORMATION:

APPLICANT: Ving, Vincent

APPLICANT: Win, Paul

APPLICANT: Gray, Gary, Gary S.

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS

CURRENT APPLICATION NUMBER: US/10/085,906

CURRENT FILING DATE: 1999-03-22

PRIOR PELING DATE: 1999-03-25

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 545

NUMBER OF SEQ ID NOS: 545

LENGTH: 15
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. 5.1e+02;
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Pred. No. 5.1e+02;
0; Mismatches 0;
                         NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPATION: (206) 622-4900
INFORMATION FOR SEQ ID NO: 545:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.4%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 5.1 Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.4%; SCOL
100.0%; Pre
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   ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity
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Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Lee
COMMENCE ADDRESS: 1279
CORRESPONDERCE Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                         GENERAL INFORMATION:
APPLICANT: Hood, Lercy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: A PACHICIN Release #1.0, Version #1.25
SOFTWARE: PACHICIN DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PILING DATE: 05-MAR-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/ACENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEPAS: (206) 682-6031
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
COUNTR: Mashington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMP
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
; Patent No. US20020150891A1
                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
STATE: Washington
COUNTRY: US
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US-09-263-959-545/c
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US-09-263-959-543
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APPLICANT: ALD CAME FIRST AND CONTROLL OF THE APPLICANT: ALD CAME APPLICANT: BESCOBEGO, Jaime APPLICANT: BESCOBEGO, Jaime TITLE OF INVENTION: Devels of Vascular Endothelial Growth Factor Receptor FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor FILE REFERENCE: MBHBO0-876-N (400/049) CURRENT APPLICATION NUMBER: US/10/138,674

CURRENT FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: Patentin Version 3.0

SEQ ID NO 9256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-287-949A-8256

US-10-287-949A-8256

Publication No. U520040102389A1

Publication No. U520040102389A1

GENERAL INPORMATION:

APPLICANT: Rabozyme Pharmaceuticals, Inc.

APPLICANT: Rabozyme Pharmaceuticals, Inc.

APPLICANT: Rabozyme Pharmaceuticals, Inc.

APPLICANT: Rabozo, Pan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT APPLICATION NUMBER: US/10/287,949A

NUMBER OF EXO ID NOS: 20822

SOFTWARE: Patentin version 3.0

SEQ ID NO 8256

LENGTH: 17
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                         Length 17;
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                                                                           0; Indels
                         DB 1; Le
5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.4%; Score 15; DB 1; I
Best Local Similarity 53.3%; Pred. No. 5.9e+02;
Matches 8; Conservative 7; Mismatches 0;
                         Query Match 0.4%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 5.5 Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                    Sequence 8256, Application US/10138674; Publication No. US20040077565A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2317 CTGTGTGTGTGTG 2331
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                                                                                                                                      1197 GGGCAAGCCCCTTGG 1211
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                                                                                                                                                                                      16 GGCAAGCCCCTTGG 2
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US-10-138-674-8256
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US-10-287-949A-8256
                                                                                                                                                                                                                                                                                                   JS-10-138-674-8256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
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10s-10-287-949A-6070
1 Sequence 6070, Application US/10287949A
1 Sequence 6070, Application US/10287949A
1 GENERAL INFORMATION:
2 APPLICANT: McSwiggen, Jim
3 APPLICANT: Richcomb, Dan
4 APPLICANT: Stinchcomb, Dan
5 APPLICANT: Stinchcomb, Dan
5 APPLICANT: Stinchcomb, Dan
5 APPLICANT: Stinchcomb, Dan
6 APPLICANT: Stinchcomb, Dan
7 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
7 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
7 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
7 CURRENT APPLICATION NUMBER: US/10/287,949A
7 CURRENT PILING DATE: 2003-04-11
7 NUMBER OF SEQ ID NOS: 20822
7 SOFT WARE: PatentIn version 3.0
7 SEG ID NO 6070
7 LENGTH: 16
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US-10-238-700-3390/c

Sequence 3390, Application US/10238700

Sequence 3390, Application US/10238700

Publication No. US20030153521A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level

FILE REFERENCE: 400/057 (MRH801-1158-A)

CURRENT APPLICATION NUMBER: US/10/238,700

CURRENT APPLICATION NUMBER: US 60/318,471

PRIOR FILING DATE: 2002-05-29

PRIOR FILING DATE: 2001-05-10

NUMBER OF SEQ ID NOS: 4666

SOFTWARE: PatentIn Version 3.0

SEQ ID NO 3390

SEQ ID NO 3390
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                                                                                                                                                                                                                                                                            Length 16;
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                                                                                                                                                                                                                                                                          0.4%; Score 15; DB 1; 1
53.3%; Pred. No. 5.5e+02;
tive 7; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 6070
LENGTH: 16
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1 GUGUGUGUGUGUGUG 15
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Matches 8; Conservative
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ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
US-10-238-700-3390
                                                                                                                                                                     TYPE: RNA
CORGANISM: Homo sapiens
US-10-138-674-6070
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TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION FILE REFERENCE: 5244118 (PERVINETION)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: TAG019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.4%; Score 15; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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US-10-310-677-45
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                                 FILE REFERENCE: 5244US (REN/PS5190USO)
CURRENT APPLICATION NUMBER: US/10/055,728
CURRENT FILING DATE: 2002-04-19
FRIOR APPLICATION NUMBER: EP 0120373.2
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-01-3
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.1
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: modified base
; LOCATION: (1)..(5)
; OTHER INFORMATION: a stands for inosine
US-10-055-728-45
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Matches 15; Conservative
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WENDUR BEAL

Sequence 21, Application US/10464158

Publication No. US20040009599A1

Sequence 21, Application US/04064158

Publication No. US2004000959A1

APPLICANT: C. Frank Bennett

APPLICANT: C. Frank Bennett

APPLICANT: C. Frank Bennett

TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APPLICANT

TITLE OF INVENTION: ANTISENSE US/10/464,158

CURRENT APPLICATION NUMBER: US/10/464,158

CURRENT FILING DATE: 2001-09-24

PRIOR FILING DATE: 1999-06-16

PRIOR PLILNG DATE: 1999-06-16

PRIOR PLILNG DATE: 1999-12-03

NUMBER OF SEQ ID NOS: 48

SEQ ID NO 21

LENGTH: 18
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Publication No. US20040072769A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods for design and selection of short double-stranded
TITLE OF INVENTION: oligonucleotides, and compounds of gene drugs
TITLE OF INVENTION: oligonucleotides, and compounds of gene drugs
TITLE OF INVENTION: 01900ucleotides, and compounds of gene drugs
TITLE OF INVENTION: 01900ucleotides, and compounds of gene drugs
CURRENT APPLICATION NUMBER: US/10/016,490C
CURRENT FILING DATE: 2002-11-22
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.4%; Score 15; DB 1; Length 19;
100.0%; Pred. No. 6.6e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Antisense Oligonucleotide
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Sequence 45, Application US/10055728;
Publication No. US20030170720A1
GENERAL INFORMATION:
APPLICANT: van der Kuyl, Antoinette C.
APPLICANT: Cornelissen, Marion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1606 CAGAAGTGCATCCAC 1620
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 CAGAAGTGCATCCAC 3
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Matches 15; Conservative
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                            TYPE: DNA ORGANISM: artificial
CURRENT FILING DATE:
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APPLICANT: Pharmacia Corp.
APPLICANT: Giere, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
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APPLICANT: Taylor, Kent D.
APPLICANT: Rotter, Jerome I.
APPLICANT: Sugiamus, Huiying
APPLICANT: Sugiamus, Kazuhito
APPLICANT: Targan, Stephan
TITLE OF INVENTION: Methods of Using a NOD2/CARD 15
TITLE OF INVENTION: Haplotype to Diagnose Crohn's Disease
FILE REFERENCE: P-CE 5451
CURRENT APPLICATION NUMBER: US/10/274,300
CURRENT FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 89
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.4%; Score 15; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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Pred. No. 7e+02;
0; Mismatches (
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-47
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Publication No. US20040132063A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pr
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                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 GGCATCAAGCTGCGG 396
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US-10-274-300-55
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                    US-10-380-124-47
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Sequence 31, Application US/09971353

Sequence 31, Application US/09971353

Sequence 31, Application No. US20030113723A1

GENERAL INFORMATION:
APPLICANT: BABL, Bharati
APPLICANT: BOSE, Melanie Anne
TITLE OF INVENTION: METHOD FOR EVALUATING MICROSATELLITE INSTABILITY IN A TUMOR SAMPL:
FILE REFRENCE: 11757-540541

CURRENT APPLICATION NUMBER: US/09/971,353

CURRENT FILING DATE: 2001-10-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PARCHING DATE: 2000-10-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PARCHING VERSION 3.1

EENGTH: 38
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Sequence 139-25

Sequence 130-157

Sequence 130-157

Sequence 130-157

Sequence 130-157

Sequence 130-157

APPLICANT: ULLMAN, EDWIN

APPLICANT: WU, MING

APPLICANT: LIU, YEN PING

TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS

FILE REFERENCE: 3817.05-1

CURRENT APPLICATION NUMBER: US/10/219,195

CURRENT APPLICATION NUMBER: 60/312,505

PRIOR FILING DATE: 2001-08-14

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Patentin Ver. 2.1

LENGTH: 39
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                                                                                                                                                                                                                                                                                                                                                          0; Indels
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7e+02;
                                                                                                                                                                                                                                                                                                          0.4%; Score 15; DB 100.0%; Pred. No. 7e+cive 0; Mismatches
                                                                                                                                                                                                              FEATURE:
COTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1491
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                 PRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1491
LENGTH: 20
2003-09-25
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Best Local Similarity 100.03
Matches 15; Conservative
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Matches 18; Conservative
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APPLICANT: ULLMAN, EDWIN
APPLICANT: WI, WING
TITLE OF INVENTION: ISOTHERWAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
TITLE OF INVENTION: ISOTHERWAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
FILE REPERENCE: 3817.05-1
CURRENT APPLICATION NUMBER: 00/312,505
PRIOR PILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE PACENTIN Ver. 2.1
IENGTH: 42
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Publication No. US20030165917A1
GENERAL INFORMATION:
APPLICANT: ULLMAN, EDMIN
APPLICANT: ULLMAN, EDMIN
APPLICANT: ULLMAN, EDMIN
TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
FILE REFERENCE: 3817.05-1
CURRENT APPLICATION NUMBER: US/10/219,195
CURRENT APPLICATION NUMBER: 60/312,505
FRIOR APPLICATION NUMBER: 60/312,505
FRIOR PLING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE PATENTING DATE: 2.1
SEQ ID NO 33
LENGTH: 42
                                                                                                                                                  Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: oligonucleotide US-10-219-195-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
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US-10-219-195-33
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Pred. No. 1.3e+03;
0; Mismatches 15; Indels
                                                                                           Query Match 0.4%; Score 15; DB 1; Length 39; Best Local Similarity 67.7%; Pred. No. 1.2e+03; Matches 21; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3262 TATTTTATTTGCTTTGTCCTTTTTCAGGAGAATTAGATT 3300
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                                                                                                                                                                                                                                             2 TITITITITITITITITITITITITITITIGCCTT 32
                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/10219195
Publication No. US20030165917A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.4%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match .0.4
Best Local Similarity 61.5
Matches 24; Conservative
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US-10-219-195-33
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0.4%; Score 15; DB 1; Length 42;

Query Match

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APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: ROWEN, Lee
APPLICANT: ROSO, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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Publication No. US20040014036Al

GENERAL INFORMATION:

APPLICAMY: Peashne, et al.,

APPLICAMY: Peashne, et al.,

TITLE OF INVENTION: Therefor

TITLE OF INVENTION: Therefor

FILE REFERENCE: 0342941-0065

CURRENT APPLICATION NUMBER: US/09/943,944E

CURRENT PAPLICATION NUMBER: US/09/943,944E

CURRENT PAPLING DATE: 2.010-08-31

NUMBER OF SEQ ID NOS: 238

SOFTWARE: Patentin Ver. 2.1
                            Gaps
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  Pred. No. 1.3e+03;
); Mismatches 15; Indels
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                                                                            3262 TATTTTATTTGCTTTGTCCTTTTTCAGGAGAATTAGATT 3300
                                                                                                                        4 rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID No: 971:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 6.76
0; Mismatches
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Best Local Similarity 61.5%; Pr
Matches 24; Conservative 0;
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Best Local Similarity 88.9
Matches 16; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Seattle
STATE: Washington
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US-09-263-959-971
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LENGTH: 18
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NAME/KEY: misc_feature
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US-10-327-805-42

Sequence 42, Application US/10327805

Sequence 42, Application US/10327805

Publication No. US20030144241A1

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD6 EXPRESSION

TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD6 EXPRESSION

TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD6

FILE REFERENCE: RTS-0045

CURRENT FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: US/109/679,298

PRIOR APPLICATION NUMBER: US/09/679,298

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 42

LENGTH: 18
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APPLICANT: Linnen, Jeffery M.
APPLICANT: Linnen, Jeffery M.
APPLICANT: Cockter, Jamel M.
APPLICANT: Getman. Damon M.
APPLICANT: Getman. Damon K.
APPLICANT: Yoshimura, Tadashi
APPLICANT: Ho-Sing-Loy, Marcy,
APPLICANT: Stringlellow, Leslie A.
TITLE OF INVENTION: Hepatitis B Virus
TITLE OF INVENTION: Hepatitis B Virus
FILE REFERENCE: GP134-02.UT
CURRENT APPLICATION NUMBER: US/10/461,790
CURRENT APPLICATION NUMBER: 60/389,393
PRIOR PRILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 142
SOFTWARE: FastSEQ for Windows Version 3.0
IENGTH: 18
                                              FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Random
OTHER INFORMATION: nucleotide sequences.
US-09-943-944E-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.4%; Score 14.8; DB 1; Length 18; Best Local Similarity 88.9%; Pred. No. 6.7e+02; Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                         Query Match
0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 6.76+02;
Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Antisense Oligonucleotide US-10-327-805-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 129, Application US/10461790
                                                                                                                                                                                                                                                                               2698 CITCCCACCTGCCCTC 2715
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                                                                                                                                                                                                                                                                                                         1 CTCCCCACCATGCCCCTC 18
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                       ORGANISM: Artificial Sequence
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ORGANISM: Hepatitis B Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Publication No. US200
GENERAL INFORMATION:
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APPLICANT: ACCOUNTS. PROCO, Pam APPLICANT: MCSwiggen, Jim APPLICANT: McSwiggen, Jim APPLICANT: Exact Dear State Comb. Dan APPLICANT: State Comb. Dan APPLICANT: State Comb. Dan APPLICANT: Escobedo, Jaime TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions ReTITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor FILE REPERENCE: MBHBOO-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1449
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2-10-138-674-3004

1 Sequence 3004, Application US/10138674

1 Sequence 3004, Application US/10138674

2 Publication No. US20040077565A1

2 Publication No. US20040077565A1

3 Publication No. US2004007565A1

4 PublicANT: Ribozyme Pharmaceuticals, Inc.

4 APPLICANT: Pavco, Pam

4 APPLICANT: Stinchcomb, Dam

4 APPLICANT: Stinchcomb, Dam

5 APPLICANT: Stinchcomb, Dam

6 APPLICANT: Scobedo, Jaime

7 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

7 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

7 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

7 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

8 TITLE REPERENCE: MBHB00-876-N (400/049)

7 CURRENT APPLICATION NUMBER: US/10/138,674

8 NUMBER OF SEQ ID NOS: 2082-2

8 OFFTARE PARENTED PARENT
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Pred. No. 6.7e+02;
4; Mismatches 2; Indels
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                                                                                                                                                                                 Query Match 0.4%; Score 14.8; DB 1; Length 18; Best Local Similarity 88.9%; Pred. No. 6.7e+02; Matches 16; Conservative 0; Mismatches 2; Indels
; LOCATION: (1)...(18)
; OTHER INFORMATION: 2'-OMe nucleotide analogs US-10-461-790-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1449, Application US/10138674
Publication No. US20040077565A1
GENERAL INFORMATION:
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Best Local Similarity 66.7%;
Matches 12; Conservative '
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Best Local Similarity 72.2
Matches 13; Conservative
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CORGANISM: Homo sapiens
US-10-138-674-1449
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CORGANISM: Mus musculus
US-10-138-674-3004
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APPLICANT: StinchComb, Dan
APPLICANT: StinchComb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MHHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 3004
LENGTH: 18
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Jesus Application US/09813289

Jesus Application US/09813289

Jesus Application US/09813289

Jesus Applicant No. US20020061571A1

JAPPLICANT: Mahadevan, M.S.

APPLICANT: Tiscornia, G

JITLE OF INVENTION: thereof

TITLE OF INVENTION: thereof

TITLE OF INVENTION: UNMER: US/09/813,289

CURRENT APPLICATION NUMBER: US 60/190,590

PRIOR PILING DATE: 2000-03-20

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 7.1e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Triticum aestivum
US-08-983-605-118
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.23
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.99
Matches 16; Conservative
                      McSwiggen, Jim
Stinchcomb, Dar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-983-605-118/c
                                                                                                                                                                                                                                                                                                                              US-10-287-949A-3004
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APPLICANT: Ravoco Pam

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MEBHBO0-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1449
                                                                                                                                                                                                             APPLICANT: Karin, Nathan
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS FOR TREATING RHEUMATOID
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS FOR TREATING RHEUMATOID
TITLE OF INVENTION OF ARTHRITS
CURRENT APPLICATION NUMBER: US/10/203,102A
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 12
LENGTH: 18
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Pred. No. 6.7e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.4%; Score 14.8; DB 1; Length 18; Best Local Similarity 88.9%; Pred. No. 6.7e+02; Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Single strand DNA oligonucleotide US-10-203-102A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 3004, Application US/10287949A; Publication No. US20040102389A1; GENERAL INFORMATION: APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                           Sequence 12, Application US/10203102A Publication No. US20040086483A1 GENERAL INFORMATION:
1678 GACTICGGCTGGCCCGG 1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1391 TCAACCTGCTGGCCCCT 1408
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1 UUAACCUGCUGGGAGCCU 18
                           1 GACUNCGCCUNGGCCCGG 18
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nes 12; Conservative
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US-10-287-949A-1449
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US-10-287-949A-3004
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Best Local S
Matches 12
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LOCATION: (1). (19)
OTHER INFORMATION: potential microsequencing oligo for 99-128-202.mis2
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1 LOCATION: 1..19

2 OTHER INFORMATION: potential microsequencing oligo for 99-148-129.misl

US-09-853-526-483
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0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 2;
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; Sequence 483, Application US/09853526
; Patent No. US20020165345A1
; GENERAL INFORMATION:
    APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
APPLICATION NUMBER: US/09/853,526
CURRENT FILING DATE: 1999-06-23
; PRIOR FILING DATE: 1999-06-23
; PRIOR FILING DATE: 1998-09-09
; PRIOR FILING DATE: 1998-12-22
; WUMBER OF SEQ ID NOS: 578
; SEQ ID NOS: 578
; SEQ ID NO 483
; LEMERH 19
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 08/996,306
PRIOR FILING DATE: 1997-12-22
PRIOR PELLING DATE: 1998-09-09
PRIOR FILING DATE: 1998-09-09
PRIOR PILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 09/218,207
PRIOR PILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 578
SSQ ID NO 546
LENGTH: 19
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-901-484A-546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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; OTHER INFORMATION: potential microsequencing oligo for 99-148-129.mis1
US-09-901-484A-483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                Query Match

0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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                                                                                                                                        FEATURE:
, OTHER INFORMATION: A mutated DMPK 3'UTR fragment
US-09-813-289-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 483, Application US/09901484A
; Sequence 483, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chunakov, Ilya
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Prostate Cancer Gene
FILE REFERENCE GEN-TILIXCADD
CURRENT APPLICATION NUMBER: US/09/901,484A
CURRENT FILING DATE: 2001-07-09
FRIOR APPLICATION NUMBER: US 60/099,658
FRIOR APPLICATION NUMBER: US 60/099,658
FRIOR APPLICATION NUMBER: US 09/218,207
FRIOR FILING DATE: 1998-09-09
FRIOR APPLICATION NUMBER: US 09/338,907
FRIOR FILING DATE: 1999-06-23
FRIOR APPLICATION NUMBER: US 09/338,907
FRIOR FILING DATE: 1999-06-23
FRIOR APPLICATION NUMBER: US 09/338,907
FRIOR FILING DATE: 1999-06-23
FRIOR APPLICATION NUMBER: US 09/338,526
FRIOR FILING DATE: 1999-06-23
FRIOR FILING DATE: 1998-05-06
FRIOR FILING DATE: 1998-05-05
FRIOR FILING DATE: 1998-05-05
FRIOR FILING DATE: 1998-06-23
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US-09-901-484A-546
; Sequence 546, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumenfeld, Marta
; APPLICANT: Chumenfeld, Marta
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; TITLE REFERENCE: GEN-TILLANGE
; FILE REFERENCE: GEN-TILLANGE
; CURRENT APPLICATION NUMBER: US/09/901,484A
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                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
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LOCATION: (1)..(19)
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                SEQ ID NO 22
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Length 19; Indels ö

Gaps

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Indels

Length 19;

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Sequence 69, Application US/10251117

Sequence 68, Application US/10251117

Sequence 68, Application US/2030170891A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James Bapression Using Short Interfering RNA

ITILE OF INVENTION: Gene Expression Using Short Interfering RNA

FILE REPERENCE: 900/042 (MHBBC2-468-A)

CURRENT APPLICATION NUMBER: US/10/251,117

CURRENT FILING DATE: 2003-02-24

FRIOR PILING DATE: 2002-06-06

FRIOR PLING DATE: 2002-05-20

FRIOR PLING DATE: 2002-05-20

FRIOR APPLICATION NUMBER: US 60/359,580

FRIOR APPLICATION NUMBER: US 60/359,580

FRIOR APPLICATION NUMBER: US 60/356,540

FRIOR APPLICATION NUMBER: US 60/356,249

FRIOR PLING DATE: 2001-07-25

FRIOR APPLICATION NUMBER: US 60/296,249

FRIOR PLING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 1213

SOFTWARE: PatentIn version 3.0

LENGTH: 19
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Sequence 180, Application US/10251117

Sequence 180, Application US/10251117

Sequence 180, Application US/10251117

Sequence 180, Application US/10251117

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

ITILE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R ITILE OF INVENTION: Gene Expression Using Short Interfering RNA

ITILE OF INVENTION: Gene Expression Using Short Interfering RNA

FILE REFERENCE: 900/042 (MBHB02-468-A)

CURRENT FAPLICATION NUMBER: US 60/393,924

PRIOR FILING DATE: 2002-02-04

PRIOR PILING DATE: 2002-06-06

PRIOR PPLICATION NUMBER: US 60/358,580

PRIOR PPLICATION NUMBER: US 60/358,580

PRIOR PPLICATION NUMBER: US 60/358,580

PRIOR PPLING DATE: 2001-07-25

PRIOR PPLING DATE: 2001-07-25

PRIOR PRILING DATE: 2001-07-25

PRIOR PRILING DATE: 2001-07-25

PRIOR PLING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 1213

SOFTWARE PATENTING NUMBER: US 60/296,249

PRIOR FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 1213
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2323 GTGTGTGTGTGTGT 2340
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SEQ ID NO 180
LENGTH: 19
TYPE: RNA
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: LOCATION: 11.19

: OTHER INFERMATION: potential microsequencing oligo for 99-128-202.mis2

US-09-853-526-546
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0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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                                                                          US-09-103-102-105

US-09-103-105-105

US-09-105-105

Patent No. US20020165345A1

GERERAL INFORMATION:

APPLICANT: Blumenfeld, Marta

TILLE REFERENCE: GENSET.18CPLCP

CURRENT PILING DATE: 109-06-23

PRIOR APPLICATION NUMBER: 09/338,907

PRIOR PILING DATE: 1999-09

PRIOR PILING DATE: 1998-09

PRIOR PILING DATE: 1998-09

PRIOR PILING DATE: 1998-09

PRIOR PILING DATE: 1998-12-22

NUMBER OF SEQ ID NOS: 578

SEQ ID NO 546

LENGTH: 19
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; OTHER INFORMATION: primer 768.348.rl
US-09-766-450-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/09766450 Publication No. US20030022166A1 GENERAL INFORMATION:
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ORGANISM: Homo Sapiens
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LENGTH: 19
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GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceutical, Inc.

APPLICANT: Ribozyme Pharmaceutical, Inc.

APPLICANT: Morrissey, David

APPLICANT: Morrissey, David

APPLICANT: Morrissey, David

APPLICANT: Morrissey, David

APPLICANT: Beigelman, Leonid

TITLE OF INVENTION: RNA Interfering Nucleic Acid (siNA)

FILE REFERENCE: 400/060 (WHHBO2-1000)

CURRENT APPLICATION NUMBER: US/10/244,647

CURRENT APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-03

PRIOR PLING DATE: 2002-07-03

PRIOR PILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: PCT US02/09187

PRIOR APPLICATION NUMBER: US 60/296,876

PRIOR APPLICATION NUMBER: US 60/296,876

PRIOR APPLICATION NUMBER: US 60/296,876

PRIOR PILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 1524

SSOCIED NOS: 1524

SSOCIED NOS: 1524

SSOCIED NOS: 1530
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                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
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; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR PILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 1213
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 429
; LENGTH: 19
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; Sequence 1161, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 515, Application US/10244647
Publication No. US20030206887A1
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ORGANISM: Artificial Sequence
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McSwiggen, James
Beigelman, Leonid
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Best Local Similarity 88.99
Matches 16; Conservative
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APPLICANT:
APPLICANT:
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor FITLE OF INVENTION: Gene Expression Using Short Interfering RNA
CURRENT APPLICATION NUMBER: US/10/251,117
CURRENT APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-02-00
                                           ; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense US-10-251-117-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibition of Epidermal Growth Factor
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US-10-251-117-317
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CURRENT APPLICATION NUMBER: US/10/251,117
CURRENT FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: US 10/163,552
PRIOR PILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-06-06
PRIOR PLING DATE: 2002-06-06
PRIOR PLING DATE: 2001-07-25
PRIOR PLING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: US 60/296,249
PRIOR PILING DATE: 2001-07-25
PRIOR PILING DATE: 2001-07-26
NUMBER OF SEQ ID NOS: 1213
SOFTWARE: PATENTIN VARSION 3.0
: SOFTWARE: PATENTIN VARSION 3.0
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                                                                                                                                                    Length 19;
                                                                                                                                           Score 14.8; DB 1; Length 1
Pred. No. 7.1e+02;
3; Mismatches 2; Indels
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: Sequence 429, Application US/10251117

: Publication No. US20030170891A1

: GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                  CUGGUGGAUGCUGAGGAG 18
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        ORGANISM: Artificial Sequence
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Best Local Similarity 72.2%;
Matches 13; Conservative
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US-10-251-117-317/c
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TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA) FILE STEREMENTS. 400/060 (MBBHB02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/389,924
PRIOR PILING DATE: 2002-02-00
PRIOR PILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-03-26
PRIOR PILING DATE: 2002-03-26
PRIOR PILING DATE: 2002-03-26
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 1161
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APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA INterference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-244-647-1161
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88.9%; Pred. No. 7.1e+02;
tive 0; Mismatches 2; Indels
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TITLE OF INVENTION: Screening method
FILE REFERENCE: PO2-0058FCT
CURRENT APPLICATION NUMBER: US/10/477,726
CURRENT FILING DATE: 2003-11-14
FRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 135
SEQ ID NO 133
LENGTH: 19
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Publication No. US20040138163A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative (
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Best Local Similarity
Matches 16; Conserve
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US-10-665-951-2244
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, OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-665-951-2244
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APPLICANT: Sirina Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Bejoglman, Leconid
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/131 (MBHB02-742-F)
FILE REFERENCE: 400/131 (MBHB02-742-F)
FILE REFERENCE: 400/131 (MBHB02-742-F)
FILE REFERENCE: 400/131 (MBHB02-742-F)
FRIOR APPLICATION NUMBER: US 10/664,668
FRIOR FILING DATE: 2003-09-18
FRIOR FILING DATE: 2003-02-29
FRIOR FILING DATE: 2002-07-29
FRIOR FILING DATE: 2002-11-04
FRIOR APPLICATION NUMBER: US 10/287,949
FRIOR FILING DATE: 2002-11-04
FRIOR FILING DATE: 2002-05-29
Gene Expression Using Short Interfering Nucleic Acid (siNA)
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                                                                                                                     PRIOR APPLICATION NUMBER: US 10/664,668
PRIOR FILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-09-18
PRIOR FILING DATE: 2003-09-20
PRIOR FILING DATE: 2003-02-20
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR PLING DATE: 2002-07-29
PRIOR PLING DATE: 2002-07-03
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-11-27
PRIOR PLING DATE: 2002-11-27
PRIOR PLING DATE: 2002-01-29
PRIOR PLING DATE: 2002-02-20
PRIOR PLING DATE: 2002-02-20
PRIOR FILING DATE: 2002-03-20
PRIOR FILING DATE: 2002-03-11
PRIOR PLING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
PRIOR PLING DATE: 2002-03-11
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                                       FILE REFERENCE: 400/131 (MBHB02-742-F)
CURRENT APPLICATION NUMBER: US/10/665,951
CURRENT FILING DATE: 2003-09-18
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Publication No. US20040138163A1
GENERAL INFORMATION:
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SEQ ID NO 2244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 19
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Sequence 34, Application US/09454394

Sequence 34, Application US/09454394

Sequence 34, Application US/094525A1

GENERAL INFORMATION:

APPLICANT: Tina McIncsh

APPLICANT: Steven Head

APPLICANT: Philip Goelet

APPLICANT: Michael T. Boyce-Jacino

ITILE OF INVENTION: Mchods for the Detection of Multiple

ITILE OF INVENTION: Mchods for the Detection of Multiple

ITILE OF INVENTION: Munder: US/09/454,394

CURRENT FILING DATE: 1999-12-03

EARLIER FILING DATE: 1999-12-03

MUMBER OF SEQ ID NOS: 72

SOFTWARE: FSEX ID NOS: 72

SOFTWARE: FSEX ID NOS: 72

SOFTWARE: FSEX ID NOS: 72

LENGTHARE: PASTESEQ for Windows Version 3.0

SEQ ID NO 34

LENGTH: 20
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APPLICANT: Steven Head
APPLICANT: Steven Head
APPLICANT: Steven Head
APPLICANT: Steven Head
APPLICANT: Michael T. Boyce-Jacino
APPLICANT: Michael T. Boyce-Jacino
APPLICANT: Michael T. Boyce-Jacino
TITLE OF INVENTION: Methods for the Detection of Multiple
TITLE OF INVENTION: Methods for the Detection of Multiple
TITLE OF INVENTION: Michael To Michael Title Polymorphisms in a Single Reaction
FILE REPERENCE: 04990.0029
CURRENT PILING DATE: 1999-12-03
EARLIER APPLICATION NUMBER: 08/216,538
EARLIER FILING DATE: 1994-03-23
EARLIER FILING DATE: 1993-11-03
NUMBER OF SEQ ID NOS: 72
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                                                                                                                                                                                                                                                                                         Length 20;
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                                                                                                                                                                                                                                                                                   Query Match

0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
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Pred. No. 7.5e+02;
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EARLIER APPLICATION NUMBER: 08/145,145
BARLIER FILING DAPE: 1993-11-03
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FREUSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 20
TYPE: DNA
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Patent No. US20020094525A1
GENERAL INFORMATION:
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Best Local Similarity 88.9
Matches 16; Conservative
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; ORGANISM: Equus caballus
US-09-454-394-34
                                                                                                                                                                                                      ORGANISM: Equus caballus US-09-454-394-33
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                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/sinA sense
US-10-665-951-2265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/09454394

Patent No. US20020004525A1

GENERAL INFORMATION:
APPLICANT: Tina McIntosh
APPLICANT: Steven Head
APPLICANT: Philip Goelet
APPLICANT: Midchael T. Boyce-Jacino
TITLE OF INVENTION: Methods for the Detection of Multiple
TITLE OF INVENTION: Single Nucleotide Polymorphisms in a Single Reaction
FILE REFERENCE: 04999.0029
CURRENT APPLICATION NUMBER: US/09/454,394
CURRENT FILING DATE: 1999-12-03
EARLIER APPLICATION WUMBER: 08/216,538
EARLIER FILING DATE: 1994-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                             PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR PILING DATE: 2002-03-11
PRIOR PLING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 7.1e+02;
Matches 13; Conservative 3; Mismatchen 2. Tran-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Itch, No. US20020082205Aluyuki
APPLICANT: Ttch, No. US20020082205Aluyuki
APPLICANT: Kavanaugh, W. Michael
ITILE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: PP-17150.001/201130.40901
CURRENT APPLICATION NUMBER: US/09/801,968
CURRENT FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 20
        APPLICATION NUMBER: US 60/358,580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Sense PCR primer US-09-801-968-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1953 CATGCGGGAGTGCTGGCA 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09801968
Patent No. US20020082205A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 CTCTGAGTGGCTGGT 1
                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 898
US-09-801-968-5/c
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US-09-454-394-33
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TOPOLOGY: linear MOLECULE TYPE: Other SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                       FILING DATE: 04-MAR-1998
APPLICATION UNDBER: 08/870,434
FILING DATE: 06-UJN-1997
APPLICATION NUMBER: 08/799,910
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/599,654
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: 08/485,573
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/386,844
FILING DATE: 10-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
                                                 FILING DATE: 07-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                  FILING DATE: 13-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 GGGAGATGACGAAGACGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGGAGTTGACGAAGATGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212)8699741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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INFORMATION FOR SEQ ID NO: 24
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       CURRENT APPLICATION
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APPLICANT: Philip Goelet
APPLICANT: Philip Goelet
TAPLICANT: Michael T. Boyce-Jacino
TITLE OF INVENTION: Methods for the Detection of Multiple
TITLE OF INVENTION: Single Nucleotide Polymorphisms in a Single Reaction
FILE REFERENCE: 04990.0029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/09924417
Patent No. US20020142441A1
GENERAL INFORMATION:
APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                              Score 14.8; DB 1; Length 20;
Pred. No. 7.5e+02;
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88.9%; Pred. No. 7.5e+02;
                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                           0; Mismatches
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CURRENT FILING DATE: 1999-12-03
FEARLIER APPLICATION NUMBER: 08/216,538
EARLIER FILING DATE: 1994-03-23
EARLIER APPLICATION NUMBER: 08/145,145
EARLIER APPLICATION NUMBER: 08/145,145
SAFARIER PILING DATE: 1993-11-03
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ VERSION 2.0
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 35 LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36, Application US/09454394
Patent No. US20020094525A1
                                                                                                                                                                                                                                                         2352
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                                                                                                                                                            0.4%;
ilarity 88.9%;
Conservative
                                                                                                                                                                                                                                                       2335 GTGTGTGTGTGTGTGC
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                                                                        ; TYPE: DNA
; ORGANISM: Equus caballus
US-09-454-394-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Equus caballus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Tina McIntosh
                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                        16;
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Sequence 1214, Application US/09263959
; Batent No. US20020150891A1
; GENERAL INFORMATION:
    APPLICANT: Road, Leroy E.
    APPLICANT: Road, Leroy E.
    APPLICANT: Road, Ben F.
    TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
    NUMBER OF SEQUENCES: 1279
    CORRESPONDENCE ADDRESS:
    ADDRESSER: Seed and Berry Lip
    STREET: 6300 Columbia Center, 701 Fifth Avenue
    CITY: Seattle
    STATE: Washington
    COUNTRY: US
    COUNTRY: US
    CONFUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: BAP PC Compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentl Release #1.0, Version #1.25
    CORPUTER: BAPLICATION DATA:
    APPLICATION NUMBER: US/09/263,959
    CLARS OF AREAL OF AMERICANEN.
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                                                             ;
0
                                                             Indels
Query Match 0.4%; Score 14.8; DB 1; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2;
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ANTI-SENSE: yes
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-996-263-11
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APPLICANT: MCKAY, Robert A.
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Wonia, Brett
APPLICANT: Wolf Brett
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS;
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS;
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS;
FILE REPERENCE: ISPH-0412
CURRENT APPLICATION NUMBER: US/09/774,809
CURRENT APPLICATION NUMBER: 09/396,902
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-08-07
PRIOR PILING DATE: 1999-08-07
PRIOR PILING DATE: 1999-08-07
PRIOR FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLICONUCLECTIDE COMPOSITIONS AND METHODS
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 7.5e+02; tive 0; Mismatches 2; Indels
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REPERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1214:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
FENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNES: single
TYPE: TOPOLOGY: linear
US-09-263-959-1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic Sequence US-09-774-809-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/09774809
Publication No. US20030004120A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/09774809 Publication No. US20030004120A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1678 GACTTCGGGCTGGCCCGG 1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3377 TTGCTGTGTGTCCCAGGC 3394
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Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 GACTTTGGCCTGGCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16, Conservative
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US-09-774-809-42
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030004325Alris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/09996263
Publication No. US20030004325A1
GENERAL INFORMATION:
APPLICANT: Phillip Dan Cook
APPLICANT: Phillip Dan Cook
TITLE OF INVENTION: Sugar Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
FOR THE MODULATION OF JNK PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.

ZIP: 19103

COMPUTER: RADABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 720 Kb

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/996,263

FILING DATE: 28-NO. US20030004325A1-2001

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/471,973

FILING DATE: <UNKNOWN>

APPLICATION NUMBER: 08/471,973

FILING DATE: <UNKNOWN>

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: ISIS-2005
TELECOMMUNICATION INFORMATION:
                     FILE REFERENCE: ISPH-0412
CURRENT APPLICATION NUMBER: US/09/774,809
CURRENT FILING DATE: 2001-01-31
                                                                                                PRIOR APPLICATION NUMBER: 09/396,902
PRIOR FILING DATE: 1999-09-15
PRIOR PRICATION NUMBER: 09/130,616
PRIOR FILING DATE: 1998-08-07
PRIOR PRICATION NUMBER: 08/910,629
PRIOR FILING DATE: 1997-08-03
NUMBER: 09 SEQ ID NOS: 165
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic Sequence US-09-774-809-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1678 GACTTCGGGCTGGCCCGG 1695
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TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                           TYPB: DNA
ORGANISM: Artificial Sequence
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US-09-776-479-311/c
                                                                                                                 US-09-776-479-311/c
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Sequence 36, Application US/09860836B

Publication No. US20030054002A1

Sequence 36, Application US/09860836B

Publication No. US20030054002A1

APPLICANT: WANGALTON:

APPLICANT: WANDSTRADT, AMY

APPLICANT: WANGEL, LAURENCE

TITLE OF INVENTION: IN INMUNE TOLERANCE

TITLE OF INVENTION: IN INMUNE TOLERANCE

FILE REFERENCE: UTSD: 122US

CURRENT APPLICATION NUMBER: US/09/860,836B

CURRENT FILING DATE: 2002-08-13

PRIOR PILING DATE: 2000-09-21
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US-09-888-326-463/C

Sequence 463, Application US/0988326

Publication No. US20030026801A1

SEGUENCE INFORMATION:

APPLICANT: Weiner, George

APPLICANT: Weiner, George

TITLE OF INVENTION: Methods for Enhancing Antibody-Induced

TITLE OF INVENTION: Cell Lysis and Treating Cancer

FILE REFERENCE: Clo39/7052 (AWS)

CURRENT APPLICATION NUMBER: US/09/888,326

CURRENT PILING DATE: 2001-06-22

PRIOR FILING DATE: 2000-06-22

PRIOR FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 848

SOFTWARE FSECSEQ for Windows Version 3.0

LENGTH: 20
Query Match 0.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic oligonucleotide NAME/KEY: misc_feature | LOCATION: (0) | LOCATION: (0) | THER INFORMATION: phosphorothioate backbone US-09-888-326-463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1678 GACTICGGCCTGCCCGG 1695
                                                                                     20 GACTITIGGCCTGGCCCGG 3
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SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 36
LENGTH: 20
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Best Local Similarity 88.9
Matches 16; Conservative
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; ORGANISM: Homo sapien
US-09-860-836B-36
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Sequence 311, Application US/09776479

Publication No. US20030087848A1

GENERAL INFORMATION:
APPLICANT: Brataler, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Deanna M.
TITLE OF INVENTION: Treatment of Asthma and Allergy
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILE REPERBUES: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479

CURRENT APPLICATION NUMBER: US 60/176,479

CURRENT APPLICATION NUMBER: US 60/176,991

PRIOR APPLICATION NUMBER: US 60/179,991

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 20
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; Sequence 311, Application US/09776479
; Publication No. US2004006790289
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 311
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0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2;
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Matches 16; Conservative
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RESULT 912

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/846,863

FILING DATE: 01-May-2001

CLASSIFICATION: CURKNOWN>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/216,538
                                                                                                                                                                                                                                                                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                           Score 14.8; DB 1;
Pred. No. 7.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I
REGISTRATION NUMBER: 32,680
REFERENCE/DOCKET NUMBER: 683-104-CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-846-863-33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 20
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TELEPHONE: (202) 383-7451
TELEFAT. (202) 383-6610
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Sense PCR primer
US-09-802-154-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Equus caballus IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-846-863-33
; Sequence 33, Application US/09846863
; Publication No. US/0030170624A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GOBLET, PHILIP KNAPP, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                               825 CTCTGCGTGGCTGGTGGT 842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 crcrcadrecordergr 1
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                  Query Match 0.4%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 915
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APPLICANT: Andrew T. Watt
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTIENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPT
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0232
CURRENT APPLICATION NUMBER: US/09/953,318
CURRENT FILING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 97
LENGTH: 20
                SQUID NO. US20030096771A1
SEQUENCE LINEARMATION:
PUBLICARTION TO US20030096771A1
GENERAL INFORMATION:
APPLICANT: Madeline M. Butler
APPLICANT: Andrew T. Watt
APPLICANT: Jacqueline Wyatt
TITE OF INVENITION: ANTISENSE MODULATION OF HORMONE-SENSITIVE LIPASE EXPRESSION
FILE REPRENCE: ISPH-0587
CURRENT FILING DATE: 2001-07-26
SEQ ID NO 132
LENGTH: 20
TENDER CONTRIBUTED TO THE 
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llarity 88.9%; Pred. No. 7.5e+02;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 0.4%; Score 14.8; DB 1; Length 20; Local Similarity 88.9%; Pred. No. 7.5e+02; hes 16; Conservative 0; Mismatches 2; Indels
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Publication No. US20030105302A1
GENERAL INFORMATION:
APPLICANT: Itch, No. US20030105302Aluyuki
APPLICANT: Kavanaugh, W. Michael
TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: PP-17149.001/201130.409
CURRENT FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Antisense Oligonucleotide US-09-915-814-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 97, Application US/09953318
Publication No. US20030105036A1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Matches 16; Conserv
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US-09-953-318-97
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| Publication No. US20030170624A1
| GENERAL INFORMATION:
| APPLICANT: GOELET, PHILIP
| KNAPP, MICHAEL R. |
| TITLE OF INVENTION: THEIR USE IN GENETIC ANALYSIS
KNAPP, MICHAEL R.
TITLE OF INVENTION: SINGEL NUCLEOTIDE POLYMORPHISMS AND
THEIR USE IN GENETIC ANALYSIS
                                                                                                                                                                                                                                             Length 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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88.9%; Pred. No: 7.5e+02;
tive 0; Mismatches 2;
                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the SEQUENCE DESCRIPTION: SEQ ID NO: 35: US-09-846-863-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
                                                                                                                                                                                           ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Equus caballus IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2335 GIGIGIGIGIGIGC 2352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
SIRANDEDNESS: single
                                                        SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                  CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                        NUMBER OF
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                                                                                                                                                  Sequence 34, Application US/09846863
Publication No. US20030170624A1
GENERAL INFORMATION:
APPLICANT: GOELET, PHILIP
TITLE OF INVENTION: SINGLE NUCLECTIDE POLYMORPHISMS AND
TITLE OF INVENTION: THEIR USE IN GENETIC ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/846,863
FILING DATE: 01-May-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION ONTA:
APPLICATION NUMBER: 08/216,538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: CURLOWN:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I
REGISTRATION NUMBER: 32,680
REFERENCE/DOCKET NUMBER: 683-104-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Score 14.8; DB 1; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 917
US-09-846-863-35/c
; Sequence 35, Application US/09846863
; Publication No. US20030170624A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Equus caballus IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2335 GTGTGTGTGTGTGTGC 2352
                    2826 ATATACATATATATAT 2843
                                          3 ATATCAATATATATAT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                          CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C. COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                    US-09-846-863-34
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APPLICANT: Monia, Brett P.
IITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
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Fublication No. US2003060268A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE OF INVENTION: IMMUNOSTIMULATORY DISEASES
FILE REFERENCE: C01039/70060(MAS)
CURRENT FILING DATE: 2002-03-29
FRICH APPLICATION NUMBER: US 60/279,642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
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88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2;
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2 OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-301
                                                                                                                                                                                                                                                                                                                              FILE NEFERENCE:
CURRENT PEDELICATION NUMBER: US/10/057,550
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: 09/506,073
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-06-8
PRIOR FILING DATE: 1998-07-06
PRIOR PILING DATE: 1996-11-26
PRIOR FILING DATE: 1996-05-31
PRIOR FILING DATE: 1996-05-31
NUMBER OF SEQ ID NOS: 130
SENGTH:: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: antisense sequence
                                                                                                                                   Sequence 27, Application US/10057550 Publication No. US20030032607A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1678 GACTTCGGGCTGGCCCGG 1695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.9<sup>5</sup>
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-112-653-301/c
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; Sequence 101, Application US/10004551
; Publication No. US20030004310A1
; Grinkral INFORMATION:
; APPLICANT: SHIMKETS, RICHARD A
; APPLICANT: FERNANDES, ELMA
; TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES ENCODED THEREBY
; FILE REPRENCE: 15966-559
; CURRENT APPLICATION NUMBER: US/10/004,551
; CURRENT APPLICATION NUMBER: 09/635,949
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 110
; SEQ ID NO 101
; SEQ ID NO 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/846,863
FILING DATE: Ol-May-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/216,538
FILING DATE: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/ACENT INFORMATION:
NAME: AUBERACH, JEFFREY:
REGISTRATION NUMBER: 32,680
REFERENCE/DOCKET NUMBER: 683-104-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFRAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.4%; Score 14.8; DB 1; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2;
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Pred. No. 7.5e+02;
0; Mismatches 2;
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US-09-846-863-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Equus caballus IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2826 ATATACATATATATAT 2843
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LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 88.9%;
Matches 16; Conservative (
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Gaps

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APPLICANT: Monia, Brett P.
TITLE OF INVENTION: Attisense Oligonucleotide Modulation of raf Gene Expression FILE REFERENCE: ISPH-0665
CURRENT APPLICATION NUMBER: US/10/173,225B
CURRENT FILING DATE: 2002-12-06
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2; Indel8
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TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION FILE REFERENCE: RTSP-0363
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88.9%; Pred. No. 7.5e+02;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-846-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Murray, James D.
APPLICANT: Maga, Elizabeth A.
APPLICANT: Maga, Elizabeth A.
APPLICANT: Anderson, Gary B.
TITLE OF INVENTION: METHOD OF GENERATING A THITLE OF INVENTION: LIVESTOCK ANIMAL.
TITLE OF INVENTION: LIVESTOCK ANIMAL.
TITLE REFERENCE: UCAL.245
CURRENT APPLICATION NUMBER: US/10/238,042
CURRENT FILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 20
                                           CURRENT APPLICATION NUMBER: US/10/181,846
CURRENT FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: PCT/US01/01416
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 09/490,692
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 176
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26, Application US/10173225B Publication No. US20030119769A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/10238042
Publication No. US20030115618A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1169 GGGAGCTGTCTCGGGCCC 1186
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                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: goat
US-10-238-042-20
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                                                                                                                                                                                                                                                   LENGTH: 20
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Sequence 72, Application US/10231302

Sequence 72, Application US/10231302

Sequence 72, Application US/20030082602A1

GENERAL INFORMATION:

APPLICANT: Yamamoto, No. US20030082602A1uko

APPLICANT: Suzuki, Tomohiro

APPLICANT: Suzuki, Tomohiro

TITLE OF INVERTION: Method for analyzing base sequence of nucleic acid

FILE REFERENCE: 03500.015203

CURRENT APPLICATION NUMBER: US/10/231,302

CURRENT FILING DATE: 2002-08-30

PRIOR FILING DATE: 2000-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                     ; Sequence 311, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: BRIATZIEN: Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; PILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR PILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FESTESEQ for Windows Version 3.0
; SEQ ID NO 311
LENGTH: 20
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88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2; Indels
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Publication No. US20303083297A1
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Lex M. Cowsert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1678 GACTTCGGGCTGGCCCGG 1695
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                            20 cacriridecciódeces
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 72
LENGTH: 20
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Best Local Similarity 88.9
Matches 16; Conservative
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Matches 16; Conservative
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CORGANISM: Homo sapiens
US-10-231-302-72
                                                                                                                             US-10-017-995-311/c
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US-10-181-846-32/c
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; CTHER INFORMATION: PCR and DNA sequencing primer for exon 7 antisense
US-10-321-555-10
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APPLICANT: Chuatacheng Song
APPLICANT: Pamposh Ganju
APPLICANT: Pamposh Ganju
APPLICANT: Pamposh Ganju
APPLICANT: Pamposh Ganju
TITIE OF INVENTION: VANTILOID RECEPTOR-RELATED NUCLEIC ACIDS
TITLE OF INVENTION: AND POLYPEPTIDES
FILE REPERENCE: 4-32048A
CURRENT APPLICATION NUMBER: 60/297,835
PRIOR APPLICATION NUMBER: 60/297,835
PRIOR APPLICATION NUMBER: 60/351,238
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/352,914
PRIOR APPLICATION NUMBER: 60/357,161
PRIOR APPLICATION NUMBER: 60/357,161
PRIOR PILING DATE: 2002-01-29
PRIOR FILING DATE: 2002-05-12
PRIOR FILING DATE: 2002-05-12
PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FASTESQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 20
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0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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                   PRIOR FILING DATE: 1999-02-10
PRIOR PLING DATE: 1998-07-03
PRIOR PLING DATE: 1998-07-03
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-05
PRIOR FILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PALENTIN VETSION 3.1
SEQ ID NO 10
PLENGTH: 20
APPLICATION NUMBER: GB 9903035.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 48, Application US/10171319
Publication No. US20030157633A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Andrea Peier
APPLICANT: Peter McIntyre
APPLICANT: Stuart Bevan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-171-319-48
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Publication No. US20030125276A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennet
APPLICANT: Kenneth Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EXF
FILE REPERENCE: RTS-0333
CURRENT APPLICATION NUMBER: US/10/008,789
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 21
LENGTH: 20
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Publication No US20030134315A1
GENERAL INFORMATION:
APPLICANT: Warenius, Hilmar Meek
APPLICANT: Seabra, Laurence Anthony
TITLE OF INVENTION: METHODS FOR DETERMINING CHEMOSENSITIVITY OF CANCER CELLS BASED UF
TITLE OF INVENTION: EXPRESSION OF NEGATIVE AND POSITIVE SIGNAL TRANSDUCTION FACTORS
FILE REFERENCE: 1417-188
FILE REFERENCE: 1417-188
FILE REFERENCE: 1417-188
FILE REFERENCE: 1417-189
FRIOR APPLICATION NUMBER: US/09/622,277
FRIOR APPLICATION NUMBER: PCT/GB99/00500
FRIOR FILING DATE: 2000-11-25
FRIOR FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-21
                   PRIOR FILING DATE: 1998-07-06
PRIOR APPLICATION NUMBER: US 08/888,982
PRIOR FILING DATE: 1997-07-07
PRIOR FILING DATE: 1997-07-07
PRIOR PILING DATE: 1996-11-26
PRIOR APPLICATION NUMBER: PCT/US95/07111
PRIOR PILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/250,856
PRIOR FILING DATE: 1994-05-31
NUMBER OF SEQ ID NOS: 109
SEQ ID NO 26
LENGTH: 20
APPLICATION NUMBER: PCT/US98/13961
                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: antisense sequence US-10-173-225B-26
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: artificial sequence
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Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                           Score 14.8; DB 1; Length 20;
Pred. No. 7.5e+02;
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                                                                                    2; Indels
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Publication No. US20030187240A1
GENERAL INFORMATION:
APPLICANT: Cook, Phillip Dan
APPLICANT: Kawasaki, Andrew
TITLE OF INVENTION: 2. Modified Oligonucleotides
FILE REFERENCE: 15155137
CURRENT PILITO DATE: 2003-01-28
FRIOR APPLICATION NUMBER: 09/389,283
PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.5e+02;
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                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               829 GCGTGGCTGGTGCTG 846
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                                                                                                                                                                                                    1 CATTGTGTATGCAGGAAT 18
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                           Query Match 0.4%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9%;
Matches 16; Conservative (
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; ORGANISM: Candida albicans
US-10-032-585-4779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 933
US-10-352-586-11/c
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Publication No. US2003170653A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: E.I. du Poward G.
TITLE OF INVENTION: Butyrolactone and its Intermediates
TITLE OF INVENTION: Butyrolactone and its Intermediates
TITLE OF INVENTION: Butyrolactone and its Intermediates
CURRENT APPLICATION NUMBER: US/10/167,547C
CURRENT APPLICATION NUMBER: 00/297198
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Microsoft Office 07
SEQ ID NO 32
LENGTH: 20
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                                                                                                                                                                                                                                                                 APPLICANT: ANGICE FEET MEINTYTE
APPLICANT: Stuar Beevan
APPLICANT: Stuar Beevan
APPLICANT: Chuanzheng Song
TITLE OF INVENTION: AND FOLYFEPTIDES
FILE REFERENCE: 4-32048A
CURRENT APPLICATION: AND FOLYFEPTIDES
FILE REFERENCE: 4-32048A
CURRENT APPLICATION: NUMBER: 60/297, 835
PRIOR FILING DATE: 2002-01-02
PRIOR FILING DATE: 2002-01-29
PRIOR PELICATION NUMBER: 60/357,161
PRIOR PELICATION NUMBER: 60/357,161
PRIOR PELICATION NUMBER: 60/381,086
PRIOR FILING DATE: 2002-02-12
PRIOR PELICATION NUMBER: 60/381,086
PRIOR PELICATION NUMBER: 60/381,086
PRIOR PELICATION NUMBER: 60/381,086
PRIOR PELICATION NUMBER: 60/381,739
PRIOR PELICATION NUMBER: 60/381,086
PRIOR PELICATION NUMBER: 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Oligonucleotide primer US-10-171-319-73
                                                                           RESULT 930

US-10-171-319-73/c

; Sequence 73, Application US/10171319

; Dublication No. US20030157633A1

; GENERAL INFORMATION:
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2 GGAGGACGAAGGTGAGGA 19
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US-10-167-547C-32
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                               APPLICANT: Ardem Patapoutian APPLICANT: Andrea Peier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 931
US-10-167-547C-32
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TITLE OF INVENTION: ALTOISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRES; FILE REPERENCE: RTS-0365; CURRENT PILLING DATE: 2002-05-31 NUMBER OF SEQ ID NO 74 SEQ ID NO 74 LENGTH: 20 TAPE: 2002-05-31 LENGTH: 20 TAPE: 2002-05-31 TAPE
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Publication No. US2003023443A1

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett

APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF CENTROMERE PROTEIN B EXPRESSION
CURRENT APPLICATION NUMBER: US/10/176,277

CURRENT FILING DATE: 2002-06-18

NUMBER OF SEQ ID NOS: 77

LENGTH: 20

LENGTH: 20
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0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-176-277-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Antisense Oligonucleotide US-10-159-856-74
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Taupier, Raymond J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu, Xiaohong
Spytek, Kimberly A.
Patturajan, Meera
Burgess, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Aggacregecagecaage 18
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APPLICANT: Tchernev, Velizar T.
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Boldog, Ferenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Gorman, Linda
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                                                                                                                                                            Sequence 97, Application US/10446373
Sequence 97, Application US/10446373
Sequence 97, Application No. US20030204076A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Andrew T. Watt
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0232
CURRENT APPLICATION NUMBER: US/10/446,373
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: US/09/953,318
PRIOR FILING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 97
LENGTH: 20
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
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; Publication No. US20030212026A1
; GENERAL INPORMATION:
; APPLICANT: Schetter, Christian
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION Immunostimulatory Nucleic Acids
; TITLE OF INVENTION Immunostimulatory Nucleic Acids
; TITLE OF INVENTION Immunostimulatory Nucleic Acids
; CURRENT APPLICATION NUMBER: US 60/156,113
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-27
; PRIOR FILING DATE: 1999-09-27
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastEEQ for Windows Version 3.0
; SEQ ID NO 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Antisense Oligonucleotide
US-10-446-373-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic Sequence US-10-314-578-311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1352 TGCAGATGATGAGATGA 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1678 GACTTCGGGCTGGCCCGG 1695
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ORGANISM: Artificial Sequence
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US-10-314-578-311/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: upstream amplification primer 99-8614 for SEQ 3898, US-10-349-143-7832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                  PRIOR FILING DATE: BARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: GARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: BARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: BARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEGO ID NO 7832
LENGTH: 20
   APPLICATION NUMBER: US 09/298,850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Siddiqui-Jain, Adam
APPLICANT: Hurley, Laurence
APPLICANT: Hurley, Laurence
APPLICANT: Grand, Cory
APPLICANT: Grand, Cory
APPLICANT: Grand, Cory
APPLICANT: Bears, David
TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
FILE REFERENCE: 53232-20004.00
CURRENT APPLICATION NUMBER: US 60/404,966
FRIOR APPLICATION NUMBER: US 60/404,966
PRIOR APPLICATION NUMBER: US 60/370,358
PRIOR PILING DATE: 2002-08-04
PRIOR FILING DATE: 2003-03-20
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PRESEE for Windows Version 4.0
SEQ ID NOS: FELLICE DATE CORD SECOND SECOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
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Publication No. US20040005601A1
GENERAL INFORMATION:
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       APPLICATION NUMBER: EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2974 CAGAGGACCAGGGCTTTT 2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2920 GGGCGGCGTGGGGGG 2937
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APPLICANT: Hurley, Laurence
APPLICANT: Farrell, Thomas
APPLICANT: Grand, Cory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGAGAACCAGGGCTTGT
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                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo Sapiens
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LOCATION: 1..20
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                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REPERENCE: 21402-230 B CURRENT APPLICATION NUMBER: US/10/094,886 CURRENT FILING DATE: 2002-03-07 PRIOR APPLICATION NUMBER: 60/274 and PRIOR APPLICATION NUMBER: 60/274 and PRIOR PILING DATE.
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Sequence 7832, Application US/10349143

Publ.tcation No. US20040005584A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Chumenfeld, Marta

APPLICANT: Chumenkov, Ilya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: 2003-01-21

FRIOR APPLICATION NUMBER: US/09/422,978

FRIOR FILING DATE: 1999-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 298
SOFTWARE: Patentin 2.1
SEQ ID NO 3.32
LENGTH: 20
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88.9%; Pred. No. 7.5e+02;
Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/274,322
PRIOR APPLICATION NUMBER: 60/213,182
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR PELICATION NUMBER: 60/318,510
PRIOR PELICATION NUMBER: 60/318,510
PRIOR APPLICATION NUMBER: 60/318,510
PRIOR APPLICATION NUMBER: 60/314,018
PRIOR PILING DATE: 2001-03-08
PRIOR PELICATION NUMBER: 60/314,018
PRIOR PELICATION NUMBER: 60/274,194
PRIOR PILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/274,194
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-09
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                                                                                                                                                                                                                                                                                                                                      Fernandes, Elma
Shimkets, Richard
                                                                                                                                                                                                                                                 Gerlach, Valerie
Pochart, Pagcal
Miller, Charles
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Matches 16; Conservative
                                          Stacie
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Publication No. US20040023379A1

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HEPATOWA-DERIVED GROWTH FACTOR EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF HEPATOWA-DERIVED GROWTH FACTOR EXPRESSION
CURRENT APPLICATION NUMBER: US/10/210, 429
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 148
SEQ ID NO 56
LENGTH: 20
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US-10-210-429-127/c
US-10-210-429-127/c
Sequence 127, Application US/10210429
PUBLICATION NO. US20040023379A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HEPATOMA-DERIVED GROWTH FACTOR EXPRESSION FILE OF INVENTION: US/10/210, 429
CURRENT APPLICATION UNMBER: US/10/210, 429
CURRENT FILING DATE: 2002-07-31
SEQ ID NO.127
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.8; DB 1; Length 20;
Pred. No. 7.5e+02;
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CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Antisense Oligonucleotide US-10-210-429-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6513
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.4%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity
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ORGANISM: H. sapiens
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Matches 16; Conserv
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US-10-210-429-127
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US-10-210-429-56
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J. Sequence 21, Application US/10422466

Publication No. US20040006036A1

GENERAL INFORMATION:

J. APPLICANT: Hu, JI-Fan

APPLICANT: Hu, JI-Fan

TITLE OF INVENTION: Silencing transcription by methylation

TITLE REPERENCE: 112029.00005

CURRENT APPLICATION NUMBER: US/10/422,466

CURRENT FILING DATE: 2000-04-22

PRIOR APPLICATION NUMBER: 09/643,128

PRIOR FILING DATE: 2000-08-21

PRIOR FILING DATE: 2000-08-21

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-06-26

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PRICENTIN VINEBER: 06/214,148

PRIOR FILING DATE: 2000-06-26

NUMBER OF SEQ ID NOS: 77

SEQ ID NO SIG ID NOS: 77

SEQ ID NO 2: 77
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                  TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA
                                              FILE REFERENCE: 53223-20004.00
CURRENT APPLICATION NUMBER: US/10/407,449
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/404,966
PRIOR FILING DATE: 2002-08-04
PRIOR FILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2003-03-20
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 6513, Application US/10289762; Publication No. US20040006218A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2920 GGGCGGGCGTGGGGGG 2937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCGGGGCGGGGGG 20
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Griffais, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-289-762-6513/c
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APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS FOR THE MODULA
TITLE OF INVENTION: OF JNK PROTEINS
FILE REFERENCE: ISPH-0726
CURRENT PAPLICATION NUMBER: US/10/345,444B
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/774,809
PRIOR APPLICATION NUMBER: US 09/396,902
PRIOR PELING DATE: 1999-09-15
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 09/287,796
PRIOR PILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
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APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3CB EXPRESSION
FILE REPERRNCE: P72.0028
CURRENT APPLICATION NUMBER: US/10/210,723
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 86
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.4%; Score 14.8; DB 1; Length 20;
88.9%; Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                Length 20,
                                                                                                                                                                                                                                                                                                                  .2; Indels
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Pred. No. 7.5e+02;
0; Mismatches .2;
                                                                                                                                                                                             ; OTHER INFORMATION: Antisense Oligonucleotide US-10-210-723-14
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CURRENT APPLICATION NUMBER: US/10/210,723
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 14
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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Publication No. US20040023382A1
GENERAL INFORMATION:
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Best Local Similarity 88.99
Matches 16; Conservative
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Matches 16; Conservative
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Sequence 50, Application US/10210479

Publication No. US20040023380A1

Publication No. US20040023380A1

GENERAL INPORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSION

TITLE OF INVENTION: ANTISENSE US/10/210,479

CURRENT APPLICATION NUMBER: US/10/210,479

CURRENT FILING DATE: 2002-07-31

NUMBER OF SEQ ID NOS: 123

SEQ ID NO 50

LENGTH: 20
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Publication No. US20040023380A1

Publication No. US200440023380A1

Publication No. US200440023380A1

APPLICANT: Brett P. Monia

APPLICANT: Renneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSION

TITLE REPERENCE: RTS-0385E

CURRENT APPLICATION NUMBER: US/10/210,479

CURRENT FILING DATE: 2002-07-31

NUMBER OF SEQ ID NOS: 123

SEQ ID NO 112

LENGTH: 20
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APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF PPPICE EXPRESSION
FILE REPERENCE: PTS-0028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match .0.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: AntiBenge Oligonucleotide US-10-210-479-50
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Publication No. US20040023382A1
GENERAL INFORMATION:
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                                                                        GCCrcrrccrcrrcarcc 1
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Best Local Similarity 88.9%;
Matches 16; Conservative
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ORGANISM: H. sapiens
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US-10-210-479-112
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APPLICANT: Smithson, Glennda
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-442A
CURRENT APPLICATION NUMBER: 108/10/236,392
CURRENT FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR PELLING DATE: 2002-09-06

PRIOR PELLING DATE: 2000-03-30

PRIOR PELLING DATE: 0860/390,155

PRIOR PELLING DATE: 2000-03-30

PRIOR PELLING DATE: 2000-03-30

PRIOR PELLING DATE: 2000-08-10

PRIOR PELLING DATE: 2002-03-15

PRIOR PELLING DATE: 2002-03-25

PRIOR PELLING DATE: 2002-03-25

PRIOR PELLING DATE: 2002-03-25

PRIOR PELLING DATE: 2000-09-12

PRIOR PELLING DATE: 2001-09-07

PRIOR PELLING DATE: 2001-09-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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; Publication No. US20040067490A1
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                                                                                                                                                                                                                                                                                                             Kekuda, Ramesh
LaRochelle, William J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adigaru, Muralidhara
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Reiger, Daniel K
Rothenberg, Mark E
Shenoy, Suresh
                                                                                                                Ellerman, Karen
Gerlach, Valerie
Gorman, Linda
Grosse, William M
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MacDougall, John R
Malyankar, Uriel M
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let, Isabelle
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Pena, Carol A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peyman, John A
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US-10-236-392-402
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Sequence 42, Application US/1034544B

Publication No. US20040029823A1

GENERAL INFORMATION:

APPLICANT: McKAY, Robert A.

APPLICANT: McKAY, Robert A.

APPLICANT: Moria, Brett

APPLICANTON NUMBER: US/10/345,44B

CURRENT FILING DATE: 2003-01-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-00-07

PRIOR PRILING DATE: 1999-00-07

PRIOR FILING DATE: 1990-00-07

PRIOR FILING DATE: 1990-00-07
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PRIOR APPLICATION NUMBER: US 08/910,629
PRIOR FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 31
LENGTH: 20
                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic Sequence US-10-345-4448-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 393, Application US/10236392
Publication No. US20040067490A1
GENERAL INFORMATION:
APPLICANT: Anderson, David W
APPLICANT: Boldog, Ferenc L
APPLICANT: Gargess, Catherine, E
APPLICANT: Casman, Stacie J
APPLICANT: Catterton, Elina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1678 GACTICGGGCTGGCCCGG 1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1678 GACTTCGGGCTGGCCCGG 1695
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-236-392-393
                                                                                                                                                                                                                                                                                 FEATURE:
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Sequence 21, Application US/10274085
Publication No. US20040077570A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Sanjay Bhanot
TITLE OF INVENTION: ANTIENSE MODULATION OF FATTY ACID SYNTHASE EXPRESSION
FILE REPERENCE: ISPH-0714
CURRENT APPLICATION NUMBER: US/10/274,085
CURRENT PILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 225
SEQ ID NO 21
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication US/10274085
Publication No. US20040077570A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Sanjay Bhanot
APPLICANT: Sanjay Bhanot
FILE REFERENCE: ISPH-0714
CURRENT APPLICATION NUMBER: US/10/274,085
CURRENT PILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 225
SEQ ID NO 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14.8; DB 1;
Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-274-085-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 7.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 88.5
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: H. :
US-10-274-085-133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ICANT: Peyman, John A
ICANT: Reiger, Danniel K
ICANT: Reiger, Danniel K
ICANT: Rothenberg, Mark B
ICANT: Shenoy, Suresh
ICANT: Shinkets, Richard A
ICANT: Smirkets, Richard A
ICANT: Smithson, Glennda
E OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
REFERENCE: 21402-442A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-236-392-402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-09-12
PRIOR FILING DATE: 2000-09-12
PRIOR PLING DATE: 2000-09-07
PRIOR PLING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US60/318,130
PRIOR PRIOR PILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
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Pred. No. 7.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/236,392
CURRENT FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R FILING DATE: 2000-03-30

R APPLICATION NUMBER: US60/390,155

R FILING DATE: 2002-06-19

R APPLICATION NUMBER: US99/635,949

R FILING DATE: 2000-08-10

R APPLICATION NUMBER: US60/318,765

R FILING DATE: 2001-09-12

R APPLICATION NUMBER: US60/357,303

R RILING DATE: 2001-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US60/367,753
FILING DATE: 2002-03-25
PAPLICATION NUMBER: US60/369,479
FILING DATE: 2002-04-02
APPLICATION NUMBER: US09/659,634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NT FILING DATE: 2002-09-06
APPLICATION NUMBER: US09/540,763
                                                                                                                                                                                                                                                                   JaRochelle, William J
                                                                                                                                                                                                                                                                                                                                                                                                           Padigaru, Muralidhara
Patturajan, Meera
Pena, Carol A
                                 Catterton, Elina
Chapoval, Andrei
Crabtree, Julie
Edinger, Shlomit, R
Ellerman, Karen
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                           MacDougall, John R
Malyankar, Uriel M
Miller, Charles E
Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                     Gorman, Linda
Grosse, William M
Gusev, Vladamir
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LENGTH: 20
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Gaps

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Sequence 24, Application US/10653872; Publication No. US20040081992A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
                                                                                                                                                                                               NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
STREET: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.8; DB 1; Length 20;
Pred. No. 7.5e+02;
0; Mismatches 2; Indels
                                                                                Query Match
0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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Sublication No. US20040102395A1

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: MODULATION OF IAP-LIKE EXPRESSION
TITLE OF INVENTION: MODULATION OF IAP-LIKE EXPRESSION
TITLE OF SEQ ID NOS: 156
UNDER OF SEQ ID NOS: 156

SEQ ID NO 47

LENGTH: 20
                                                                                                                                                                                                                                                                                          RESULT 958
US-10-302-027-105
Sequence 105, Application US/10302027
Sequence 105, Application US/10302027
Sublication No. US20040102391A1
GENERAL INFORMATION:
TITLORY: Micholas M. Dean
APPLICANT: Kenneth W. Dobie
TITLORY: Kenneth W. Dobie
FITLE REFERENCE: PTS-0068
CURRENT APPLICATION NUMBER: US/10/302,027
CURRENT FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 135
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antisense Oligonucleotide US-10-303-325-47
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-302-027-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 960
US-10-688-706-153
; Sequence 153, Application US/10688706
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                                                                                                                                                                                     1447 GCGGCCAAGGGTAACCTG 1464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-302-027-105
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0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Nicholas M. Dean

APPLICANT: Nicholas M. Dean

TITLE OF INVENTION: MODULATION OF GANKYRIN EXPRESSION

TITLE OF INVENTION: MODULATION OF GANKYRIN EXPRESSION

CURRENT APPLICATION NUMBER: US/10/302,027

CURRENT FILING DATE: 2002-11-21

NUMBER OF SEQ ID NOS: 135

LENGTH: 20
                                                                 CUDDITKE: USAS

CUDDITKE: USAS

ZIP: 10036-2711

COMPUTER READABLE FORM:
    MBDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ Version 2.0
    SOFTWARE: PastSEQ Version 2.0
    SPELICATION NUMBER: US/10/653,872
    PRIOR APPLICATION NUMBER: US/09/924,417
    APPLICATION NUMBER: US/09/924,417
    APPLICATION NUMBER: US/09/924,417
    APPLICATION NUMBER: US/09/924,417
    APPLICATION NUMBER: US/09/934,286
    APPLICATION NUMBER: US/09/934,286
    APPLICATION NUMBER: US/09/934,286
    APPLICATION NUMBER: US/09/934,286
    APPLICATION NUMBER: 08/870,434
    FILING DATE: 0-UN-1997
    APPLICATION NUMBER: 08/89,654
    FILING DATE: 09-FEB-1996
    APPLICATION NUMBER: 08/89,573
    FILING DATE: 09-FEB-1995
    APPLICATION NUMBER: 08/89,573
    FILING DATE: 10-FEB-1995
    APPLICATION NUMBER: 08/89,573
    FILING DATE: 10-FEB-1995
    APPLICATION NUMBER: 08/386,844
    FILING DATE: 10-FEB-1995
    APPLICATION NUMBER: 30,742
    REFERENCE/DOCKET NUMBER: 30,742
    REFERENCE/DOCKET NUMBER: 30,742
    REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-653-872-24
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212)8699741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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ORGANISM: Artificial Sequence
          CITY: New York
STATE: NY
                                                            COUNTRY: USA
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1473 TCTGCGGCGCGCGCCC 1490
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PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin version 3.2
SEQ ID NO 507
LENGTH: 20
                                                                                                                TYPE: DNA ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: artificial
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US-10-688-706-828
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APPLICANT: Pharmacia Corp.
TITLE OF INVENTE: RYSY
FILE REFERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT APPLICATION NUMBER: 05/119,268
FRIOR APPLICATION NUMBER: 60/419,268
PRIOR APPLICATION NUMBER: 60/419,268
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin version 3.2
SEQ ID NO 285
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels
                                                              APPLICANT: Broechat, Kay
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/419,268
PRIOR PILICATION NUMBER: 60/419,268
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin Version 3.2
LENGTH: 20
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TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION FILE REFERENCE: 01393/1
CURRENT APPLICATION VUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/419,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: human GFAT antisense US-10-688-706-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: human GFAT antisense US-10-688-706-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 507, Application US/10688706 Publication No. US20040102412A1 GENERAL INFORMATION: APPLICANT: Pharmacia Corp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 285, Application US/10688706; Publication No. US20040102412A1; GENERAL INFORMATION:
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    Publication No. US20040102412A1
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Best Local Similarity 88.9
Matches 16; Conservative
                         GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
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ORGANISM: artificial
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| Publication No. US20040102412A1
| GENERAL INPORMATION:
| APPLICANT: Pharmacia Corp.
| APPLICANT: Pharmacia Corp.
| APPLICANT: Pharmacia Corp.
| APPLICANT: Broschat, Kay
| TITLE OF INVENTION: ANTISENSE MODULATION OF GRAT EXPRESSION
| FILE REFERENCE: 01393/1
| CURRENT APPLICATION NUMBER: US/10/688,706
| CURRENT APPLICATION NUMBER: 60/419,268
| PRIOR APPLICATION NUMBER: 60/419,268
| PRIOR FILING DATE: 2002-10-17
| NUMBER OF SEQ ID NOS: 3071
| SOFTWARE: Patentin Version 3.2
| SEQ ID NO 508
| LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.4%; Score 14.8; DB 1; Length 20; Best Local Similarity 88.9%; Pred. No. 7.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                 Length 20;
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TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01393/11
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT PELING DATE: 2003-10-17
PRIOR PILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin version 3.2
LENGTH: 20
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0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
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OTHER INFORMATION: human GFAT antisense
) OTHER INFORMATION: human GFAT antisense US-10-688-706-507
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Publication No. US20040102412A1
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
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US-10-660-897-9
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                              0.4%; Score 14.8; DB 1; Length 20; 88.9%; Pred. No. 7.5e+02; tive 0; Mismatches 2; Indels
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                            Sequence 56. Application US/10316243

Publication No. US20040110147A1

GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION:

FILE REFERENCE: RTS-0462

CURRENT APPLICATION NUMBER: US/10/316,243

NUMBER OF SEQ ID NOS: 168

SEQ ID NO 96

LENGTH: 20
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US-10-31-67/c
US-10-31-67/c
Sequence 167, Application US/10316243
Publication No. US20040110147A1
GENERAL INFORMATION:
APPLICANT: Ravi Jain
TITLE OF INVENTION: MODULATION OF BAF53 EXPRESSION
FILE REFERENCE: RTS-0462
CURRENT APPLICATION NUMBER: US/10/316,243
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 167
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Antisense Oligonucleotide US-10-316-243-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 9, Application US/10660897; Publication No. US20040115706A1; GENERAL INFORMATION:
                                                                                                          1473 TCTGCGGCGCGCGCC 1490
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Best Local Similarity 88.9
Matches 16; Conservative
                                    Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: H. sapiens
US-10-688-706-828
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US-10-316-243-96
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APPLICANT: Chung, Mary
APPLICANT: Siddigui-Jain, Adam
APPLICANT: Siddigui-Jain, Adam
APPLICANT: Mitten, Jeffrey
APPLICANT: Mitten, Jeffrey
APPLICANT: Mitten, Jeffrey
TITLE OF INVENTION: QUADRUPLEX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
FILE REFERENCE: 532232000800
FILE REPERENCE: 53223200800
CURRENT APPLICATION NUMBER: US/10/660,897
CURRENT APPLICATION NUMBER: 60/410,475
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 40
SOFTHARE: FASESEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 20
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Sequence 42, Application US/10303588

Sequence 42, Application US/10303588

Sequence 42, Application US/10303588

Sequence 42, Application US/10303588

GENERAL INFORMATION: Mobile

TITLE OF INVENTION: MODULATION OF DEATH-ASSOCIATED PROTEIN KINASE 1 EXPRESSION

TITLE REFRENCE: HTS-0010-11-22

CURRENT FILING DATE: 2002-11-22

NUMBER OF SEQ ID NOS: 78

SEQ ID NO 42

LENGTH: 20
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| Sequence 42, Application US/10303588 |
| Publication No. US20040116364A1 |
| Publication No. US20040116364A1 |
| GENERAL INFORMATION: |
| APPLICANT: Kenneth W. Dobie |
| TITLE OF INVENTION: MODULATION OF DEATH-ASSOCIATED PROTEIN KINASE 1 EXPRESSION |
| FILE REPERENCE: HTS-0071 |
| CURRENT APPLICATION NUMBER: US/10/303,588 |
| CURRENT PILING DATE: 2002-11-22 |
| SEQ ID NO 42 |
| SEQ ID NO 42 |
| LENGTH: 20
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0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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88.9%; Pred. No. 7.5e+02;
tive 0; Mismatches 2;
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ORGANISM: Artificial Sequence
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Matches 16; Conservative
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0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
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88.9%; Pred. No. 7.5e+02;
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                                                                                                                                       Sequence 18, Application US/10316540 Publication No. US20040126761A1 GENERAL INFORMATION:
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  921 CTTCTTCCTGTTCATCCT 938
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Best Local Similarity
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                                                                                                                      US-10-316-540-18
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                                                                                                   Length 20;
                                                                                              Score 14.8; DB 1; Length 2
Pred. No. 7.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FREESEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/763,992
FILING DATE: 22-Jan.2004
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/418,887
FILING DATE: 15-OCT-1999
APPLICATION NUMBER: US/08/946,869
FILING DATE: 08-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BECKEY, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5697.US.P1
TELECOMMUNICATION INFORMATION:
                       ; PEATURE:
-1 OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-588-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-763-992-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: 11
                                                                                                                                                                                                                                                                                                                                                                                                                             GORDON, Julian
HODGES, Steven C.
KLASS, Michael R.
KRATOCHVIL, Jon D.
                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/10763992
Publication No. US20040121397A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROBERTS-RAPP, Lisa
RUSSELL, John C.
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: COHEN, Maurice
FRIEDMAN, Paula N.
                                                                                                                                                                                   2824 ATATATACATATATAT 2841
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
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                                                                                                                                                                                                                       19 ATATGTATATATATA 2
                                                                                                   Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
ORGANISM: Artificial Sequence
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CORRESPONDENCE ADDRESS:
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US-10-763-992-21
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Sequence 1039, Application Us/10671395
Publication No. US20040132063A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTIERNSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
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Publication No. US20040126761A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ravi Jain
TITLE OF INVENTION: MODILATION OF ALPHA-METHYLACYL-COA RACEMASE EXPRESSION
TILE REPERENCE: RTS-0471
CURRENT APPLICATION NUMBER: US/10/316,540
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 95
LENGTH: 20
APPLICANT: Renach W. Dobie
APPLICANT: Ravi Jain
TITLE OF INVENTION: MODULATION OF ALPHA-METHYLACYL-COA RACEMASE EXPRESSION
FILE REPERENCE: RTS-0471
CURRENT APPLICATION NUMBER: US/10/316,540
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 156
SEGO ID NO 18
LENGTH: 20
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Sequence 1366, Application US/10671395
Publication No. US20040132063A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blarmacia Corp.
APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTACLANDIN E2 SYNTHASE
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTACLANDIN E2 SYNTHASE
TITLE OF INVENTION: ANTISENSE US/10/671,395
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SEQ ID NO 1366
LENGTH: 20
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                                                                                                                                    Query Match
0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2;
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1343
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ORGANISM: artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                          US-10-671-395-1343/c
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## Sequence 1219, Application US/10671395

## Sequence 1219, Application US/10671395

## Sequence 1219, Application No. US20040132063A1

## SEQUENCE INFORMATION: BARBESSION

## APPLICANT: Pharmacia Corp.

## TITLE OF INVENTION: BARBESSION

## TITLE OF INVENTION: BARBESSION

## TITLE OF INVENTION: BARBESSION

## FILE REFERENCE: 1179/1/US

## CURRENT APPLICATION NUMBER: US/10/671,395

## CURRENT APPLICATION NUMBER: 60/413,549

## PRIOR PILING DATE: 2002-09-25

## NUMBER OF SEQ ID NOS: 1809

## SOFTWARE: PatentIn version 3.2

## SOFTWARE: PatentIn version 3.2

## ENGTH: 20
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| Sequence 1106, Application US/10671395
| Sequence 1106, Application US/10671395
| Sequence 1106, Application No. US20040132063A1
| Publication No. US20040132063A1
| GENERAL INFORMATION:
| APPLICANT: Pharmacia Corp. |
| TITLE OF INVENTION: BXPRESSION |
| TITLE OF INVENTION: BXPRESSION |
| FILE REFERENCE: 1179/1/US |
| CURRENT APPLICATION NUMBER: US/10/671,395 |
| CURRENT FILING DATE: 2003-09-25 |
| PRIOR FILING DATE: 2003-09-25 |
| NUMBER OF SEQ ID NOS: 1809 |
| SOFTWARE PATENTING NOS: 1809 |
| SEQ ID NO 106 |
| LENGTH: 20
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Pred. No. 7.5e+02;
0; Mismatches 2; Indels
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                                                                                                                                                              ; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; CTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1106
  CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION WUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
SEQ ID NO 1039
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                     19 GTGGGCCTGTGTGTGTGC 2
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-671-395-1219/c
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APPLICANT: Hiromitsu, TAKASE
APPLICANT: Hiroyuki, HASHINOTO
TITLE OF INVENTION: METHOD OF ANALYZING PROBE CARRIER USING TIME-OF-FLIGHT SECONDARY
TITLE OF INVENTION: ION MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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APPLICANT: Ireland, James S.
APPLICANT: Ireland, James S.
APPLICANT: Lander, Extc S.
TITLE CANT: Lander, Extc S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REPERENCE: 2825.2008-001
CURRENT APPLICATION NUMBER: US/09/765,081
CURRENT PILING DATE: 2001-01-18
PRIOR FILING DATE: 2000-01-19
NUMBER: OF SEQ ID NOS: 461
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.4%; Score 14.8; DB 1;
Local Similarity 88.9%; Pred. No. 7.5e+02;
les 16; Conservative 0; Mismarche.
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Pred. No. 7.9e+02;
0; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/10/744,730
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: US 2003-190010
PRIOR PLING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: UP 2002-191391
PRIOR PLING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: UP 2002-191414
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.2
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Sequence for Target
US-10-744-730-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 266, Application US/09765081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 37, Application US/09765081 Patent No. US20020037508A1 GENERAL INFORMATION:
                                                                Sequence 5, Application US/10744730 Publication No. US20040137491A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2695 CCACTTCCCACCTGCCC 2712
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                                                                                                                                 APPLICANT: Tadashi, OKAMOTO
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Best Local Similarity 88.9
Matches 16; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial
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US-09-765-081-266/c
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Matches
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APPLICANT: Pharmacia Corp.
APPLICANT: Glerse, James K
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT APPLICATION NUMBER: 60/413,549
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR PILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
SEQ ID NO 1728
LENGTH: 20
                                                                                                                                                                                                                                                                                                  APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
LENGTH: 20
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                          2; Indels
    Pred. No. 7.5e+02;
                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Human PGE2 antisense
                                                                                                                                                                                                                  sequence 1597, Application US/10671395; Publication No. US20040132063A1; GENERAL INFORMATION: APPLICANT: Pharmacia Corp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1728, Application US/10671395; Publication No. US20040132063A1; GENERAL INFORMATION:
                                                                   2315 GTCTGTGTGTGTGTGT 2332
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                                                                                                      20 GTATGTGTGTGTATGT 3
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Matches 16; Conservative
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Best Local Similarity 88.99
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: artificial
                                                                                                                                                                            RESULT 978
US-10-671-395-1597/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-671-395-1728/c
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TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative
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; OTHER INFORMATION: Synthetic
US-09-864-426A-1134
                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                              Query Match 0.4
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 985
US-09-864-426A-1134
                                                                                                                                                                                                                                                      US-09-864-636A-1134
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                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43, Application US/09932300
| Publication No. US20030032788A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: GRAVER, Exic
| APPLICANT: ISRAEL, Yedy
| TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION
| FILE REFERENCE: 9855-310
| CURRENT FPLICATION NUMBER: US/09/932,300
| CURRENT FILING DATE: 201-08-20
| FRIOR APPLICATION NUMBER: US 09/109,663
| FRIOR FILING DATE: 1993-07-03
| FRIOR FILING DATE: 1993-07-02
| NUMBER OF SEQ ID NOS: 111
| SOFTWARE: PARENTIN Ver. 2.1
| LEARTH OF SEQ ID NOS: 111
| SOFTWARE: 21-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Candidate; OTHER INFORMATION: TNF(alpha) ASO
US-09-932-300-43
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.8; DB 1; Length 21;
Pred. No. 7.9e+02;
1; Mismatches 3; Indels
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               GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLECTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2008-001
CURRENT APPLICATION NUMBER: US/09/765,081
CURRENT PILING DATE: 2001-01-18
PRIOR PILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 266
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1134, Application US/09864636A
Publication No. US20030104378A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Allwai, Hatim
APPLICANT: Bartholomay, Christian
APPLICANT: Chehak, LuAnne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2082 GIACTCCCGGGTGGCCAGG 2101
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Best Local Similarity 80.0%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9°
Matches 16; Conservative
Patent No. US20020037508A1
                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-765-081-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 984
US-09-864-636A-1134
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APPLICANT: Kavanagh, T.
APPLICANT: Lao, N.
TITLE OF INVENTION: A NOVEL PLASTID-TARGETING NUCLBIC ACID SEQUENCE, A
TITLE OF INVENTION: A NOVEL BETA-AMYLASE SEQUENCE, A STIMULUS-RESPONSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 14.8; DB 1; Length 21;
88.9%; Pred. No. 7.9e+02;
tive: 0; Mismatches 2; Indels
                                                                                                                                                                                         TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: U.S.A. COUNTER: U.S.A. COUNTER: LIBEBB COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURSOFTWARE: MICROSOFT WORD VERSION 2.0C
CURSOFTRATION DATA:
RILING DATE: 29-ADY-2002
CLASSIFICATION: «UNKNOWN»
ATTORNEY/AGBNT INPORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                            I. DU PONT DE NEMOURS
                                                                    Sequence 46, Application US/10023066A
Publication No. US20030056242A1
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature LOCATION: 1..21
OTHER INFORMATION: /prc
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Publication No. US20030074690A1
GENERAL INFORMATION:
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TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                     AND COMPANY
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STRANDEDNESS: single
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ADDRESSEE: E. I. D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligonucleotide"
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Best Local Similarity 88.99
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
                                                                                                                                                                       COMPANY
                                                JS-10-023-066A-46/c
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SEQUENCE 490, Application US/10085906

Publication No. US20030054371A1

SERVERAL INFORMATION:

APPLICANT: Wid, Paul

APPLICANT: Wid, Paul

APPLICANT: Wid, Paul

APPLICANT: GIAY, GAY, GAY, S.

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: UNMBER: US/10/085,906

CURRENT APPLICATION NUMBER: US 60/126,215

PRIOR FILING DATE: 1999-03-25

PRIOR FILING DATE: 1999-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 545

SEQ ID NO 490

LENGTH: 21
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MEDIUM TYPE: Diskette-3.5 inch, 1.44 MB storage COMPUTER: PC compatible OPERATING SYSTEMS Windows 95 SOFTWARE: Word 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/016,505
FILING DATE: 10-Dec-2001
CLIASSIFICATION: cUNKNOWN-
APPLICATION APPLICATION: cUNKNOWN-
FILING DATE: May 14, 1999
ATTORNEY/AGENT INFORMATION:
NAME: Barry L. Davison
REGISTRATION NUMBER: 47/309
TELECOMMUNICATION INFORMATION:
TELEBRONE, [206] 628-7621
TELEBRONE; (206) 628-7621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-016-505-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  857 AGGAGCTGGTGGAGGCTG
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-085-906-490/c
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Gaps

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APPLICANT: Hayden, Michael R.
APPLICANT: Brooks-Wilson, Angela R.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
         ; OTHER INFORMATION: Description of Artificial Sequence:oligomucleotide
US-10-311-946-21
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                                                                                          Length 21;
                                                                                                                                  Indels
                                                                                     0.4%; Score 14.8; DB 1;
88.9%; Pred. No. 7.9e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: FORS-06666
CURRENT APPLICATION NUMBER: US/10/084,839
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: Patentin version 3.1
SEQ ID NO 1134
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Vedvík, Kevin L.
TITLE OF INVENTION: RNA Detection Assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Allawi, Hatim
Argue, Brad T.
Bartholomay, Christian T.
Chehak, LuAnne
Curtis, Michelle L.
                                                                                                                                                                                                                                                                                                                                         Sequence 1134, Application US/10084839 Publication No. US20030186238A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 204, Application US/10452510 Publication No. US20040005666A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schaefer, James J.
Skrzypczynski, Zbigniew
Takova, Tsetska Y.
Thompson, Lisa C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neri, Bruce P.
Olson, Sarah M.
Olson-Munoz, Marilyn C.
                                                                                                                                                                                 2700 TCCCACCCTGCCCTCAG 2717
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Third Wave Technologies
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                                                                                                                                                                                                                       3 rccacccccccrcag 20
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Lukowiak, Andrew A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic US-10-084-839-1134
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                                                                                          Query Match 0.4
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaiser, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ip, Hon S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 16; Conserv
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US-10-452-510-204
  FEATURE:
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| Bublication 0. US20030109481A1
| GREATION 0. US20030109481A1
| GREATION 0. US20030109481A1
| GREATION 0. US20030109481A1
| TITLE OF INVENTION: THROUT CG11 Specific Gene Expression and its Use in Cancer Therap FILE REPERENCE: 1-3152021/FM1
| CURRENT APPLICATION NUMBER: US/10/311,946
| UNMBER OF SEQ ID NOS: 37
| SOFTWARE: Patentin Ver. 2.1
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| Sequence 49, Application US/10090011
| Publication No. US2030082810A1
| APPLICANT: Serup, Palle
| APPLICANT: Gradwohl Gerard
| TITLE OF INVENTION: Methods For Generating Insulin-Secreting
| TITLE OF INVENTION: Methods For Transplantation
| FILE REFERENCE: 6246-2200-US
| CURRENT APPLICATION NUMBER: US/10/090,011
| CURRENT FILING DATE: 2002-02-26
| PRIOR APPLICATION NUMBER: US 60/271,474
| PRIOR FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-261-189-5
                                                                                                                                                                                                                                                                                                                                                                   0.4%; Score 14.8; DB 1; Length 21; ilarity 88.9%; Pred. No. 7.9e+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21;
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Pred. No. 7.9e+02;
0; Mismatches 2;
PROMOTER AND USES THEREOF
                     FILE REFERENCE: 9341-017
CURRENT APPLICATION NUMBER: US/10/261,189
CURRENT FILING DATE: 2002-09-30
FRIOR APPLICATION NUMBER: US/09/375,140
FRIOR FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 21
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                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
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ORGANISM: Homo Sapien
US-10-090-011-49
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Matches 16; Conserva
    TITLE OF INVENTION:
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LENGTH: 21
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Query Match
Best Local Similarity
Matches 16; Conserv
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| Sequence 135, Application US/10401520
| Publication No. US20040009506A1
| GENERAL INFORMATION:
| APPLICANT: Stephen, Jean-Philippe F. APPLICANT: Stephen, Jean-Philippe F. APPLICANT: Wong, Wai Lee Tan
| TITLE OF INVENTION: Quantitation of Nucleic Acid Analytes
| TITLE OF INVENTION: Quantitation of Nucleic Acid Analytes
| TITLE OF INVENTION: Quantitation of Nucleic Acid Analytes
| TILL OF INTING DATE: 2003-03-03
| CURRENT FILING DATE: 2002-03-03
| PRIOR PLICATION NUMBER: US 60/368,669
| NUMBER OF SEQ ID NOS: 138
| LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bayer AG
TILLE OF INVENTION: REGULATION OF HUMAN ADENYLATE CYCLASE, TYPE IV
FILE REFERENCE: RCK-6 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/398,757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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larity 88.9%; Pred. No. 7.9e+02;
Conservative 0; Mismatches 2; Indels
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CURRENT APPLICATION NUMBER: US/10/452,510
CURRENT FILING DATE: 2003-66-02
PRIOR APPLICATION NUMBER: US 09/526,193
PRIOR FILING DATE: 2000-03-15
PRIOR PLING DATE: 1999-03-15
PRIOR PLING DATE: 1999-06-08
PRIOR PLING DATE: 1999-06-08
PRIOR PLING DATE: 1999-06-08
PRIOR PLING DATE: 1999-06-17
PRIOR PLING DATE: 1999-06-17
PRIOR PLING DATE: 1999-06-17
PRIOR PLING DATE: 1999-06-17
PRIOR PLING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 287
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 204
LENGTH: 21
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Publication No. US20040029247A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-10-452-510-204
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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Sequence 311, Application US/10648593

Publication No. US20040106132A1

GENERAL INFORMATION:

A APPLICANT: Bristol-Wyers Squibb Company

TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT

TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS

PILE REFERENCE: D0273 NP

TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS

CURRENT APPLICATION NUMBER: US/10/648,593

CURRENT APPLICATION NUMBER: US/10/648,593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ## Sequence 204, Application US/10617334

## Sequence 204, Application US/10617334

## Sequence 204, Application US/06869A1

## Sequence 204, Application US/060869A1

## Septication No. US20040058869A1

## SEPTICANT: HAYGAR, Michael R.

## APPLICANT: HAYGAR, Michael R.

## TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS

## TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS

## CURRENT PAPLICATION NUMBER: US/10/617,334

## CURRENT PILING DATE: 2003-07-10

## PRIOR PILING DATE: 1999-03-15

## PRIOR PILING DATE: 1999-06-19

## PRIOR PILING DATE: 1999-06-11

## PRIOR PILING DATE: 1999-06-17

## PRIOR PILING DATE: 1999-09-01

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Pred. No. 7.9e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US 60/24:
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
; OTHER INFORMATĪON: Primer: AC4-L1
US-10-398-757-3
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Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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US-10-617-334-204
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US-10-665-951-2275

Publication No. US20040138163A1

Sequence 2275, Application US/1066991

Publication No. US20040138163A1

Sequence 2275, Application No. US20040138163A1

Sepulcant Siran Therapeutics, Inc.

APPLICANT: Belgelman, Leonid

APPLICANT: Pavco, Pamela

APPLICANT: Pavco, Pamela

APPLICANT: Pavco, Pamela

APPLICANT: Pavco, Pamela

ITILE OF INVENTION: Grow The Rector and Vascular Endothelial

TITLE OF INVENTION: Grow The Rector and Vascular Endothelial

TITLE OF INVENTION: Grow The Rector and Vascular Endothelial

TITLE OF INVENTION: Grow The Rector and Vascular Endothelial

TITLE OF INVENTION: Grow The Rector and Vascular Endothelial

TITLE OF INVENTION: Grow The Rector and Vascular Endothelial

TITLE OF INVENTION: Grow The Rector and Vascular Endothelial

CURRENT PAPLICATION WUMBER: US 10/664,668

PRIOR PLILNG DATE: 2003-09-18

PRIOR PLILNG DATE: 2003-09-18

PRIOR PLILNG DATE: 2002-07-29

PRIOR PLILNG DATE: 2002-07-29

PRIOR PLILNG DATE: 2002-07-03

PRIOR PLILNG DATE
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Pred. No. 7.9e+02;
0; Mismatches 2; Indels
                                   PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: US 09/526,193
PRIOR PILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/213,958
PRIOR PILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 256
SOFTWARE: Word for Windows Version 6.0 (ASCII Text)
LENGTH: 21
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         PRIOR APPLICATION NUMBER: US 60/151,977
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.4%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: homo sapien
US-10-745-377-118
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APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN

TITLE OF INVENTION: KINASE

FILE REFERENCE: AM101071

CURRENT APPLICATION NUMBER: US/10/702,496

CURRENT FILING DATE: 2003-11-07

PRIOR APPLICATION NUMBER: 60/429,381

PRIOR APPLICATION NUMBER: 60/429,381

NUMBER OF SEQ ID NOS: 306

SOFTWARE: Patentin version 3.2

LENGTH: 21

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; Sequence 118, Application US/10745377
; Publication No. US20040137423A1
; GABERAL INFORMATION:
; APPLICANT: Hyden, Wichael R.
; APPLICANT: Pimstone, Simon
; APPLICANT: Clee, Susanne, M.
; TITLE OF INVENTION: Compositions and Methods for Modulating
; TITLE OF INVENTION: DLC Cholesterol and Triglyceride Levels
; FILE REFERENCE: 76005-109
; CURRENT APPLICATION NUMBER: US/10/745,377
; CURRENT PILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR PILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: US 60/134,600
; PRIOR APPLICATION NUMBER: US 60/139,600
; PRIOR APPLICATION NUMBER: US 60/139,600
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Pred. No. 7.9e+02;
0; Mismatches 2; Indels
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PRIOR APPLICATION NUMBER: 60/406,385
PRIOR FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 557
SOFTWARE: Patentin version 3.2
SEQ ID NO 311
LENGTH: 21
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Matches 16; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-311
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McSwiggen, James
Beigelman, Leonid
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| Sequence 2278, Application US/1065951
| Sequence 2278, Application Wo. US20040138163A1
| Sequence 2278, Application No. US20040138163A1
| Sequence 2278, Application No. US20040138163A1
| Sequence 2278, Application No. US20040138163A1
| APPLICANT: BitTA Therefore Interference Mediated Inhibition of Vascular Endothelial
| TITLE OF INVENTION: RAW Interference Mediated Inhibition of Vascular Endothelial
| TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
| TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
| TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
| TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
| TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
| TITLE OF INVENTION NUMBER: US/065,951
| CURRENT FILING DATE: 2003-09-18
| PRIOR FILIAGE DATE: 2003-09-18
| PRIOR FILIAGE DATE: 2002-07-29
| PRIOR FILIAGE DATE: 2002-07-29
| PRIOR FILIAGE DATE: 2002-07-29
| PRIOR FILIAGE DATE: 2002-07-39
| PRIOR FILIAGE DATE: 2002-07-39
| PRIOR FILIAGE DATE: 2002-07-39
| PRIOR PRIOR APPLICATION NUMBER: US 60/393,124
| PRIOR FILIAGE DATE: 2002-06-06
| PRIOR FILIAGE DATE: 2008-06-06
| PRIOR F
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ch 0.4%; Score 14.8; DB 1; Length 21; I Similarity 72.2%; Pred. No. 7.9e+02; 13; Conservative 3; Mismatches 2; Indels
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// DCATION: (20)...(21)

OTHER INFORMATION: n stands for thymidine

US-10-665-951-2278
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                                                                                                                                                  1953 CATGCGGGAGTGCTGGCA 1970
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                                                                                                                                                                                            1 CAUGCUGGACUGCUGGCA 18
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ORGANISM: Artificial Sequence
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Matches
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| APERICANT: Bestgamm, leconid | Court | Estaconid | Process | Pro
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88.9%; Pred. No. 7.9e+02;
tive 0; Mismatches 2;
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                                                                                 497 ACACGCTGGACGTGCTGG 514
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative
  Best Local Similarity 88.9
Matches 16; Conservative
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APPLICANT: Hayden, Michael R.
APPLICANT: Hayden, Michael R.
APPLICANT: Brooks-Wilson, Angela R.
APPLICANT: Pinatone, Simon N.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
FILE REFERENCE: 760050-92
CURRENT APPLICATION NUMBER: US/10/744,465
CURRENT FILING DATE: 2003-12-23
FRIOR APPLICATION NUMBER: US 09/526,193
FRIOR APPLICATION NUMBER: 00/124,702
FRIOR PILING DATE: 1999-06-15
FRIOR FILING DATE: 1999-06-17
FRIOR FILING DATE: 1999-06-17
FRIOR APPLICATION NUMBER: 60/139,600
FRIOR PILING DATE: 1999-06-17
FRIOR PILING DATE: 1999-06-17
FRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 287
LENGTH RESERVED FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: sinh antisense region
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Pred. No. 7.9e+02;
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                           PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/393,796
PRIOR PILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 10/287,949
PRIOR FILING DATE: 2002-11-04
PRIOR PILING DATE: 2002-11-07
PRIOR PLILING DATE: 2002-11-07
PRIOR PLILING DATE: 2002-11-27
PRIOR PLILING DATE: 2002-05-29
PRIOR PLILING DATE: 2002-02-0
PRIOR PELING DATE: 2002-02-0
PRIOR PELING DATE: 2002-02-0
PRIOR PELING DATE: 2002-02-0
PRIOR PELING DATE: 2002-03-11
PRIOR PELING DATE: 2002-03-11
PRIOR PELING DATE: 2002-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature; LOCATION: (20)...(21); OTHER INFORMATION: n stands for thymidine US-10-665-951-2386
                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 2455 SOFTWARE: Patentin version 3.2
        US 60/399,348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 204, Application US/10744465 Publication No. US20040157250A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9%;
Matches 16; Conservative
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0.4%; Score 14.8; DB 1; Length 21;

Query Match

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APPLICANT: DAILNOWIN, UNLILCA
APPLICANT: HOFFMEYER, SVEN
APPLICANT: HOFFMEYER, SVEN
APPLICANT: HOFFMEYER, SVEN
APPLICANT: MORNHINWEG, ESTHER
TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDRUG
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
FILE REFERENCE: VOS-42 CON
CURRENT APPLICATION NUMBER: US/10/627,253A
CURRENT APPLICATION NUMBER: PCT/EPO2/00796
PRIOR PRILING DATE: 2003-07-24
PRIOR PPLICATION NUMBER: EP 01101651.6
PRIOR APPLICATION NUMBER: EP 01101651.6
PRIOR APPLICATION NUMBER: EP 01101651.6
SOUTH OF SEQ ID NOS: 406
SOUTHARD OF SEQ ID NOS: 406
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HOFFWEYER, SVEN
APPLICANT: HOFFWEYER, SVEN
TITLE OF INVENTION: POLYMORPHISMS IN THE HUMAN GENE FOR THE MULTIDBUG
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
CURRENT APPLICATION NUMBER: US/10/627,253A
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: PCT/EP02/00796
PRIOR PILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 406
SOFTHARE: PATEUTI VETSION 3.2
SEQ ID NO 245
LENGTH: 21
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US-10-627-253A-246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide US-10-627-253A-245
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Pred. No. 7.9e+02;
0; Mismatches 2;
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US-10-786-720-3818/c
US-10-786-720-3818/c
US-10-786-720-3818/c
Publication No. US20040191818A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: WYeth
APPLICANT: U., Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 011896-023000 (AM101331L)
CURRENT PALING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 3818
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US-10-786-720-3819
US-10-786-720-3819
Sequence 3819, Application US/10786720
Sequence 3819, Application US/10786720
Sequence 3819, Application US/20040191818A1
Sequence 3819, Application
APPLICANT: Wyeth
APPLICANT: O'Toole, Margot
APPLICANT: O'Toole, Margot
APPLICANT: Liu, well
APPLICANT: O'Toole, Margot
APPLICANT: O'Toole, 
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0.4%; Score 14.8; DB 1; Length 21;
1larity 88.9%; Pred. No. 7.9e+02;
Conservative 0; Mismatches 2; Indels
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0.4%; Score 14.8; DB 1;
Best Local Similarity 72.2%; Pred. No. 7.9e+02;
Matches 13; Conservative 3; Mismatches 2;
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0.4%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2;
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ORGANISM: RNAi-antisense strand
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   Query Match
Best Local Similarity
Matches 16; Conserv
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US-10-786-720-3817/C
Sequence 3817/C
Sequence 3817, Application US/10786720
Sequence 3817, Application US/10786720
Sequence 3817, Application US-10786720
Sequence 3817, Application No. US-0040191818A1
SEPLICANT: Weth
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
FILE REPERBRECE: 031896-023000 (AM101331L)
CURRENT PAPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SEQ ID NOS: 21135
SEQ ID NO 3817
LENGTH: 21
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                     Sequence 204, Application US/10833679

Sequence 204, Application US/10833679

Publication No. US20040185508A1

GENERAL INPORMATION:

APPLICANT: Hayden, Michael R.

APPLICANT: Hayden, Michael R.

APPLICANT: Pinactone, Simon N.

TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS

FILE REPERENCE: 760050-135

CURRENT APPLICATION NUMBER: US/10/833,679

CURRENT PELLING DATE: 2004-04-28

FRIOR APPLICATION NUMBER: 10/612,510

PRIOR APPLICATION NUMBER: 10/617,334

PRIOR PILLING DATE: 2003-07-10

PRIOR APPLICATION NUMBER: 60/134,702

PRIOR PILLING DATE: 1999-06-08

PRIOR PILLING DATE: 1999-06-08

PRIOR FILLING DATE: 1999-06-01

PRIOR FILLING DATE: 1999-06-07

PRIOR PELLING DATE: 1999-06-07

NUMBER OF SEQ ID NOS: 287

SOFTWARE: PATENTH: 21
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11arity 88.9%; Pred. No. 7.9e+02;
Conservative 0; Mismatches 2; Indels
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                                                                                                                                                      2791 TACATTTCTATAAATAGA 2808
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; ORGANISM: Homo sapiens
US-10-833-679-204
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US-10-786-720-3817
   Query Match
Best Local Similarity
Matches 16; Conserv
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APPLICANT: 0'Toole, Margot
APPLICANT: 10'Toole, Margot
APPLICANT: Liu, Mil
APPLICANT: DISEASES
TITLE OF INVENTION: DISEASES
TITLE REPERENCE: 01896-023000 (AM101331L)
CURRENT APPLICANTON NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 4527
LENGTH: 21
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GENERAL INFORMATION:
APPLICANT: 0'Toole, Margot
APPLICANT: Wyeth: Compositions and methods for diagnosmic applicants in the weight and methods for diagnosmic applicant: Liu, Wei TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES FILE REPERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135 '
SOGTWARE: Patentin version 3.2
SEQ ID NO 4526
LENGTH: 21
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0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2: Thanh
                                                                               Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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Pred. No. 7.9e+02;
3; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: RNAi-antisense strand US-10-786-720-4527
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Best Local Similarity 72.2%;
Matches 13; Conservative
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                  ; ORGANISM: Homo sapiens
US-10-786-720-4525
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US-10-786-720-4527
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               APPLICANT: Wyeth
APPLICANT: O'TOOLe, Margot
APPLICANT: O'TOOLe, Margot
APPLICANT: Liu, Weil
APPLICANT: Liu, Will
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
TITLE REPERENTE OF 1896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 3320
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Sequence 3822, Application US/10786720
Publication No. US20040191818A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wiweth
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: US/1078010 AM 01331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT PILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SSEQ ID NO 3822
LENGTH: 21
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Pred. No. 7.9e+02;
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Pred. No. 7.9e+02;
3; Mismatches 2; Indels
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US-10-786-720-3822
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                    TYPE: DNA
COCANISM: Homo sapiens
US-10-786-720-3820
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Best Local Similarity
GENERAL INFORMATION:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES

CURRENT APPLICATION NUMBER: US/10/786,720

CURRENT APPLICATION NUMBER: US/10/786,720

CURRENT FILING DATE: 2004-02-26

NUMBER OF SEQ ID NOS: 21135

SOFTWARE: Patentin version 3.2

SEQ ID NO 5.58

LENGTH: 21
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APPLICANT: Liu, Wei
TITLE O'INVENTION: DISEASES
FILE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
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Pred. No. 7.9e+02;
0; Mismatches 2;
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Pred. No. 7.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                         497 ACACGCTGGACGTGCTGG 514
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US-10-786-720-5259
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 5257
LENGTH: 21
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SEQ ID NO 5259
LENGTH: 21
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Best Local Similarity 88.9%;
Matches 16; Conservative
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; ORGANISM: RNAi-sense strand
US-10-786-720-5258
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Best Local Similarity 72.23
Matches 13; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-10-786-720-5257
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                                            Sequence 4528, Application US/10786720

Forguence 4528, Application US/10786720

Fublication No. US20040191818A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: O'TOOLE, Margot
TITLE OF INVENTION: DISEASES
TITLE OF INVENTION: DISEASES
TITLE OF INVENTION: DISEASES
TITLE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOUTHWARE: Patentin version 3.2
SEQ ID NO 4528
LENGTH: 21
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Sequence 4530, Application US/10786720
Publication No. US20040191818A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: O'TOOLE, Margot
APPLICANT: Will Wei
APPLICANT: O'TOOLE, WEI
APPLICANT: O'TOOLE, WEI
APPLICANT: US, WEI

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APPLICANT: Liu, Wei
TITLE O' INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 0.4%; Score 14.8; DB 1; Length 21; Local Similarity 88.9%; Pred. No. 7.9e+02; 16; Conservative 0; Mismatches 2; Indels
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7.9e+02;
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Pred. No. 7.
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FILE REFERENCE: 031896-023000 (AMI01331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5257, Application US/10786720 Publication No. US20040191818A1 GENERAL INFORMATION: APPLICANT: Wyeth
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ilarity 72.2%;
Conservative
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; ORGANISM: Homo sapiens
US-10-786-720-4528
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Best Local Similarity
RESULT 1016
US-10-786-720-4528/c
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APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Liu, Weith APPLICANT: Liu, Weith APPLICANT: Liu, Weith COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION: DISEASES
TILE REFERENCE: 031896 023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 11108
LENGTH: 21
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Liu, Weith
APPLICANT: Liu, Weith
TITLE NO'TOOLE,
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L.)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT APPLICATION NUMBER: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 21
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0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2: Indele
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                                                                                                                                                                                                                                                                                                           Score 14.8; DB 1;
Pred. No. 7.9e+02;
0; Mismatches 2;
                        FILE REFERENCE: 031896-023000 (AMI01331L)
CURRENT PEDLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17096
LENGTH: 21
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Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                                                       ; ORGANISM: RNAi-sense strand US-10-786-720-17096
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                                                                                                                                                                                                              TYPE: RNA
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US-10-786-720-5262
US-10-786-720-5262
Sequence 5262, Application US/10786720
Publication No. US20040191818A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: O'TOOLE, Margot
APPLICANT: UNW WEIL
TITLE OF INVENTION: DISBASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION UNDHER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
                                                                                                                                                  Sequence 5260, Application US/10786720
Sequence 5260, Application US/10786720
Publication No. US20040191818A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Liu, Wed
APPLICANT: Liu, Wed
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 011896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT PILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
SEQ ID NO 5-260
LENGTH: 21
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GENERAL INFORMATION:
APPLICANT: Wyeth APPLICANT: Weth APPLICANT: O'Toole, Margot APPLICANT: Liu, Wei TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE TITLE OF INVENTION:
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Pred. No. 7.9e+02;
3; Mismatches 2; Indels
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2 ACACGCUGUACGUGCUCG 19
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; ORGANISM; RNAi-antisense strand
US-10-786-720-5262
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Best Local Similarity 72.2
Matches 13; Conservative
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CRGANISM: Homo sapiens
US-10-786-720-5260
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US-10-786-720-17096/c
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LENGTH: 21
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APPLICANT: O'TOOLE, Margot

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE

TITLE OF INVENTION: DISEASES

FILE REFERENCE: 031896-023000 (AM101331L)

CURRENT APPLICATION NUMBER: US/10/786,720

CURRENT FILING DATE: 2004-02-26

NUMBER OF SEQ ID NOS: 21135

SOFTWARE: PATENTIN VERSION 3.2

SEQ ID NO 18293

LENGTH. 21

TYPE. no.
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Sequence 20057, Application US/10786720

Sequence 20057, Application No. US20040191818A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER:
TITLE OF INVENTION:
CURRENT FILING DATE: 2004-02-26

NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2

LENGTH: 21

LENGTH: 21
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Publication No. US20040191818A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: O'Toole, Margot
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: Patentin version 3.2
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88.9%; Pred. No. 7.9e+02;
tive 0; Mismatches 2;
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Pred. No. 7.9e+02;
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9°
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US-10-786-720-20857
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SEQ ID NO 20859
LENGTH: 21
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| Publication No. US20040191818A1
| Publication No. US20040191818A1
| GENERAL INFORMATION:
| APPLICANT: Wyeth
| TITLE OF INVENTION: DISEASES
| TITLE OF INVENTION:
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Sequence 18290, Application US/10786720

Sequence 18290, Application US/10786720

Sequence 18290, Application US/10786720

Sequence 18290, Application US/10786720

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Liu, Wei

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE

TITLE OF INVENTION: DISEASES

STILE OF INVENTION: DISEASES

STILE OF INVENTION: DISEASES

TITLE OF INVENTION: DISEASES

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tive 0; Mismatches 2
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                   2322 TGTGTGTGTGCGTGTG 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2332 TGCGTGTGTGTGTGTG 2349
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ORGANISM: RNAi-sense strand
US-10-786-720-18281
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                           16; Conservative
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Best Local Similarity
Matches 16; Conserval
                                                                                                                                                                       Best Local Similarity
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US-10-786-720-18281/c
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JUNEARL INFORMATION:

JUNEARL TOWNSTAIL THE METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLING TITLE OF INVENTION: THE METHOD

FILE REFERENCE: 199953USOXDIV

CURRENT PILLING DATE: 2000-11-29

PRIOR APPLICATION NUMBER: US 09/556,127

PRIOR APPLICATION NUMBER: US 09/556,127

PRIOR APPLICATION NUMBER: UP 1999-111601

PRIOR FILLING DATE: 1999-04-20

NUMBER OF SEQ ID NOS: 70

SEQ ID NO 6

LENGTH: 30
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Sequence 7, Application US/09725265

Sequence 7, Application Wo. US20010000175A1

GENERAL INFORMATION:

APPLICANT: KRANGANA, TAKAHIRO

APPLICANT: KANAGATA, YOICHI

APPLICANT: KANAGATA, YOICHI

APPLICANT: YOKOMAKU, TOYOKAZU

APPLICANT: YOKOMAKU, TOYOKAZU

APPLICANT: KOYOMAKU, TOYOKAZU

APPLICANT: WOKOMAKU, TOYOKAZU

APPLICANT: WOKOMAKU

APPLICANT: WOWOMAKU

APPLICANT: WOKOMAKU

APPLICANT: WOWOMAKU

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APPLICANT: WOWOMAKU

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0.4%; Score 14.8; DB 1;
Best Local Similarity 73.1%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3259 AGATATTTTATTTGCCTTTTT 3284
   3309 ATTTTTTAGGAGATTTATTTTT 3334
                                                                                                                                                                                                                                                             Sequence 6, Application US/09725265 Publication No. US20010000175A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: SYNTHETIC DNA US-09-725-265-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: ARTIFICIAL SEQUENCE FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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US-10-786-720-20990/C
i Gequence 20990, Application US/10786720
i Publication No. US20040191818A1
i GENERAL INFORMATION:
i APPLICANT: Wyeth
i APPLICANT: Liu, Wei
i TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
i TITLE OF INVENTION: DISEASES
i FILE REFERENCE: 031896-023000 (AM101331L)
i CURRENT APPLICATION UNDERER: US/10/786,720
i CURRENT FILING DATE: 2004-02-26
i NUMBER OF SEQ ID NOS: 21135
i SOGTWARE: Patentin Version 3.2
i ENGTH: 21
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j Sequence 144, Application US/10085906

j Publication No. US20030054371A1

j GREREAL INFORMATION:
   APPLICANT: Ying, Vincent
   APPLICANT: Wu, Paul
   APPLICANT: Gray, Gary S.
   TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
   TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
   TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
   TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
   TITLE OF INVENTION: UNBER: US 5/10/085, 906
   CURRENT FILING DATE: 100-02-27
   PRIOR APPLICATION NUMBER: US 60/126,215
   PRIOR APPLICATION NUMBER: US 60/126,215
   PRIOR APPLICATION NUMBER: PCT/US00/07938
   PRIOR PRILING DATE: 2000-03-24
   NUMBER OF SEQ ID NOS: 545
   NUMBER OF SEQ ID NOS: 545
   LENGTH: 26

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                                                                                                         Score 14.8; DB 1; Length 21;
Pred. No. 7.9e+02;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                 1350 GATGGAGATGATGAAGAT 1367
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                                                                                                                                                                                                                                                                                                            GAUGAAGAGGAUGAAGAU 18
j ORGANISM: RNAi-antisense strand
US-10-786-720-20859
                                                                                                             Query Match 0.4%;
Best Local Similarity 72.2%;
Matches 13; Conservative
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 73.1%;
Matches 19; Conservative
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CRGANISM: RNAi-sense strand
US-10-786-720-20990
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ORGANISM: Homo sapiens
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APPLICANT: TORINURA, MASAKI

APPLICANT: TORINURA, MASAKI

APPLICANT: TORINURA, SHINYA

APPLICANT: YAMADA, KAZUTAKA

APPLICANT: YAMADA, KAZUTAKA

APPLICANT: YAMADA, KAZUTAKA

APPLICANT: YOKOWAKU, TOYOKAZU

TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA

TITLE OF INVENTION: METHOD

TITLE OF INVENTION: METHOD

TITLE OF INVENTION: METHOD

FILE REFERENCE: 2003-204-163-0-X

CURRENT APPLICATION NUMBER: US/09/891,517

CURRENT APPLICATION NUMBER: US/2000-193133

PRIOR APPLICATION NUMBER: US/2000-193133

PRIOR PILING DATE: 2000-06-27

PRIOR PILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

NUMBER OF SEQ ID NOS: 108

SEQ ID NO 12

LENGTH: 30

***LENGTH: 30
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Best Local Similarity 73.1%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

0.4%; Score 14.8; DB 1;
Best Local Similarity 73.1%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 7;
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PRIOR APPLICATION NUMBER: JP2000-193133
PRIOR FILIMG DATE: 2000-066-27
PRIOR PLING DATE: 2000-06-23
PRIOR FILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Version 3.1
SEQ ID NO 7
LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09891517
Patent No. US2002010653A1
GENERAL INFORMATION:
APPLICANT: KURANE, RYUICHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAMA, TAKAHIRO
APPLICANT: TANAGAMA, TAKAHIRO
APPLICANT: TORIWURA, MASAKI
APPLICANT: TORIWURA, MASAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 6, Application US/10209608; Publication No. US20030082592A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic DNA US-09-891-517-7
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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APPLICANT: KURANE, RYUCHIRO
APPLICANT: KANAGAMA, TAKAHIRO
APPLICANT: KANAGAMA, TAKAHIRO
APPLICANT: KANADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: KOYAMA, OSAMU
APPLICANT: KOYAMA, OSAMU
APPLICANT: KOYAMA, OSAMU
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
TITLE OF INVENTION: NUMBER: US/09/725,265
TITLE OF INVENTION NUMBER: US/09/725,265
CURRENT PELLING DATE: 2000-11-29
PRIOR FILING DATE: 2000-1-29
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
TANDE. NUMBER
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APPLICANT: KAMAGAWA, TAKAHIRO
APPLICANT: KAMAGATA, YOICHI
APPLICANT: TORIMURA, SHINYA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOMAZU,
TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: METHOD FOR ANALYZING DATA
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: METHOD FOR ANALYZING DATA
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TITLE OF INVENTION: METHOD
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                                                                                                                                                                                              Score 14.8; DB 1; Length 30;
Pred. No. 1.1e+03;
0; Mismatches 7; Indels
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Patent No. US20020106653A1
GENERAL INFORMATION:
APPLICANT: KURANE, RYUICHIRO
APPLICANT: KANAGANA, TAKAHIRO
APPLICANT: KAMAGATA, YOLCHI
APPLICANT: TORIMURA, MASAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09725265 Publication No. US20010000175A1 GENERAL INFORMATION:
                                                        ; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: SYNTHETIC DNA US-09-725-265-12
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            ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                      Query Match 0.4%;
Best Local Similarity 73.1%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOWAKU, TOYOKAZU
APPLICANT: KOYAMA, OSAWU
APPLICANT: WINCHICANTON: WEITHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID PROBES FOR THE METHOD FOR ANALYZING DATY;
TITLE OF INVENTION: THE METHOD
TITLE OF INVENTION: THE METHOD
TITLE OF INVENTION: WINMER: US/10/209,608
TITLE REFERENCE: 199953USOXDIV
CURRENT APPLICATION NUMBER: US/09/725,265
PRIOR APPLICATION NUMBER: US/09/725,265
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 1999-111601
PRIOR PILING DATE: 1999-111601
PRIOR PILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATEURIN VERSION 3.1
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APPLICANT: KANAGANA, TAKAHRO
APPLICANT: KANAGANA, YOLCHI
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOWAKU, TOYOKAZU
APPLICANT: YOKOWAKU, TOYOKAZU
APPLICANT: YOKOWAKU, TOYOKAZU
APPLICANT: YOLWAN, OSAMU
APPLICANT: FUNUSHO, KENTA
TITLE OF INVENTION: MUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATH
TITLE OF INVENTION: THE METHOD
FILE REFERENCE: 0163-0758-0%
CURRENT PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US/09/556,127
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                                      Gaps
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                                      Indels
73.1%; Pred. No. 1.1e+03;
tive 0; Mismatches 7
                                                                                                                3259 AGATATTTATTTGCTTTGTCCTTTT 3284
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PRIOR APPLICATION NUMBER: JP 1999-111601
PRIOR FILING DATE: 1999-04-20
                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/10209608
Publication No. US20030082592A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10683386
Publication No. US20040063137A1
GENERAL INFORMATION:
APPLICANT: KURANE, RYUICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: SYNTHETIC DNA US-10-209-608-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KURANE, RYUICHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KAMAGATA, YOICHI
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
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Best Local Similarity 73.1
Matches 19; Conservative
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                       APPLICANT: KANAGAMA, TAKAHINO
APPLICANT: KANAGAMA, TAKAHINO
APPLICANT: KANAGAMA, YOYCHI
APPLICANT: YAMANA, YOYCHI
APPLICANT: YAMANA, YOYCHI
APPLICANT: YOKOMAKU, TOYCKAZU
APPLICANT: YOKOMAKU, TOYCKAZU
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: METHOD
TITLE OF INVENTION NUMBER: US/10/209,608
TITLE OF INVENTION NUMBER: US/09/725,265
PRIOR PELLING DATE: 2000-11-29
PRIOR PILLING DATE: 2000-11-29
PRIOR FILLING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 6
LEAST TARGET TO NO 6
LEAST TARGET TO NO 6
LEAST TARGET TO TARGET 
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APPLICANT: YANADA, KAZUTAKA
APPLICANT: YANADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: KOYKOMAKU, TOYOKAZU
APPLICANT: KOYKOMAKU, TOYOKAZU
APPLICANT: KOYKOMAKU, TOYOKAZU

TITLE OF INVENTION: MUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
TITLE OF INVENTION: NUCLEEC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
TITLE OF INVENTION: THE METHOD
FILE REFERENCE: 199953USOXDIV
CURRENT FALLING DATE: 2002-08-01
PRIOR PLILING DATE: 2000-04-20
PRIOR PRILING DATE: 2000-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-111601
PRIOR FILING DATE: 1999-14-20
NUMBER OF SEQ ID NOS: 70
SEQ ID NO 7
LENGTH: 30
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Pred. No. 1.1e+03;
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Publication No. US20030082592A1
GENERAL INFORMATION:
APPLICANT: KURANE, RYLICHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KAMAGAMA, YOLCHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-6
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ORGANISM: ARTIFICIAL SEQUENCE
   KURANE, RYUICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 73.1
Matches 19; Conservative
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APPLICANT: ULLMAN, EDMIN
APPLICANT: ULLMAN, EDMIN
APPLICANT: ULLMAN, EDMIN
APPLICANT: LIU, YEN PING
TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLBIC ACID ANALYSIS
FILE REFERENCE: 3817.05-1
CURRENT APPLICATION NUMBER: US/10/219,195
CURRENT APPLICATION NUMBER: 60/312,505
PRIOR APPLICATION NUMBER: 60/312,505
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 39
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Publication No. US20030165917A1
GENERAL INFORMATION:
APPLICANT: ULLMAN, EDWIN
APPLICANT: WU, MING
APPLICANT: LIU, YEN PING
TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
FILE REPERENCE: 3817.05-1
CURRENT APPLICATION NUMBER: US/10/219,195
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  TITLE OF INVENTION: NUCLEIC ACID PROBES FOR TITLE OF INVENTION: THE METHOD FILE OF INVENTION: THE METHOD FILE REFERENCE: 0163-0758-0X CURRENT PELLING DATE: 2000-04-20 PRIOR APPLICATION NUMBER: US/99/556,127 PRIOR APPLICATION NUMBER: US/99/556,127 PRIOR APPLICATION NUMBER: US/99/556,127 PRIOR FILING DATE: 2000-04-20 PRIOR FILING DATE: 1999-04-20 NUMBER OF SEQ ID NOS: 70 SEQ ID NO 12
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Sequence 30, Application US/10219195
Publication No. US20030165917A1
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ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: KUNANE, RYUICHIRO
APPLICANT: KANAGAMA, TAKAHIRO
APPLICANT: KANAGAMA, TAKAHIRO
APPLICANT: KANAGAMA, TAKAHIRO
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: PUNCHTION: MUTHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: THE METHOD
TITLE OF INVENTION NUMBER: US/09/556,127
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SEQ ID NO 7
LENGTH: 30
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TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOU
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Pred. No. 1.1e+03;
0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/10683386
Publication No. US20040063137A1
GENERAL INFORMATION:
APPLICANT: KURANE, RYUICHIRO
                                                                                                                                                                                 ; OTHER INFORMATION: SYNTHETIC DNA US-10-683-386-6
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APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KAMAGATA, VOICHI
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: KOKOMAKU, TOYOKAZU
APPLICANT: KOKOMAKU, TOYOKAZU
                                                                                                            TYPE: DNA ORGANISM: ARTIFICIAL SEQUENCE
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       NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                    Query Match 0.4%;
Best Local Similarity 73.1%;
Matches 19; Conservative
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                                                               SEQ ID NO 6
                                                                                                                                                                    FEATURE:
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Patent No. US2002000971641
; GRNERAL INFORMATION:
APPLICANT: Abarzua, Petricio
TITLE OF INVENTION: Extension
TITLE OF INVENTION: Extension
FILE REFERENCE: 469290-55
CURRENT APPLICATION UNMER: US/09/827,289
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: U.S. 60/194843
PRIOR APPLICATION NUMBER: U.S. 60/194843
PRIOR PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE Patent IN Ver. 2.1
: SEQ ID NO 18
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; Sequence 14, Application US/09827289
; Patent No. US20020009716A1
; GREERAL INFORMATION:
APPLICANT: Abarzua, Patricio
; TITLE OF INVENTION: Extension
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT PILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; RING FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Pl primer for ; OTHER INFORMATION: use in allele discrimination US-09-827-289-18
                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
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Pred. No. 1.4e+03;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                     ch 0.4%; Score 14.8; DB 1; Length 39; 1 Similarity 73.1%; Pred. No. 1.3e+03; 19; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   3262 TATTTTATTTGCTTTGTCCTTTTTCA 3287
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CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION WUMBER: 60/312,505
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO LENGTH: 39
                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.4%;
Best Local Similarity 73.1%;
Matches 19; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                           US-10-219-195-31
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                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                        FEATURE:
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Sequence 2, Application US/10362010
Publication No. US20040038247A1
GENERAL INFORMATION
Sequence 2, Application Wo. US20040038247A1
GENERAL INFORMATION
Sequence 3, Sidney
APPLICAMY: Prominer, Sidney
APPLICAMY: Venkatesh, Byrappa
APPLICAMY: Tan, Yin, Heee
APPLICAMY: Tan, Yin, Heee
TITLE OF INVENTION: NUCLEIC ACTIC CONSTRUCTS INCLUDING A NOVEL T-CELL ACTIVE PROMOTER,
TITLE OF INVENTION: AND PHARMACETTICAL COMPOSITIONS AND METHODS UTILIZING SAME FOR
TITLE OF INVENTION: REGULATING T-CELL MEDIATED INMUNE RESPONSE
FILE REPERENCE: 01/22004
CURRENT APPLICATION NUMBER: US/10/362,010
CURRENT FILING DATE: 2003-08-19
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TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
CHERTURE:
OTHER INFORMATION: Description of Artificial Sequence: P1 primer for OTHER INFORMATION: use in allele discrimination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DIA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Pl primer for
OTHER INFORMATION: use in allele discrimination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Abazaua, Patricio
TITLE OF INVENTION: Process for Allele Discrimination Using Primer
TITLE OF INVENTION: Extension
FILE BREFRENCE: 469290-52
CURRENT APPLICATION NUMBER: US/09/827,289
CURRENT APPLICATION NUMBER: US. 60/194843
PRIOR APPLICATION NUMBER: US. 60/194843
PRIOR PILING DATE: 2001-04-05
SOFTWARE: PLANG DATE: 2001-04-05
SOFTWARE: PLANG PATE: 2001-04-05
SOFTWARE: PLANG PATE: 2001-04-05
SOFTWARE: PATENTI VET: 2.1
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0.4%; Score 14.8; DB 1; Length 45;
Best Local Similarity 59.5%; Pred. No. 1.4e+03;
Matches 25; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1353 GGAGATGATGATGATGGTGGGAAACACAAAAACATCATCAA 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Single strand DNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                           3262 TATTITATTIGCTTTGTCCTTTTTCA 3287
                                                                                                                                                                                                                                                                                                                                                                                                    12 rrrrrrrrrrrrrrrrrrrrrrrrrrrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/09827289
Patent No. US20020009716A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA US-09-828-034-1
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                                                                                              APPLICANT: Lobse, Peter APPLICANT: Wagner, Richard TITLE OF INVENTION: Peptide Acceptor Ligation Methods FILE REFERENCE: 50036/031002
CURRENT APPLICATION NUMBER: US/10/208,357
CURRENT FILING DATE: 2002-0/7-30
FRIOR APPLICATION NUMBER: US/09/619,103
FRIOR APPLICATION NUMBER: 06/145,834
FRIOR APPLICATION NUMBER: 60/145,834
FRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: designed sequence to act as a linker
US-10-208-357-4
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0.4%; Score 14.6; DB 1;
Best Local Similarity 69.0%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 9;
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; Patent No. US20020064771A1
; GENERAL INFORMATION:
   APPLICANT: Thong, Weidong
; APPLICANT: Thong, Meidong
; APPLICANT: Ferrari, Eric
; TITLE OP INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: INO1165
; CURRENT APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; PRIOR FILING DATE: 2000-04-06
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 1
LENGTH: 40
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Publication No. US20020182687A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 524, Application US/09263959
Sequence 524, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
CITY: Seattle
CITY: Seattle
CITY: Manhington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Score 14.6; DB 1; Length 20; Best Local Similarity 70.0%; Pred. No. 8e+02; Matches 14; Conservative 2; Mismatches 4; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: The PC Compatible
COMPUTER: The PC Compatible
COMPUTER: The PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLIASSIFICATION:
NAME: McMasters, David D.
REGISTRATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 320010.426C2
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 524:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3264 TTTTATTTGCTTTGTCCTTTT 3284
                                             FEATURE:
NAME/KEY: misc feature
LOCATION: (9) ...(9)
OTHER INFORMATION: Any nucleotide
FEATURE:
NAME/KEY: misc.feature
LOCATION: (12)...(12)
OTHER INFORMATION: Any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                        1750 AAGTGGATGGCGCCTGAGGC 1769
  LOCATION: (6)..(6)
OTHER INFORMATION: Any nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Washington
COUNTRY: US
ZIP: 98104-7092
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Gaps

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Sequence 867, Application US/09876143; Publication No. US20040081958A1; GENERAL INFORMATION: APPLICANT: Infigen Inc. APPLICANT: ELLERTSEN, KENNETH J.
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RESULT 1051 US-10-208-357-4/c

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Gaps

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Length 40; Indels

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Sequeix.

Patent No. US2002013502

Patent No. US2002013502

GENERAL INFORMATION:

APPLICANT: Rowen, Lee

APPLICANT
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Pred. No. 6.8e+02;
0; Mismatches 1; Indels
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Publication No. US20020127634A1
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Woodring E. Wright
APPLICANT: Blizabeth Blackburn
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTY: US
ZIP: 98104-7092
COUNTY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: MCMASLERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 544:
LENGTH: 16 base pairs
                                                                                                                                                                                                                                                                                                      Sequence 544, Application US/09263959 Patent No. US20020150891A1
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3465 TATATATCTATATA 3480
                                                            3463 TATATATATCTATATA 3478
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Best Local Similarity 93.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: LOB Angeles
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Patent No. US20020150891A1

GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.

APPLICANT: Rowen, Lee

APPLICANT: Koop, Ben F.

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:
APPLICANT: ENSEYTHE, TODD
APPLICANT: FORSYTHE, TODD
TITLE OF INVENTION: IDENTIFICATION AND USE OF MOLECULAR MARKERS INDICATING
TITLE OF INVENTION: CELLULAR REPROGRAMMING
FILE REFERENCE: 028040-0202
CURRENT APPLICATION NUMBER: US/09/876,143
CURRENT FILING DATE: 2001-06-06
PRIOR PILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 1744
SOFTWARE: Patentin Version 3.0
LENGTHARE: Patentin Version 3.0
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Pred. No. 1.4e+03;
0; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
BLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3306 AGGATTTTTTTAGGAGATTTATTTTT 3334
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NAME: MCMASters, David D.
RECISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEFAN: (206) 622-4900
TELEFAN: (206) 622-4900
INFORMATION FOR SEQ ID NO: 541:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 69.0%;
Matches 20; Conservative
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EDNESS: single
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Best Local Similarity
Matches 15; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA; ORGANISM: Bovine US-09-876-143-867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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Sequence 540, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.

APPLICANT: Rowen, Lee

APPLICANT: ROWEN, Lee

APPLICANT: ROWEN, Lee

APPLICANT: ADDRESS: 1279

CORRESPONDENCE ADDRESS: 1279

CORRESPONDENCE ADDRESS: Seed and Berry Lip

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STREET: MANAGEMEN COLUMBIA CENTER, 701 Fifth Avenue

CITY: Seattle

STREET: ADDRESSES: 1279

CONTRESSED: 1270

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STREET: MANAGEMEN COLUMBIA CENTER, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPASSIBLE
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
TURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
PTI.ING DATE: 05-MAR-1999
                                            920010.426C2
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (206) 622-4900
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 9200;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 540:
SEQUENCE CHARACTER.STICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
US-09-263-959-540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-263-959-540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Fatent No. US20020150891A1

GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.

APPLICANT: Rowen, Lee

APPLICANTON: 1279

CORRESPONDENCE ADDRESS:

ADDRESSE: Seed and Berry LLP

STRATE: Washington

COUNTRY: Seattle

STRATE: Washington

COUNTRY: US ABLIGATION

MEDIUM TYPE: Ploppy disk

COMPUTER: IBW PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PREADALE FORM:

MEDIUM TYPE: IBW PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PERCENTIN RELABER: US/09/263,959

FILING DATE:

APPLICATION NUMBER: US/09/263,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" DISKETS: 3.5" DISKET: 3.5" DISKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2318 TGTGTGTGTGTGTG 2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
TTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 93.8
Matches 15; Conservative
                  California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-463-404-57
                                                                          90071-2066
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APPLICANT: LI, YUAN
APPLICANT: HERMIDA, LEANDRO C.
APPLICANT: HERMIDA, LEANDRO C.
APPLICANT: HOPPA, NANCY L.
TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG
TITLE OF INVENTION: LIBRARIES OF CDNAS
FILE REFERENCE: 0109015/026
CURRENT PILLING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 14.4; DB 1; Length 16; 93.8%; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEOLOMERE LENGTH AND/OR TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FEBSEEG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,927A
FILING DATE: 29-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
APPLICATION NUMBER: 08/09/378,535
FILING DATE: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONDITIONS RELATED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Pifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Mceachern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-232-927A-80
; Sequence 80, Application US/10232927A
; Publication No. US20030190638A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2315 GTCTGTGTGTGTGT 2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Michael D. West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nam Woo Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-885-28
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Sequence 231, Application US/10085906

Subjication No. US2003064371A1

GENERAL INFORMATION:

APPLICANT: Ying, Vincent

APPLICANT: Gray, Gary S.

TITLE OF INVENTION: POLYMORRPHIC ELEMENTS IN THE

TITLE OF INVENTION: POLYMORRPHIC ELEMENTS IN THE

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/085,906

CURRENT FILING DATE: 2002-02-25

PRIOR APPLICATION NUMBER: US 60/126,215

PRIOR APPLICATION NUMBER: PS 60/126,215

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: PCT/US00/07938

SOFTWARE: FARESQ for Windows Version 4.0

SEG ID NO.23

LENGEN. 1.
                                                                                     APPLICANT: Ying, Vincent
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
APPLICANT: Wu, Paul
APPLICANT: Gray, Gary, Gary
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
FILE REFERENCE: GNN-5343CP2
CURRENT APPLICATION NUMBER: US/10/085,906
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR APPLICATION NUMBER: US 99534,061
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR SPC IING DATE: 2000-03-24
SRIOR PILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SSC ID NOS: 545
SSC ID NO 231
FEATURE OF SEC FOR WINDOWS VERSION 4.0
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                  Sequence 231, Application US/10085906
Publication No. US20030054371A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 15; Conserva
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ઠે 셤 RESULT 1061 US-10-092-885-28

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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Parmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: Stanchcomb, Jam
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Scobedo, Jaime
APPLICANT: Scobedo, Jaime
APPLICANT: Becobedo, Jaime
APPLICANT: Becopedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Lacobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
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                                                                                                                                                                                                                         Score 14.4; DB 1; Length 16; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                               3; Mismatches
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; Sequence 5819, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6071, Application US/10138674
Publication No. US20040077565A1
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NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 5819
LENGTH: 16
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5848
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1 GUGUGUGUGUGGGGU 16
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Best Local Similarity 75.0%;
Matches 12; Conservative
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Best Local Similarity 50.0°
Matches 8; Conservative
                                                                                                                                      , ORGANISM: Homo sapiens
US-10-138-674-5848
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ORGANISM: Homo sapiens
US-10-138-674-6071
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US-10-287-949A-5819
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Publication No. US20040077565A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ravco, Pam
APPLICANT: Stinchcodu, Dan
APPLICANT: Escobedo, Jaim
APPLICANT: Escobedo, Jaim
APPLICANT: Escobedo, Jaim
APPLICANT: MENBOO-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT APPLICATION NUMBER: US/10/138,674
SOFTWARE: Patentin Version 3.0
SEQ ID NOS: 20822
SOFTWARE: Patentin Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-138674

US-10-138674

Sequence 5848, Application US/10138674

Publication No. US200400775651

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Parco, Pam

APPLICANT: Binchcomb, Dam

APPLICANT: Stinchcomb, Dam

APPLICANT: Stinchcomb, Dam

APPLICANT: Stinchcomb, Dam

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

CURRENT APPLICANTON NUMBER: US/10/138,674

CURRENT PILING DATE: 2002-05-03
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0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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                         NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REGISTRATION NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELERAX: (213) 955-0440
TELERAX: (213) 955-0440
TELERAX: (7-3510
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: 80: US-10-232-927A-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318 TGTGTGTGTGTGTG 2333
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Best Local Similarity 75.0
Matches 12; Conservative
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ORGANISM: Homo sapiens
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Woodring E. Wright
Elizabeth Blackburn
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TELOMERASE ACTIVITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/691,633
FILING DATE: 22-Oct-2003
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/060,952C
FILING DATE: May 13,1993
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: MATCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTR: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
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REFERENCE/DOCKET NUMBER: 202/045
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-691-633-57
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2002, Application US/09866108
Patent No. US20020048800A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard J.
                               Sequence 57, Application US/10691633
Publication No. US20040198659A1
GENERAL INFORMATION:
APPLICANT: Michael D. West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2318 TGTGTGTGTGTGTG 2333
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INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
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APPLICANT: GU, Yizhong
APPLICANT: H, Yonggang
APPLICANT: PENN, Sharton G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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      US-10-691-633-57
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Publication No. US20040102389A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: Actinchemb, Dam

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Refrige RIBERGE: MBHB00-876-N (400/049)

CURRENT PILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: Patentin Version 3.0

SEQ ID NO 5848
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US-10-287-949A-6071
Sequence 6071, Application US/10287949A
Sequence 6071, Application US/10289A1
Sequence 6071, Application US/10289A1
Sequence 6071, Application US/20040102389A1
SEQUENCE STATE S
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Pred. No. 6.8e+02;
3; Mismatches 1; Indels
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                                  1; Indels
Best Local Similarity 75.0%; Pred. No. 6.8e+02; Matches 12; Conservative 3; Mismatches 1
                                                                                                1295 TGAAGATGCTGAAAGA 1310
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NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2321 GTGTGTGTGTGCGT 2336
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1 UGAAAUGCUGAAAGA 16
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Best Local Similarity 75.0%;
Matches 12; Conservative
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Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
CORGANISM: Homo sapiens
US-10-287-949A-6071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-287-949A-5848
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MAR.
ITILE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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Best Local Similarity 93.8°
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-2003
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                                   APPLICANT: SHANN, MAIN.

TITLE OF INVERTION: MASSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE TILE BETERENCE: AEGMICA-7

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-30

PRIOR PI
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Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: JI, Yongqang
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: SHANK, David R.
APPLICANT: SHANK, David R.
APPLICANT: SHANK, David R.
APPLICANT: SHANK, Mark
TITLE OF INVENTION: MACK
FILE REFERENCE: AEOMICA-7
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CURRENT FILING DATE: 2001-05-25
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04
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                   CHEN, Wensheng
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US-09-866-108-2002
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                   APPLICANT
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Gaps

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APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITIE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
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0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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CURRENT PELING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-6
PRIOR PILING DATE: 2000-06-6
PRIOR PILING DATE: 2000-09-7
PRIOR PILING DATE: 2000-09-27
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 20
                                      PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SEQ ID NO 2006
SEQ ID NO 2006
PRIOR APPLICATION NUMBER: PCT/US01/00670
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Patent No. US20020048800A1
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Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: HAISE, Parron G.
APPLICANT: HAISE, David K.
APPLICANT: HAISE, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MAS.
TITLE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-01-30
PRIOR PILING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2001-01-65
NUMBER OF SEQ ID NOS: 15752
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acomica Sequence Listing Engine SEQ ID NO 2005
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00661
FILING DATE: 2001-01-30
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CORGANISM: Homo sapiens
US-09-866-108-2005
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US-09-730-289B-156

US-09-730-289B-156

Sequence 156, Application US/09730289B

Publication Wo. US20030050259A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: McSwigen, Jim

TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease

FILE REFERENCE: WHB800-864-A (400/006)

CURRENT APPLICATION NUMBER: US/09/730,289B

CURRENT PILING DATE: 2000-12-06

PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 3897

SOFTWARE: PatentIn version 3.0

SEQ ID NO 156

INNGTH. 17
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; Sequence 1807, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
APPLICANT: Blatt, Larry
; APPLICANT: GLOWITLEA Bharat
APPLICANT: CONVILLA: Bharat
; APPLICANT: Haeberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO GENE
; TILE REFERENCE: MHENBO, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US 60/181,797
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR APPLICATION NUMBER: US 60/181,797
; RIOR APPLICATION NUMBER: US 60/181,797
; RIOR APPLICATION NUMBER: US 800-02-11
; NUMBER OF SEQ ID NOS: 6679
; SEQ ID NOS: 6679
; SEQ ID NOS: 6679
; SEQ ID NOS: 679
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0.4%; Score 14.4; DB 1;
Best Local Similarity 75.0%; Pred. No. 7.2e+02;
Matches 12; Conservative 3; Mismatches 1;
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; Sequence 41, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
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1 UUUAGUUUUAAAACUG 16
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   1 ACCATCAAGCAGCTGG 16
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US-09-730-289B-156
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US-09-780-533A-1807
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TYPE: RNA
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APPLICANT: GIV, YiAhong
APPLICANT: AND STANK, Sharton G.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SIANNON, MASIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ADOMICA-7
CURRENT APPLICANTON NUMBER: US/09/866,108
CURRENT APPLICANTON NUMBER: US/09/866,108
FRIOR APPLICANTON NUMBER: US/00/65-25
FRIOR APPLICANTON NUMBER: PCT/US01/0066
FRIOR APPLICANTON NUMBER: PCT/US01/0066
FRIOR PLING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-3
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                                                                                                                               Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 7.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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Patent No. US20020048800A1
                                                                                                                                                                                                                                                                     1992 CACCTTCAAGCAGCTG 2007
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7995
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ORGANISM: Homo sapiens
US-09-866-108-7997
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us-op-s77-478-2009

bublication US/09871478

publication No. US200300663301A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: McSwiggen, Jaw

TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication

FILE REFERENCE: MBHB00-445-H (400/029)

CURRENT APPLICATION NUMBER: US 07/882,712

PRIOR FILING DATE: 2000-13-20

PRIOR PLING DATE: 2000-03-20

PRIOR PLING DATE: 2000-03-20

PRIOR PRIOR APPLICATION NUMBER: US 09/636,347

PRIOR PLING DATE: 2000-00-8-09

PRIOR PLING DATE: 2000-00-8-09

PRIOR PLING DATE: 1994-02-07

PRIOR APPLICATION NUMBER: US 08/433,993

PRIOR PLING DATE: 1994-02-07

PRIOR APPLICATION NUMBER: US 08/434,504

PRIOR APPLICATION NUMBER: US 09/436,430

PRIOR APPLICATION NUMBER: US 08/434,504

PRIOR APPLICATION NUMBER: US 08/436,430

PRIOR PLING DATE: 1999-11-08

PRIOR PLING DATE: 1999-11-08
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US-09-848-754A-2482
Sequence 2482, Application US/09848754A
Publication No. US20030073207A1
GENERAL INFORMATION:
APPLICANT: Riboryme Parameceuticals, Inc.
TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
TITLE OF INVENTION: USABBOD-958-1 (400/018)
CURRENT PEDLICATION UNDER: 12(90/018)
CURRENT PILING DATE: 2001-05-03
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Pred. No. 7.2e+02;
5; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     853 GAGGAGGAGCTGGTGG 868
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Best Local Similarity 62.5%;
Matches 10; Conservative
                                                                          TYPE: RNA

ORGANISM: Hepatitis B virus
US-09-877-478-1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // TYPE: RNA
// ORGANISM: Hepatitis B virus
US-09-877-478-2089
SEQ ID NO 1412
LENGTH: 17
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                                                                 APPLICANT: McSwiggen, Jim
FILE OF INVENTYOR: McHod and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBH300-845-H (400/029)
CURRENT FILING DATE: 2001-12-31
FRIOR PAPLICATION NUMBER: US 09/837,478
PRIOR FILING DATE: 1992-05-14
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 1099-05-04
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1995-05-04
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APPLICANT: Bibozyme Pharmaceuticals, Inc.
APPLICANT: Bratt, Larry
APPLICANT: Bratt, Larry
APPLICANT: Bratt, Larry
APPLICANT: Bratt, Larry
APPLICANT: Morsiseev, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBHB00-845-H (400/029)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT APPLICATION NUMBER: US 07/882,712
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR PELING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
PRIOR PELING DATE: 2000-08-09
PRIOR PELING DATE: 2000-08-09
PRIOR PELING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 08/433,993
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR PELING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR PELING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-05-04
PRIOR FILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 6866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3626 GGGCCCTGAGTCTGGG 3641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: RNA; ORGANISM: Hepatitis B virus US-09-877-478-41
    Draper, Kenneth
Blatt, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-877-478-1412/c
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RESULT 1086
US-05-827-395A-424
| Sequence 424, Application US/09827395A
| Fublication No. US20030113891A1
| GENERAL INFORMATION:
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: Dawrence Blatt
| APPLICANT: Dames McSwiggen
| APPLICANT: Dames McSwiggen
| APPLICANT: Dames McSwiggen
| TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Receptor G
| FILE REPERENCE: MHHB00-878-C (400/017)
| CURRENT APPLICATION NUMBER: US/09/827,395A
                                                                         Sequence 391, Application US/09930423

Publication No. US20030092003A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease;
FILE REPERENCE: MBHB00, 918-A 400/027
CURRENT APPLICATION NUMBER: US/09/930, 423
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: Patentin version 3.0
SEQ ID NO 391
LINGTH: 17
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iS-09-780-164-723
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Best Local Similarity 75.0%; Pred. No. 7.2e+02;
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TYPE: RNA
CRGANISM: Homo sapiens
US-09-780-164-723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Homo Sapiens
US-09-930-423-391
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Sequence 2907, Application US/09848754A

Sequence 2907, Application US/09848754A

Publication No. US20030073207A1.

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors

CURRENT APPLICATION UNDERS: US/09/848,754A

CURRENT FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 9645

SEQ ID NO 2907

SEQ ID NO 2907
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US-09-930-423-390/c
; Sequence 390, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McGwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease;
; RIER REFRERNES: MEHBOO, 918-A 400/027
; CURRENT FILING DATE: 2001-08-15
; UNMBER OF SEQ ID NOS: 4553
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 390
; LENGTH: 17
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                                                                                                                                                                                                                                                                                   Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 75.0%; Pred. No. 7.2e+02; Matches 12; Conservative 3; Mismatches 1; Indels
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NUMBER OF SEQ ID NOS: 9645
SOPTWARE: Patentin version 3.0
SEQ ID NO 2482
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                                                                                                                                        ; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-2482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
CRGANISM: Homo sapiens
US-09-848-754A-2907
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CORGANISM: Homo Sapiens
US-09-930-423-390
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Best Local Similarity
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Best Local S.
Matches 12
                                                                                                              LENGTH: 17
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APPLICANT: Von Carlowitz, Ira
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Hamblin, Paul
APPLICANT: Hamblin, Paul
APPLICANT: Bills, Jonathan
ITILE OF INVENTION: (GRID) Gene
FILE REFERENCE: MBH00-901-A (400/013)
FULE REFERENCE: MBH00-901-A (400/013)
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304
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US-09-745-237A-390/C
US-09-745-237A-390/C
Sequence 390, Application US/09745237A
Sequence 390, Application US.0030143708A1
Sequence 390, Application No. US20030143708A1
SENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
SAPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
TITLE OF INVENTION: Wethod and Reagent for the Treatment of Alzheimer's Disease
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: PatentIn version 3.0
SEQ ID NO 390
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0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 7.2e+02;
Matches 12; Conservative 3; Mismatches 1; Indels
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0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                           0.4%; Score 14.4; DB 1; Length 17; 75.0%; Pred. No. 7.2e+02;
                                                                                                                                                                                                                   3; Mismatches
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Jarvis, Thale
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 880, Application US/09792818 Publication No. US20030134806A1
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                                                                                                                                                              Query Match
Best Local Similarity 75.0
Matches 12; Conservative
                                                    TYPE: RNA
CRGANISM: Homo sapiens
US-09-792-818-645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
CRGANISM: Homo sapiens
US-09-792-818-880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
CORGANISM: Homo sapiens
US-09-745-237A-390
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1089
US-09-792-818-880
     ; SEQ ID NO 645
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publication No. US20030134806A1

GENERAL INFORMATION:
APPLICANT: Stbozyme Pharmaceuticals, Inc.
APPLICANT: Stbozyme Pharmaceuticals, Inc.
APPLICANT: Won Carlowitz, Ira
APPLICANT: McSwiggen, Jim
APPLICANT: Hamblin, Paul
APPLICANT: GRID) Gene
TITLE OF INVENTION: GRID) Gene
TITLE OF INVENTION: GRID) Gene
CURRENT APPLICATION NUMBER: US/09/792,818
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304
SOFTWARE: Patentin version 3.0
SEQ ID NO 382
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Publication No. US20030134806A1
GENERAL INFORMATION:
APPLICANT: RIDOZYME Pharmaccuticals, Inc.
APPLICANT: Azvis, Thale
APPLICANT: McSwiggen, Jim
APPLICANT: Hamblin, Paul
APPLICANT: Blis, Jonathan
APPLICANT: Blis, Jonathan
APPLICANT: Blis, Jonathan
APPLICANT: Ramblin, Paul
APPLICANT: Blis, Jonathan
APPLICANT: RILIS, JONATHON: Mathoo.901-A (400/013)
CURRENT APPLICANTION: MUMBER: US/09/792,818
CURRENT PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304
SOFTWARE: PatentIn version 3.0
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Pred. No. 7.2e+02;
2; Mismatches 1; Indels
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CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/780,533
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER: OF SEQ ID NOS: 2617
SOFTWARE: PAEGENTIN VETSION 3.0
SEQ ID NO 424
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Best Local Similarity 81.2%
Matches 13, Conservative
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ORGANISM: Homo sapiens
US-09-792-818-382
                                                                                                                                                                                                                                                 TYPE: RNA
CORGANISM: Homo sapiens
US-09-827-395A-424
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US-10-238-700-3350/c

i Sequence 3350, Application US/10238700

i Publication No. US2030153521A1

i Publication No. US2030153521A1

i GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

ITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level

FILE REFERENCE: 400/057 (MBHB01-1158-A)

CURRENT APPLICATION NUMBER: US/10/238,700

CURRENT FILING DATE: 2002-09-18

PRIOR APPLICATION NUMBER: DCT/US 02/16840

PRIOR APPLICATION NUMBER: US 60/318,471

PRIOR PILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 4666

SOFTWARE: Patentin version 3.0

SEQ ID NO 3330

LENGTH: 17
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Publication No US2003016622941

JERNERAL INFORMATION:
APPLICANT'S Shannon, Mark
TITLE OF INVENTION: HUWAN POSH-LIKE PROTEIN 1
FILE REFRENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US 02/16840 PRIOR FILING DATE: 2002-05-29 PRIOR APPLICATION NUMBER: US 60/318,471 PRIOR FILING DATE: 2001-09-10 NUMBER OF SEQ ID NOS: 4666 SOFTWARE: PATENTIN VERSION 3.0 SEQ ID NO 2806
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US-10-238-700-2806
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US-10-238-700-3350
                                                                                                                                                                                                                                  TYPE: RNA
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Sequence 2806, Application US/10238700

Publication No. US20030153521A1

Sequence 2806, Application US/10238700

Publication No. US20030153521A1

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level

FILE REFERENCE: 400/0218 105/10/238,700

CURRENT APPLICATION NUMBER: US/10/238,700
                                                                                                                                                     Fublication US/09745237A

Sequence 391, Application US/09745237A

Publication No. US20030143708A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: McSwiggen, Jim

APPLICANT: McSwiggen, Jim

TITLE OF INVENTYON: Method and Reagent for the Treatment of Alzheimer's Disease

TILE REFERENCE: 400/007 (MBHB00-918-A)

CURRENT FILING DATE: 2002-04-15

NUMBER OF SEQ ID NOS: 4550

SOFTWARE: Patentin Version 3.0

SEQ ID NO 391
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US-10-21-059-166/C
Sequence 166, Application US/10211059
Publication No. US20030100495A1
GENERAL INFORMATION:
APPLICANT: Zhang, Jian
FILE REFERENCE: PB0149
CURRENT APPLICATION NUMBER: US/10/211,059
CURRENT APPLICATION NUMBER: US/0/211,059
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/311,034
PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 322
SEQ ID NO 166
SEQ ID NO 166
LENGTHERS AFORMICA SEQUENCE LISTING Engine
SEQ ID NO 166
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     GCCTGCAGGCCCTGG 2
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                     RESULT 1091
US-09-745-237A-391/c
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US-10-061-201-444
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Fublication No. US20030166229A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PROLTS
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT APPLICATION NUMBER: PCT/US01/00666
FRIOR PRIOR PELICATION NUMBER: PCT/US01/00667
FRIOR APPLICATION NUMBER: PCT/US01/00667
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR PELICATION NUMBER: PCT/US01/00669
FRIOR PELICATION NUMBER: PCT/US01/00669
FRIOR APPLICATION NUMBER: PCT/US01/00669
FRIOR FILING DATE: 2001-01-30
FRIOR APPLICATION NUMBER: PCT/US01/00670
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR APPLICATION NUMBER: US 60/328,205
FRIOR APPLICATION NUMBER: US 60/328,205
FRIOR APPLICATION NUMBER: US 60/328,205
FRIOR FILING DATE: 2001-01-30
FRIOR APPLICATION NUMBER: US 60/328,205
           PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-05-23
PRIOR PLILING DATE: 2001-05-23
PRIOR PLILING DATE: 2001-05-23
PRIOR PLILING DATE: 2001-10-10
NUMBER: US 60/328,205
NUMBER OF SEQ ID NOS: 4162
SEQ ID NO 441
APPLICATION NUMBER: PCT/US01/00668
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CORGANISM: Homo sapiens
US-10-061-201-441
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; ORGANISM: Homo sapiens
US-10-061-201-443
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| Pacipacies 444, Application 104/1061201 |
| Publication Nov. US2001662294 |
| PUBLICATION NOVER: US101-101-101 |
| PUBLICATION NOVER: US101-101-
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US-10-342-902-1412,

US-10-342-902-1412,

Sequence 1412, Application US/10342902

Publication No. US20040054156A1

SEMERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: Morrissey, Dave

ITILE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication

FILE REFERENCE: 400/075 (MRHB00-845-1)

CURRENT PILING DATE: 2001-06-08

FRIOR APPLICATION NUMBER: US/10/342,902

CURRENT PILING DATE: 2000-03-20

FRIOR APPLICATION NUMBER: US 09/877,478

PRIOR FILING DATE: 2000-03-20

PRIOR PLING DATE: 2000-08-09

PRIOR PLICATION NUMBER: US 09/636,385

PRIOR FILING DATE: 2000-03-20

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR FILING DATE: 2000-02-4

PRIOR PLING DATE: 1994-02-07

PRIOR APPLICATION NUMBER: US 09/436,430

PRIOR PLING DATE: 1992-05-14

PRIOR PLING DATE: 1990-05-14

PRIOR PLING DATE: 1900-03-20

PRIOR APPLICATION NUMBER: US 07/882,712

PRIOR APPLICATION NUMBER: US 07/882,712

PRIOR PLING DATE: 1990-05-14

PRIOR PLING DATE: 1990-05-14

PRIOR PLING DATE: 1900-03-20

PRIOR APPLICATION NUMBER: US 09/436,430

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR APPLICATION NUMBER: US 09/696,347

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PRIOR APPLICATION NUMBER: US 09/436,430

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR APPLICATION NUMBER: US 09/436,430

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR APPLICATION NUMBER: US 09/696,347

PRIOR APPLICATION NUMBER: US 09/696,347
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
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                                                         FILE KEFEKANICH (10) (WIRER: US/10/342,902)
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2000-08
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-03-20
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 1994-02-07
PRIOR PILING DATE: 1994-02-07
PRIOR FILING DATE: 1994-02-07
PRIOR FILING DATE: 1992-05-14
PRIOR FILING DATE: 1992-05-14
PRIOR FILING DATE: 1992-05-14
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SEQTHARRE: PATENTIN VEREIGN 3.2
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Best Local Similarity 93.8°
Matches 15; Conservative
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Best Local Similarity
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APPLICANT: Lawrence Blatt
APPLICANT: Lawrence Blatt
APPLICANT: James McSwiggen
APPLICANT: Bharat Chowrira
APPLICANT: Bharat Chowrira
APPLICANT: Bharat Chowrira
APPLICANT: Bharat Chowrira
APPLICANT: Peter Habberi
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
FILE REFERENCE: BHBBOO-878 H 4 (400/112)
CURRENT APPLICATION NUMBER: US/10/430,882
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 09/780,533
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-11
PRIOR PLING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
SPRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 2617
SSOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.4%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 7.2e+02;
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   PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/328,205
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 424, Application US/10430882
Publication No. US20030203870A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 41, Application US/10342902
Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Blact, Kenneth
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1312 GATGCCACTGACAAGG 1327
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
US-10-061-201-445
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US-10-430-882-424
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Page 282

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Sequence 4753, Application US/10138674

Sequence 4753, Application US/10138674

Sequence 4753, Application No. US20040077555A1

Sequence 4753, Application No. US20040077555A1

Sequence 4753, Application No. US20040077555A1

Sequence 4753, Application No. US200400, Inc.

APPLICANT: Richcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel)

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: WINNER: US/10/138,674

CURRENT PILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4753
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APPLICANT: AZOCO, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Standboamb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/10/138, 674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 6732
LENGTH: 17
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Pred. No. 7.2e+02;
1; Mismatches 1; Indels
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                                                                    Score 14.4; DB 1;
Pred. No. 7.2e+02;
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Publication No. US20040077565A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1393 AACCTGCTGGGCGCCT 1408
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1 Similarity 87.5%;
14; Conservative
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                                                                    Query Match 0.4%;
Best Local Similarity 81.2%;
Matches 13; Conservative ;
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Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-10-138-674-4753
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US-10-138-674-6732
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Best Local Similarity
Matches 14; Conserv
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US-10-138-674-2650
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; Sequence 2650, Application US/20136541
; GENERAL INFORMATION:
    APPLICANT: Rhozyme Pharmaceuticals, Inc.
    APPLICANT: Racocow, Dam
    APPLICANT: Stinchcomb, Dan
    APPLIC
                                                                                                                                                                                                                                                                                                                     Sequence 2089, Application US/10342902

Publication No. US20040054156A1

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: Moxidgen, Jim

APPLICANT: Moxidgen, Jim

APPLICANT: Moxidgen, Jim

APPLICANT: Working Blatt, Larry

APPLICANT: Moxidgen, Jim

APPLICANT: 2001-05.08

PRIOR PILING DATE: 2001-06-08

PRIOR FILING DATE: 2000-08-09

PRIOR PILING DATE: 1994-02-07

PRIOR PILING DATE: 1994-02-07

PRIOR FILING DATE: 1994-02-07

PRIOR FILING DATE: 1995-02-07

PRIOR PRIOR
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ilarity 62.5%; Pred. No. 7.2e+02;
Conservative 5; Mismatches 1; Indels
    Indels
            ;
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                                                                                    853 GAGGAGCAGCTGGTGG 868
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                                                                                                                                                            GAGGAGCACCTGCTGG 1
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            15; Conservative
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ORGANISM: Mus musculus
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Best Local Similarity
Matches 10; Conserve
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US-10-342-902-2089
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            Matches
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TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor CURRENT APPLICATION NUMBER: US/10/287, 949A CURRENT FILING DATE: 2003-04-11 NUMBER OF SEQ ID NOS: 20822 SOFTWARE Patentin version 3.0 SEQ ID NO 2650 LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4753, Application US/10287949A
; Sequence 4753, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Bacobed, Jam
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobed, Jaim
; APPLICANT: Escobed, Jaim
; APPLICANT: Escobed, Jaim
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4753
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US-10-287-949A-6732

Sequence 6712, Application US/10287949A

Sequence 6712, Application US/10287949A

Sequence 6712, Application US/10289A1

GENERAL INFORMATION:

APPLICANT: Riboryme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, Jim

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Becobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBH800-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822
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                                                                                                                                                                                                                                                                                                                                Query Match

0.4%; Score 14.4; DB 1;
Best Local Similarity 81.2%; Pred. No. 7.2e+02;
Matches 13; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1608 GAAGTGCATCCACAGG 1623
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Best Local Similarity 75.v.
Them 12; Conservative
Escobedo, Jaime
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CORGANISM: Homo sapiens
US-10-287-949A-4753
                                                                                                                                                                                                                                       TYPE: RNA
CORGANISM: Mus musculus
US-10-287-949A-2650
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Forginary 7632, Application US/10138674

Fublication No. US20040077565A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Parco, Pam
APPLICANT: Racopen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674

CURRENT FILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 20822

SOFTWARE: Patentin Version 3.0

SEQ ID NO 7632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 75.0%; Pred. No. 7.2e+02; Matches 12; Conservative 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1397 TGCTGGGCGCCTGCAC 1412
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Best Local Similarity 75.0
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-10-138-674-7632
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US-10-138-674-7696
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publication No. US20040102413A1
GENERAL INPOWATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Rosiggen, Jim
APPLICANT: Chowrira, Bharat
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Bnzyme
FILE REFERENCE: MHHOO-882-C (400/019)
CURRENT FILING DATE: 2003-11-13
PRIOR PELICATION NUMBER: US/10/712,672
CURRENT FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 5586
SOFTWARE: PATENT VERSION 3.0
SEQ ID NO 526
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ## APPLICANT: Ribozyme Pharmaceuticals, Inc.
### APPLICANT: Ribozyme Pharmaceuticals, Inc.
#### APPLICANT: Ribozyme Pharmaceuticals, Inc.
#### APPLICANT: McSwiggen, Jim
### APPLICANT: Stinchcomb, Dan
### APPLICANT: Stinchcomb, Dan
### TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
### TITLE OF INVENTION: Wethod and Reagent for the Inhibition of Telomerase Enzyme
### TITLE OF INVENTION: WHERE: US/01/012,672
### CURRENT APPLICATION NUMBER: US/09/653,225
### PRIOR PELING DATE: 2000-08-31
### PRIOR PELING DATE: 2000-08-31
### PRIOR PELING DATE: 1099-08-31
### PRIOR PILING DATE: 1999-08-31
### PRIOR PILING DATE: 1999-08-31
### WUMBER OF SEQ ID NOS: 5586
### SOFTWARE: PatentIn version 3.0
### SECTION OF THE PATENTIAL PAT
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Pred. No. 7.2e+02;
3; Mismatches 1; Indels
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              Indels
         3; Mismatches
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Publication No. US20040102413A1
GENERAL INFORMATION:
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Best Local Similarity 75.0%;
Matches 12; Conservative 3
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12; Conservative
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US-10-712-672-526
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              Matches
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i Sequence 7632, Application US/10287949A

i Sequence 7632, Application US/10287949A

j Publication No. US20040102389A1

i SEQUENCE TO THE CONTROL OF 
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; Bublication No. US20040102389A1
; Bublication No. US20040102389A1
; GENDRAL INFORMATION:
; APPLICANT: Rarco, Pan Application No. McDiana Applicant: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Barco, Pan
; APPLICANT: Barco, Pan
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Becobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; TITLE REFERENCE: MRH800-876-N (400/049)
; CURRENT APPLICATION UMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 7696
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                                                                                                                                                                                                                                                                                                                            Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 7.2e+02; Matches 14; Conservative 1; Mismatches 1; Indels
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         SOFTWARE: PatentIn version 3.0 SEQ ID NO 6732
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7696
                                                                                                                                                      ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-6732
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Best Local Similarity
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Sequence 2682, Application US/10712672

Sequence 2682, Application US/10712672

Publication No. US20040102413A1

GENERAL INFORMATION:

APPLICANT: Bloozyme Pharmaceuticals, Inc.

APPLICANT: Chowrira, Bharat

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TILE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme

FILE REFERENCE: MBHB00-882-C (400/019)

CURRENT APPLICATION NUMBER: US/09/653,225

PRIOR PILING DATE: 2003-11-13

PRIOR PILING DATE: 2000-08-31

PRIOR PILING DATE: 2000-04-14

PRIOR PILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 5586

SOFTWARE: PatentIn version 3.0

LENGTH - 17
                                                                                                                                                                                                                                                  ## Sequence 2341, Application US/10712672

| Sequence 2341, Application No. US2004010241341
| Publication No. US2004010241341
| Publication No. US2004010241341
| GENERAL INFORMATION:
| APPLICANT: Bloozyme Pharmaceuticals, Inc.
| APPLICANT: Chowrier, Bharat
| APPLICANT: Chowrier, Bharat
| APPLICANT: Stinchcomb, Dan
| TILE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
| FILE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
| FILE REPERBNCE: MBHB00-882-C (400/019)
| CURRENT APPLICATION NUMBER: US/09/653,225
| PRIOR FILING DATE: 2000-08-31
| PRIOR FILING DATE: 2000-04-14
| PRIOR SEQ ID NOS: 5586
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 2: 5586
| SOFTWARE: Patentin version 3.0
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0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 7.2e+02;
Matches 13; Conservative 2; Mismatches 1; Indels
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1479 GGCGCGGCGCCCCG 1494
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CORGANISM: Homo sapiens
US-10-712-672-2682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-2341
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## Sequence 2330, Application US/10712672

## Publication No. US20040102413A1

## GENERAL INPORMATION:

## APPLICANT: Ribozyme Pharate

## APPLICANT: Chowrira, Bharat

## APPLICANT: Ribozyme Pharate

## APPLICANT: Action Now Pharate

## APPLICANT: Action Now Pharate

## APPLICANT: Action Now Pharate

## APPLICANT: APPLICANT: MEHBOO-882-C (400/019)

## CURRENT APPLICANT: We had and Reagent for the Inhibition of Telomerase Enzyme

## PILE REFERENCE: MEHBOO-882-C (400/019)

## CURRENT APPLICATION NUMBER: US/09/653,225

## PRIOR PILING DATE: 2000-00-31

## PRIOR PILING DATE: 2000-00-31

## PRIOR PILING DATE: 1999-08-31

## PRIOR PLING DATE: 1999-08-31

## WUMBER OF SEQ ID NOS: 5586

## SOFTWARE: PatentIn version 3.0

## SEQ ID NO 2330

## EDMORTH: 1790-08-31

## EDMORTH: PATENCE P
                                                                                                                                                                                                                                                                                                               Sequence 2019, Application US/10712672

Sequence 2019, Application US/10712672

Sequence 2019, Application US/20040102413A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharat

APPLICANT: Chowrira, Bharat

APPLICANT: Action of Telomerase Enzyme

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TILE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme

TILE OF INVENTION: Method and Reagent for 2003-11-13

CURRENT PILING DATE: 2003-11-13

PRIOR PLILING DATE: 2000-04-14

PRIOR PLILING DATE: 2000-04-14

PRIOR PLILING DATE: 2000-04-14

PRIOR PLILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-08-31

PRIOR FILING DATE: 2000-08-31
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                                           1563 CTGTGCCTACCAGGTG 1578
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Best Local Similarity 93.8
Matches 15; Conservative
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CORGANISM: Homo sapiens
US-10-712-672-2019
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CRGANISM: Homo sapiens
US-10-712-672-2330
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TITLE OF INVENTION: O'LIGGOUCLEGOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAN
TITLE OF INVENTION: O'LIGGOUCLEGOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAN
TITLE OF INVENTION: VIRUS REPLICATION
FILE REFERENCE: 400/042US (WHHB02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR PELING DATE: 2001-10-24
PRIOR PELING DATE: 2001-06-09
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-34
PRIOR PELICATION NUMBER: US 60/337,055
PRIOR PELING DATE: 2001-10-34
PRIOR PELING DATE: 2001-10-3-1
PRIOR PELING DATE: 2001-10-3-1
PRIOR PELING DATE: 2000-13-1
PRIOR FILING DATE: 2000-13-1
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR PELING DATE: 2000-12-18
PRIOR PELING DATE: 2000-00-15
PRIOR FILING DATE: 2000-11
PRIOR FILING DATE: 2000-11
PRIOR FILING DATE: 2000-00-15
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APPLICANT: Patrice, Lee
APPLICANT: Patrice, Lee
APPLICANT: Remeth, Draper
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIE OF INVENTION: VIRUS REPLICATION
TITLE OF INVENTION: VIRUS REPLICATION
FILE REFERENCE: 400/404US (MBHB02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILLING DATE: 2003-09-23
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James, McSwiggen
David, Morrissey
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APPLICANT: David, Morrissey
APPLICANT: David, Morrissey
APPLICANT: Panela, Pavco
APPLICANT: Panela, Pavco
APPLICANT: Partice, Lee
APPLICANT: Renneth, Draper
APPLICANT: Renneth, Draper
APPLICANT: Renneth, Draper
APPLICANT: Elisabeth, Roberts
ITILE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
ITILE OF INVENTION: UNGER: 400/0420S (MEHBO2-249-E)
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-26
PRIOR FILING DATE: 2001-10-26
PRIOR PLING DATE: 2002-03-20
PRIOR PLING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US 60/337,055
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2002-03-20
PRIOR PLING DATE: 2001-03-26
PRIOR PLING DATE: 2000-03-21
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NUMBER OF SEQ ID NOS: 16207
SOFTWARE: PatentIn version 3.0
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Pred. No. 7.2e+02;
0; Mismatches 1; Indels
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; Sequence 1412, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
   APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
                                                                                                                                                                    US-10-669-841-41/c
; Sequence 41, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         APPLICANT: Sirna Therapeutics, Inc. APPLICANT: Lawrence, Blatt APPLICANT: Dennis, Macejak APPLICANT: James, McSwiggen
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1 AGGGAGGGGGGGCCC 16
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Best Local Similarity 93.8%;
Matches 15; Conservative
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                      Query Match

0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 7.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Publication No. US20040137589A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3194 CCCCGGAGCTGGAGGA 3209
                                                                                                                            3194 CCCCGGAGCTGGAGGA 3209
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2003
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US-10-723-361-2005/c
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Publication No. US20040137589A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GU, Xizhong

APPLICANT: GU, Xizhong

APPLICANT: GU, Xizhong

APPLICANT: HANZEL, David R.

APPLICANT: RANGEL, David R.

APPLICANT: SIGN, WHEREL US/0/23, 361

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: US/0/20, 456

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR PRILING DATE: 2001-01-04

PRIOR PLILING DATE: 2001-01-30

PRIOR PRIOR PRILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-
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SOFTWARE: Aeomica Sequence Listing Engine
                                                                                                                                                                                                                                                                             - See File Wrapper or PALM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.4%; Score 14.4; DB 1; Length 17; 62.5%; Pred. No. 7.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR PILIG DATE: 2002-03-11
PRIOR PILIG DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-26
PRIOR PRILICATION NUMBER: US 09/740,332
PRIOR PILING DATE: 2000-07-07
PRIOR PILIGATION NUMBER: US 09/611,931
PRIOR PILIGATION NUMBER: US 09/504,321
PRIOR PILIGATION NUMBER: US 09/504,321
PRIOR PILING DATE: 2000-02-15
PRIOR PILING DATE: 2000-02-15
NUMBER: OF SEQ ID NOS: 16207
SEQ ID NOS: 16207
SEQ ID NOS: 16207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2776 TTCCGGAAACTAGTGT 2791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 UUCCGGAAACUACUGU 16
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ORGANISM: Hepatitis B Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
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CORGANISM: Homo sapiens
US-10-723-361-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1122
US-10-723-361-2002/c
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: FENN: JI, Yonggang
APPLICANT: FENN: JI, Yonggang
APPLICANT: RANZE, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: GHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
FILE REFERENCE: PB0105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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CURRENT PAPLICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR PAPLICATION NUMBER: US 09/866,108
PRIOR PLING DATE: 2001-05-25
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-00-06-46
PRIOR FILING DATE: 2000-09-27
PRIOR PLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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                                                       PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.4; DB 1; Length 17; Pred. No. 7.2e+02;
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SEQ ID NO 7995
LENGTH: 17
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7995, Application US/10723361
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Best Local Similarity 93.8%;
Matches 15; Conservative
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CORGANISM: Homo sapiens
US-10-723-361-2006
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US-10-723-361-7995
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Best Local Similarity
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                 APPLICANT: CHEN, Wensheng
APPLICANT: GHAN, Wark Wensheng
APPLICANT: SHANNOW, MARK
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILE REFRENCE: P0105
CURRENT PELLON NUMBER: US 09/866,108
FRIOR PLILING DATE: 2003-11-26
FRIOR APPLICATION NUMBER: US 60/207,456
FRIOR PLILING DATE: 2000-05-26
FRIOR PLILING DATE: 2000-05-26
FRIOR PLILING DATE: 2000-05-26
FRIOR PLILING DATE: 2000-05-26
FRIOR PLILING DATE: 2000-00-27
FRIOR PLILING DATE: 2000-01-30
FRIOR PLILING DATE: 2001-01-30
FRIOR PLICATION NUMBER: PCT/USOI/0669
FRIOR PLILING DATE: 2001-01-30
FRIOR PLILING
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### APPLICANT: GU, Yizhong
### APPLICANT: GU, Yizhong
### APPLICANT: GU, Yizhong
### APPLICANT: David K.
### APPLICANT: PENN, Sharron G.
### APPLICANT: PENNON, Mark
### APPLICANT: PENNON, Mark
### PENNON, Mark
### PENNON PENLON NUMBER: US 09/866,108
### PRIOR PILING DATE: 2000-10-24
### PRIOR PELING DATE: 2000-10-04
### PRIOR PELING DATE: 2001-01-30
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Publication No. US20040137589A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1487 GGCCCCCGGGCCTGGA 1502
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Best Local Similarity 93.8
Matches 15; Conservative
RANK, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-723-361-2006/c
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                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell
Leigh & Whinston, LLP
STREET: One World Trade Center, Suite
1600, 121 S.W. Salmon Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Word97 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/892,325
FILING DATE: 26-Jun-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION NUMBER: 09/058,947
PILING DATE: cUnknown>
ATTORNEY/AGENT INPORMATION:
ATTORNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 41,401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 97204-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3.5-inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3658 GCCTGCAGGGCCATGG 3673
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18 base pairs
Massachusetts: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
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FUDICATION TO USZOUG137583A1

SEQUENCE THOROMATURON:

APPLICAMT: GU, Yizhong

APPLICAMT: GU, Yizhong

APPLICAMT: BENN, Sharron G,

APPLICAMT: BENN, Sharron G,

APPLICAMT: HANNEL, David R.

APPLICAMT: APPLICAMT: BENNON, MARK

TITLE OF INTENTION UNDERRE: US/10/723,361

CURRENT PAPLICATION NUMBER: US/201-126

FRIOR APPLICATION NUMBER: US/201-126

FRIOR APPLICATION NUMBER: US/201-05-25

FRIOR APPLICATION NUMBER: US/201-05-26

FRIOR APPLICATION NUMBER: US/201-05-26

FRIOR APPLICATION NUMBER: US/201-05-26

FRIOR APPLICATION NUMBER: US/201-06-26

FRIOR APPLICATION NUMBER: US/201-06-26

FRIOR APPLICATION NUMBER: US/201-06-26

FRIOR APPLICATION NUMBER: PCT/US01/00666

FRIOR APPLICATION NUMBER: PCT/US01/00666

FRIOR APPLICATION NUMBER: PCT/US01/00669

FRIOR PLING DATE: 2001-01-30

FRIOR FLING DATE: 2001-01-30

FRIOR PLING DATE: 2001-01-30

FRIOR APPLICATION NUMBER: PCT/US01/00669

FRIOR APPLICATION NUMBER: PCT/US01/00669
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     Gaps
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
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CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.4%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 7.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels
     1; Indels
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/09350206
Patent No. US20020099199A1
GENERAL INFORMATION:
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                                                     1992 CACCTTCAAGCAGCTG 2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ACCATCAAGCAGCTGG 16
                                                                                                       2 CACCATCAAGCAGCTG 17
  15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7997
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     Matches
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Gaps
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1 Sequence 395, Application US/09969373

1 Sequence 395, Application US/09969373

2 Patent No. US20020133852A1

3 Patent No. US20020133852A1

3 Patent No. US2002013385A1

3 APPLICANT: Hauge, Brian M.

3 APPLICANT: Hauge, Brian M.

3 TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping File REFERENCE: 38-10(5.5679) A

3 CURRENT APPLICATION NUMBER: US/09/969,373

5 CURRENT PILING DATE: 2001-10-02

7 PRIOR PILING DATE: 2001-01-05

7 PRIOR FILING DATE: 2001-01-13

7 PRIOR PILING DATE: 2001-01-13
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Pred. No. 7.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                 APPLICATION NUMBER: PCT/US99/23089
                                                   APPLICATION NUMBER: PCT/US99/28214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 229, Application US/09909088B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GCTGTCCACAGGGGAG 18
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Best Local Similarity 93.8%;
Matches 15; Conservative
                             LING DATE: 1999-10-05
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ORGANISM: Glycine max
US-09-969-373-3935
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US-09-909-088B-229
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PPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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REFERENCE/DOCKET NUMBER: 5493-50032/DJE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 10.90-14
CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: ECT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-18
PRIOR PLILING DATE: 1999-09-18
PRIOR PLILING DATE: 1999-09-18
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
                                                                                                                                                                                                                                  TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-892-325-6
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 229, Application US/09909320 Patent No. US20020132240A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Godowski, Paul J.
Grimaldi, Christopher J.
                        TELECOMMUNICATION INFORMATION TELEPHONE: (503) 226-739
                                                                         TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3106 GGCGGAGAGTTTTAAT 3121
                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GrcGGAGAGTTTTAAT 17
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gao, Wei-Qiang
Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicholas F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kljavin, Ivar J.
Mather, Jennie P.
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Hillan, Kenneth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL NY.
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLE REFERENCE: 10466-14
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Paoni, Nich
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                       ;
0
                                                                                            Length 18;
                                                                                                                                                    Indels
                                                                                      Query Match 0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR PAPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PAPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
   ; OTHER INFORMATION: oligonucleotide probe US-09-909-088B-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
FILLING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-27
APPLICATION NUMBER: PCT/US99/28313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 229, Application US/09905291A Patent No. US20020160374A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
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tewart, Timothy A.
umas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E
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Pan, James
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Botstein, David
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Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Genentech, Inc
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Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard, A.
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ACIGGS ENCOLATING LIES SCHEENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/909,088B

CURRENT FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: DCT/USO9/0414

PRIOR FILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                              Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Stewart, Timothy A.
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan, James
Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                          Gerber, Hanspeter
Gerritsen, Mary B
                                                    APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Betstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                  Gao, Wei-Qiang
Patent No. US20020146709A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumas. Daniel
                                                                                                                                                                                                                                                                                                                                                                                        Goddard, A.
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Gaps
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Patent No. US20020168708A1

GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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0.4%; Score 14.4; DB 1; Length 18;
illarity 93.8%; Pred. No. 7.7e+02;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICALLO...

PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/09/042,780
FILING DATE:
APPLICATION NUMBER: US 08/985,090
FILING DATE: 04-DEC-1997
ATTORNEY, AGENT INFORMATION:
NAME: Blizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REGISTRATION NUMBER: 33,505
FEFERENCE/DOCKET NUMBER: MNI-032CF
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                3658 GCCTGCAGGGCCATGG 3673
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INPORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Baton, David
APPLICANT: Baton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic aci
                              Best_Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                             JS-09-166-334-24
                Query Match
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                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Oligonucleotide probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/09349755
Patent No. US20020166131A1
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
APPLICANT INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
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COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IDM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/349,755

FILING DATE: OB-Jul-1999

CLASSIFICATION NUMBER: US/09/042,780

FILING DATE: CURROWN

APPLICATION NUMBER: US/09/042,780

FILING DATE: OB-DC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Elizabeth A. Hanley

REGISTRATION NUMBER: 33,505

REGISTRATION NUMBER: 33,505

TELERCOMMUNICATION NUMBER: MI-032CP

TELERCOMMUNICATION NUMBER: MI-032CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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STREET: 28 State Street
           PRIOR APPLICATION NUMBER: FLICT.
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SQ ID NO 229
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MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-349-755-24
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INFORMATION FOR SEQ ID NO: 24:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT PILING DATE: 2001-07-17
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-2
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/2094
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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PRIOR FILING DATE: 1999-11-29
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PRIOR FILING DATE: 1999-11-30
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APPLICATION NUMBER: PCT/US99/30911
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                                                                                                         Sequence 229, Application US/09907824 Publication No. US20020197671A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      Godowski, Paul J.
Grimaldi, Christopher J.
3 GCTGTCCACAGGGAG 18
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                                                                                                                        Godowski, Paul J.
Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
                                                                        Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
                                                          Wei-Qiang
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FILING DATE: 1999-12-20 APPLICATION NUMBER: PCT/US99/30999 FILING DATE: 1999-12-20

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Gaps

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APPLICANT: Williams, Wickey
APPLICANT: William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
                                                                                                                                                                                                                                     CTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Oligonucleotide probe
US-09-907-841-229
                                                                                                                                                                                                                                                                                                                                            Query Match
0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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PRIOR PILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/USO0/04114
PRIOR PILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
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US-09-904-011-229
IS-09-904-011-229
; Sequence 229, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                    , OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-907-824-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PELING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
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CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11-20
             PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 229, Application US/09907841 Publication No. US20020198366A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerbor, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Stewart, Timothy A.
Tumas, Daniel
                                                                                                                          LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
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Paoni, Nicholas F.
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Mather, Jennie P.
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APPLICANT: Abkenazi, Avi
APPLICANT: Bottefin, David
APPLICANT: Beton, Dar Luc
APPLICANT: Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                           FEATURE:
, OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-903-640-229
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CURRENT APPLICATION NUMBER: US/09/908,093
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PRIOR DATE: 1999-07-07
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PRIOR DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
    PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Godowski, Paul J.
Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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Eaton, Dan L.
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REPRENCE: 10466-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-904-011-229
CURRENT APPLICATION NUMBER: US/09/903,640 CURRENT FILING DATE: 2001-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 229, Application US/09903640 Publication No. US20030017463A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
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Best Local Similarity 93.8
Matches 15; Conservative
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US-09-903-640-229
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PRIOR PELLING DATE: 1999-07-07
PRIOR PELLING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PILLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-09-18
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR PELLING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-15
PRIOR PLING DATE: 1999-10-29
PRIOR PLING DATE: 1999-10-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PCT/US00/04414
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Publication No. US20
GENERAL INFORMATION
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PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-908-093-229
       PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23189
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
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CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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ilvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth,
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Mather, Jennie P.
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, OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-906-742-229
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR PELING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-18
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR PELICATION NUMBER: PCT/US99/28564

PRIOR PELING DATE: 1990-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR PLING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-16

PRIOR PILING DATE: 1999-12-16

PRIOR PILING DATE: 1999-12-20

PRIOR PILIN
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
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Grimaldi, Christopher J.
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Mather, Jennie P.
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Hillan, Kenneth,
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                                                                                                                                                                                                                                                                       APPLICANY: Williams, Daniel
APPLICANY: Williams, Daniel
APPLICANY: Williams, D. Mickey
APPLICANY: Williams, D. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-00-16
PRIOR APPLICATION NUMBER: D606/0411
PRIOR FILING DATE: 2008-00-18
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PRIUNG DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-15
PRIOR PLING DATE: 1999-07-15
PRIOR PLING DATE: 1999-07-15
PRIOR PRIUGE DATE: 1999-10-10
PRIOR PRIUGE DATE: 1999-11-29
PRIOR PRIUGE DATE: 1999-11-29
PRIOR PRIUGE DATE: 1999-11-29
PRIOR PRIUGE DATE: 1999-11-29
PRIOR PRIUGE PRIUGE: POPPLICATION NUMBER: PCT/US99/1099
PRIOR PRIUGE DATE: 1999-12-00
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Stewart, Timothy A.
Tumas, Daniel
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                                                                                                                                   Nicholas F.
Kljavin, Ivar J.
Mather, Jennie P
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Oligonucleotide probe

US-09-907-613-229 .
. Sequence 229, Application US/09907613 ; Publication No. US20030027145A1 ; GENERAL INFORMATION:

TYPE: DNA ORGANISM: Artificial Sequence FEATURE:

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Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Oligonucleotide probe
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
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PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PELLOGATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
                         PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION WHRBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US99/30911
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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PRIOR APPLICATION NUMBER: 09/665,350
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Sequence 229, Application US/09904859
Publication No. US20030036060A1
GENERAL INFORMATION:
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and
TITLE OF INVENTION: Acids Encod
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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                               Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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Publication No. US20030027146A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goo, Wei-Qiang
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: oligonucleotide probe
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                                                      CURRENT PILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: DCT/USO0/04414
PRIOR PILING DATE: 2000-02-27
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
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5. US20030036094A1
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gerritsen, Mary E.
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Best Local Similarity, 93.8°
Matches 15; Conservative
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Botstein, David
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Gao, Wei-Qiang
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Publication No. US2(
GENERAL INFORMATION
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                  PRIOR PLINING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PLINING DATE: 1999-09-15
PRIOR PLINING DATE: 1999-09-15
PRIOR PLINING DATE: 1999-00-15
PRIOR PLINING DATE: 1999-10-05
PRIOR PLINING DATE: 1999-11-29
PRIOR PLINING DATE: 1999-11-29
PRIOR PLINING DATE: 1999-11-20
PRIOR PLINING DATE: 1999-11-20
PRIOR PLINING DATE: 1999-12-02
PRIOR PRILING DATE: 1999-12-02
PRIOR PLINING DATE: 1999-12-02
PRIOR PLINING DATE: 1999-12-02
PRIOR PLINING DATE: 1999-12-02
PRIOR PLINING DATE: 1999-12-06
PRIOR PLINING DATE: 2000-01-05
FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
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Publication No. US20030036061A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Glang
Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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ORGANISM: Artificial Sequence
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Mather, Jennie P
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,786
CURRENT FILING DATE: 2001-07-12
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Pred. No. 7.7e+02;
0; Mismatches 1;
                     Application US/09904786
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PRIOR FILING DATE: 2000-00-10
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Grimaldi, Christopher J.
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Stewart, Timothy A
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ORGANISM: Artificial Sequence
PEATURE:
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Best Local Similarity 93.8%;
Matches 15; Conservative
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Publication No. US20030039971A1
GENERAL INFORMATION:
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Gerritsen, Mary B
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Mather, Jennie P.
Pan, James
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Eaton, Dan L.
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                                                                                                                  : Genentech, Inc.
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SEQ ID NO 229
LENGTH: 18
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URRENT APPLICATION NUMBER: US/09/904,820
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APPLICATION NUMBER: PCT/US00/04414
FILING DATE: 2000-02-22
APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
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APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/28565
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APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US99/30999
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FILING DATE: 2000-01-05
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APPLICATION NUMBER: PCT/US99/20944
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PLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/28564
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APPLICATION NUMBER: US 60/146,222
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APPLICATION NUMBER: 09/665,350
                           Christopher J.
                                                                                                                                                                                                                                                                                                                           Williams, P. Mickey Wood, William, I.
                                                       Gurney, Austin L.
Hillan, Kenneth, J.
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ORGANISM: Artificial Sequence
                                                                                                               Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy I
Tumas, Daniel
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Godowski, Paul J
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Best Local Similarity 93.8
Matches 15; Conservative
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Godowski, Paul J. Grimaldi, Christopher J. errara, Napoleone Gerritsen, Mary E. Goddard, A. Gerber, Hanspeter ilvaroff, Ellen ong, Sherman

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HILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IILE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/906,700

CURRENT FILING DATE: 2000-09-18

PRIOR PELICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1090-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594
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FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
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PRIOR APPLICATION NUMBER: PCT/USO0/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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PRIOR APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/21547
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FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Mather, Jennie P.
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                                                                                                                                                                                                                                    Wei-Qiang
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ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide probe
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PRIOR APPLICATION NUMBER: US 60/145,048
PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PELING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-18
PRIOR PLING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PELING DATE: 1999-10-15
PRIOR PELING DATE: 1999-10-15
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-03
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APPLICATION NUMBER: PCT/US00/04414
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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SEQ ID NO 229
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APPLICANT:
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TYPE: DNA

GRANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide probe

US-09-906-700-229 ; Sequence 229, Application US/09906700 ; Publication No. US20030039972A1

RESULT 1151

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-903-786-229
             PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-20
PRIOR PELLOR DATE: 1999-12-20
PRIOR PELLOR DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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PRIOR APPLICATION NUMBER: PCT/USO/04414
PRIOR PILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 229, Application US/09902903
Publication No. US20030044839A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Desnoyers, Luc
APPLICANT: Besteein, David
APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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APPLICANT:
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                                      0.4%; Score 14.4; DB 1; Length 18; ilarity 93.8%; Pred. No. 7.7e+02; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/09/903,786
CURRENT FILING DATE: 2001-07-11
PRIOR PELICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PRICATION NUMBER: US 60/145,698
PRIOR PRICATION NUMBER: US 60/145,698
PRIOR PRICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PRILING DATE: 1999-07-28
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
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PPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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PAPLICKATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
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                                                                                                                                                                                                                                                                              Sequence 229, Application US/09903786 Publication No. US20030044793A1 GENERAL INFORMATION: APPLICANT: Genentech, Inc.
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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ilvaroff, Ellen
ong, Sherman
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Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goddard, A.
                                          Query Match
Best Local Similarity
Matches 15; Conserv
US-09-906-700-229
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) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: oligonucleotide probe US-09-903-749A-229
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Acids Encoding the Same
                                                            CURRENT AFFILMS DATE: 2001-07-11
PRIOR APPLICATION NUMBER: PT/US00/04414
PRIOR PILING DATE: 2000-02-2
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-13-03
                                            CURRENT APPLICATION NUMBER: US/09/903,749A CURRENT FILING DATE: 2001-07-11
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5. US20030049621A1
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Filvaroff, Ellen
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APPLICANT: Genentech, Inc., APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
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Best Local Similarity 93.8
Matches 15; Conservative
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Gao, Wei-Qiang
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Publication No.
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                                  US-09-903-749A-229; Application US/09903749A; Publication No. US20030045693A1; GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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ORGANISM: Artificial Sequence
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Gerritsen, Mary E.
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Paoni, Nicholas F.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Beton, Dan L.
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RESULT 1156
US-09-904-956-229
Sequence 229, Application US/09904956
; Publication No. US20030049622A1
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Grimaldi, Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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Eaton, Dan L.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ACIDS ENCOLLING LIE SAME
CURRENT APPLICATION NUMBER: US/09/904,119
CURRENT FILING BATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-07
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
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1101 GCTGTCCTCAGGGGAG 1116

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APPLICANT: Williams, Daniel,
APPLICANT: Williams, Daniel,
APPLICANT: Williams, I.
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION WINGER: US/09/904,956
CURRENT APPLICATION WINGER: US/06/143,048
PRIOR APPLICATION WINGER: US/06/143,048
PRIOR APPLICATION WINGER: US/06/145,208
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-18
PRIOR PELING DATE: 1999-07-18
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PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-12
PRIOR APPLICATION WINBER: PCT/US99/2019
PRIOR PILING DATE: 1999-11-20
PRIOR APPLICATION WINBER: PCT/US99/2019
PRIOR PILING DATE: 1999-11-20
PRIOR APPLICATION WINBER: PCT/US99/2019
PRIOR PILING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-30
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
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CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PULING DATE: 1999-07-07
PRIOR PULING DATE: 1999-07-07
                                        PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 18
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Paoni, Nicholas F.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,736
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04114
PRIOR PILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR FILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21090
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                                                ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: oligonucleotide probe
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                                                                                                                                            0.4%; Score 14.4; DB 1; Length 18; 93.8%; Pred. No. 7.7e+02; tive 0; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
ORGANISM: Artificial Sequence FEATURE:
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Gerritsen, Mary E.
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Paoni, Nicholas F.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Matches 15, Conservative
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File Reference: 10466-14 CURRENT APPLICATION NUMBER: US/09/903,943 CURRENT FILING DATE: 2001-07-11
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                                                                                                                                                                                                    CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 99/665,350
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 1900-07-22
PRIOR PLING DATE: 1999-07-07
PRIOR FLING DATE: 1999-07-06
PRIOR FLING DATE: 1999-07-26
PRIOR FLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-09-09
PRIOR PLING DATE: 1999-09-03
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PRIOR FILING DATE: 2000-01-05
WUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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FILING DATE: 1999-10-05
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
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PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-
PRIOR APPLICATION NUMBER: PCT/US99/28565
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APPLICATION NUMBER: PCT/US99/23089
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o. US20030054351A1
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Stewart, Timothy A.
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ORGANISM: Artificial Sequence
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Desnoyers, Luc
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Publication No. US20
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-907-794-229
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-01-15
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR PRIOR PLING DATE: 1999-12-20
PRIOR PRIOR DATE: 1999-12-20
                        ION NUMBER: US 60/146,222
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Publication No. US20030054349A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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ORGANISM: Artificial Sequence
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Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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FILING DATE: 1999-07-26
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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RRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: US 60/143,048
RRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
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CURRENT APPLICATION NUMBER: US/09/907,925
CURRENT FILING DATE: 2001-07-17
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PELLICATION NUMBER: PCT/US99/20944
FILLING DATE: 1999-09-13
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APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/21090
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PRIOR FILING DATE: 1999-11-29
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Publication No. US20030054352A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
                       1101 GCTGTCCTCAGGGGAG 1116
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
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Gerritsen, Mary E
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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Gao, Wei-Qiang
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/904,462

CURRENT PILLING DATE: 2001-07-13

PRIOR PLING DATE: 2000-09-18

PRIOR PLING DATE: 2000-09-18

PRIOR PLING DATE: 2000-09-18

PRIOR PLING DATE: 2000-02-22

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-15

PRIOR PLING DATE: 1999-10-15

PRIOR PLING DATE: 1999-11-30

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-07

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 1999-12-20
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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ORGANISM: Artificial Sequence
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Stewart, Timothy A
Ferrara, Napoleone
Filvaroff, Ellen
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                                                                                                              Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                   Wei-Qiang
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
                                          PRIOR FILING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28113
PRIOR APPLICATION NUMBER: PCT/US99/28113
PRIOR PILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NOWER OF SEQ ID NOS: 423
SEQ ID NO 229
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PRIOR APPLICATION NUMBER: 09/665,350
APPLICATION NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 229, Application US/09903520 Publication No. US20030054401A1 GENERAL INFORMATION:
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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PLICANT: Tumas, Daniel
PLICANT: Tumas, Daniel
PLICANT: Williams, P. Mickey
PLICANT: Wood, William, I.
PLICANT: Wood, William, I.
TIE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TIE OF INVENTION: Acids Encoding the Same
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-907-925-229
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PRIOR PILING DATE: 1209-02-22
PRIOR PILING DATE: 1299-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1299-07-26
PRIOR PILING DATE: 1299-07-26
PRIOR PILING DATE: 1299-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
  PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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Publication No. US20030054400A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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ilvaroff, Ellen
                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth,
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Wood, William, 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same PLICATION NUMBER: US/09/905.056

CURRENT FILING DATE: 2000-02-22

PRIOR PELING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-09-08

PRIOR PELING DATE: 1999-09-08

PRIOR PELING DATE: 1999-09-01

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-29

PRIOR PELING DATE: 1999-10-30

PRIOR PELING DATE: 1999-10
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
CHER INFORMATION: Oligonucleotide probe
19.09-905-056-229
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; Sequence 229, Application US/09909064
; Publication No. US20030059772A1
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Stewart, Timothy A.
Tumas, Daniel
Hillan, Kenneth, J.
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                                                                                                                                             aoni, Nicholas F.
                                          lljavin, Ivar J.
Iather, Jennie P.
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SEQ ID NO 229
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                                                         PRIOR PILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-02
                                  LICATION NUMBER: PCT/US00/04414
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Grimaldi, Christopher J.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Forgy, Sherman
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ORGANISM: Artificial Sequence
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Gerber, Hanspeter
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SEQ ID NO 229
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RESULT 1166
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PPLICANT: Stewart, Timothy A.
PPLICANT: Tunas, Daniel
PPLICANT: Williams, P. Mickey
PPLICANT: Williams, P. Mickey
PPLICANT: Wood, William, I.
TILE OF INVENTION: Secreted and Transmembrane Polypeptiges and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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CRGANISM: Artificial Sequence
FEATURE:
CHER INFORMATION: Description of Artificial Sequence: Synthetic
CTHER INFORMATION: oligonucleotide probe
US-09-909-064-229
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CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT PELIGNE DATE: 2001-07-18
PRIOR PPLICATION NUMBER: PCT/USOO/04414
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-18
PRIOR PELING DATE: 1999-09-19
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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ilvaroff, Ellen
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Ashkenazi, Avi
Botstein, David
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ao, Wei-Qiang
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APPLICANT: Tumas, Dannel, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBNCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,553
CURRENT FILING DATE: 2000-02-22
PRIOR PILING DATE: 2000-02-22
PRIOR PAPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
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Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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PRIOR APPLICATION NUMBER: PCT/US99/21547
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                                                                                                                                                                                                                                                                                                                    sequence 229, Application US/09904553; Publication No. US20030059828A1
FENERAL INFORMATION: APPLICANT: Genentech, Inc.
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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ilvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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TANT: Williams, P. Mickey
TANT: Wood, William, I.
OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-905-381-229
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TITLE OF INVENTION: Acids Encoding the Same
                                | PRIOR APPLICATION NUMBER: PCT/US99/21090
| PRIOR PLING DATE: 1999-09-15
| PRIOR FILING DATE: 1999-09-15
| PRIOR FLING DATE: 1999-0-15
| PRIOR FLING DATE: 1999-10-05
| PRIOR PLING DATE: 1999-10-05
| PRIOR APPLICATION NUMBER: PCT/US99/28313
| PRIOR PLING DATE: 1999-11-29
| PRIOR PLING DATE: 1999-11-30
| PRIOR PLING DATE: 1999-11-30
| PRIOR PLING DATE: 1999-12-02
| PRIOR PLING DATE: 1999-12-03
| PRIOR PLING DATE: 1999-12-04
| PRIOR PLING DATE: 1999-12-05
| PRIOR PLING DATE: 1999-12-06
| PRIOR PLING DATE: 1999-12-16
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Grimaldi, Christopher J.
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerritsen, Mary B
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide probe
US-09-904-553-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/09/905,381
CURRENT FILING DATE: 2001-07-13
PRIOR PELICATION NUMBER: 09/665,350
PRIOR PLING DATE: 2000-09-18
PRIOR PELICATION NUMBER: PCT/US00/04414
PRIOR PLING DATE: 2000-02-2
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
             PRIOR FILING DALL.
PRIOR APPLICATION NUMBER: PCI/USS//
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
APPLICATION NUMBER: PCT/US99/30911
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APPLICATION NUMBER: PCT/US99/20944
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Glang
Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
FILE SPECIATION NUMBER: US/09/05,348
CURRENT PALICATION NUMBER: US/09/05,348
CURRENT PALICATION NUMBER: PCT/US00/04114
PRIOR FLILING DATE: 1090-07-07
PRIOR PLILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-09-18
PRIOR PLILING DATE: 1999-10-10
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-11-05
PRIOR PLILING
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                      Godowski, Paul J.
Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
                                                                                        Gurney, Austin L.
Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ścierczeczeczecze 18
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APPLICANT:
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FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: 05/66.350

CURRENT FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: 09/665.350

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-12-07

PRIOR PRIOR FILING DATE: 1999-12-07

PRIOR PRIOR FILING DATE: 1999-12-07

PRIOR PRIOR FILING DATE: 1999-12-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1101 GCTGTCCTCAGGGGAG 1116
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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US-09-905-348-229
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                          0.4%; Score 14.4; DB 1; Length 18; 93.8%; Pred. No. 7.7e+02; tive 0; Mismatches 1; Indels
                                                   FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-905-088-229
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PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR PLILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PILING DATE: 1999-09-13
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FILING DATE: 1999-09-15
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FILING DATE: 1999-11-29
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FILING DATE: 1999-11-30
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APPLICATION NUMBER: PCT/US99/28564
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Publication No. US20030073079A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
TYPE: DNA
ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                          Query Match 0.4
Best Local Similarity 93.8
Matches 15; Conservative
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Gao, Wei-Qiang
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APPLICANT:
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PPLICANT: Stewart, Timothy A.
PPLICANT: Stewart, Timothy A.
PPLICANT: Tunas, Daniel
PPLICANT: Williams, P. Mickey
PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-07-12
PRIOR PILING DATE: 2001-07-12
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
                           Application US/09905088
5. US20030073077A1
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Paoni, Nicholas F
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Mather, Jennie P.
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Botstein, David
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Eaton, Dan L.
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APPLICANT: KOY, MAIGGATEL AND
APPLICANT: Stewart, Timothy A.
APPLICANT: Tames, Daniel
APPLICANT: Twas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,759
CURRENT PILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PRILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PRILING DATE: 1999-07-26
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                                                                   Score 14.4; DB 1; Length 18;
Pred. No. 7.7e+02;
0; Mismatches 1; Indels
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/28564
FILLING DATE: 1999-12-02
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FILING DATE: 1999-12-02
; OTHER INFORMATION; Oligonuclectide probe US-09-905-075-229
                                                                                                                                                                                                                                                                                                                                                 Sequence 229, Application US/09902759
Publication No. US20030077654A1
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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aoni, Nicholas F.
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                                                                        Ouery Match 0.4%;
Best Local Similarity 93.8%;
Matches 15; Conservative
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Mather, Jennie P.
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Eaton, Dan L.
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERRORS: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,075
CURRENT FILING DATE: 2001-07-13
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                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic CTHER INFORMATION: oligonucleotide probe US-09-907-575-229
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               PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION WUMBER: PCT/US99/28565
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PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-0
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 18
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Publication No. US20030077583A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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NUMBER OF SEQ ID NOS: 423
LENGTH: 18
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TYPE: DNA
ORGANISM: Artificial Sequence
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Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
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ORGANISM: Artificial Sequence
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Bettein, David
APPLICANT: Desnoyers, Iuc
APPLICANT: Baton, Dan L.
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Tumas, Daniel
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                         PRIOR APPLICATION NUMBER: PCT/US99/2134/
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/2854
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-04
PRIOR PILING DATE: 1999-12-05
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1900-01-05
NUMBER OF SEQ ID NOS: 423
                                                 FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
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5. US20030082541A1
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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NPLICANT: Ashkenazi, Avi
NPLICANT: Botstein, David
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Eaton, Dan L.
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Publication No. US20
GENERAL INFORMATION:
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FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/665,350
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
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CTHER INFORMATION: Description of Artificial Sequence: Synthetic
CTHER INFORMATION: Oligonuclectide probe
US-09-902-759-229
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                                            PRIOR APPLICATION NUMBER: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PAPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 18
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT EPLING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US/09/907,979
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonuclectide probe
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR PILING DATE: 2001-07-17
PRIOR PLING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-18
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PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-15
PRIOR PAPLICATION NUMBER: PCT/US99/2094
PRIOR PILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PAPLICATION NUMBER: PCT/US99/2091
PRIOR PLING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28309
PRIOR PLING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/30091
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30091
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-03
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
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ORGANISM: Artificial Sequence
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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CTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-902-713-229
PILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,713
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-22
PRIOR PLICATION NUMBER: US 60/145,048
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PRIOR DATE: 1999-10-05
PRIOR PRIOR DATE: 1999-11-29
PRIOR PRIOR DATE: 1999-11-29
PRIOR PRIOR DATE: 1999-11-29
PRIOR PRILICATION NUMBER: PCT/US99/20564
PRIOR PRILICATION NUMBER: PCT/US99/20564
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PRILICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-06
PRIOR PRILICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-06
PRIOR PRILICATION NUMBER: PCT/US99/30095
PRIOR PRILICATION NUMBER: PCT/US99/30099
PRIOR PLING DATE: 1999-12-06
PRIOR PRILICATION NUMBER: PCT/US99/30099
PRIOR PLING DATE: 1999-12-20
PRIOR PPELICATION NUMBER: PCT/US99/30099
PRIOR PLING DATE: 1999-12-20
PRIOR PPELICATION NUMBER: PCT/US99/30099
PRIOR PERIOR PRILICATION NUMBER: PCT/US99/30099
PRIOR PERIOR DATE: 1999-12-20
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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i Sequence 229, Application US/09907979
i Publication No. US20030082542A1
general information:
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERBENCS: 10466-14
CURRENT APPLICATION NUMBER: US/09/903,925
CURRENT FILING DATE: 2001-07-11
PRIOR PIPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR PLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-903-925-229
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PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PRILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 18
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PRIOR APPLICATION NUMBER: PCT/US99/20944
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PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-10-05
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PRIOR FILING DATE: 1999-11-29
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APPLICATION NUMBER: PCT/US99/20594
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PRIOR FILING DATE: 1999-07-07
PRIOR PLICATION UNMBER: US 60/145,698
PRIOR PLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PLICATION NUMBER: PCT/US99/20594
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US-09-906-760A-229
; Sequence 229, Application US/09906760A
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Jumas, Daniel
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                         ljavin, Ivar J.
ather, Jennie P.
                                                                                                Nicholas F
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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CURRENT FILING DATE: 2001-12-14
Application US/09902615 or US20030092002A1
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Grimaldi, Christopher J.
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Publication No. US20030096233A1
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Grimaldi, Christopher J.
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
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ORGANISM: Artificial Sequence
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ilvaroff, Ellen
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Filvaroff, Ellen
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Hillan, Kenneth, J
Kljavin, Ivar J.
Mather, Jennie P.
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Gao, Wei-Qiang
Gerber, Hanspeter
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Paoni, Nicholas F
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Botstein, David
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Eaton, Dan L.
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                                             GENERAL INFORMATION
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PLING DATE: 1999-09-13
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CURRENT APPLICATION NUMBER: US/09/903,823
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
; OTHER INFORMATION: oligonucleotide probe US-09-906-760A-229
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-11-30
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 229, Application US/09903823
Publication No. US20030104381A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Hillan, Kenneth, J
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Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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Eaton, Dan L.
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PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
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PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PPLICATION NUMBER: PCT/US99/30095
PRIOR PELICATION NUMBER: PCT/US99/30099
PRIOR PLING DATE: 1999-12-06
PRIOR PPLING DATE: 1999-12-06
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CURRENT APPLICATION NUMBER: US/09/906,760A
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                            Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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tewart, Timothy A.
Tumas, Daniel
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ilvaroff, Ellen
ong, Sherman
           tion No. US20030096340A1
INFORMATION:
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Paoni, Nicholas F.
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Gerber, Hanspeter
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Mather, Jennie P.
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and Transmembrane Polypeptides and Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                     PRIOR FILLING DATE: 1999-09-15
PRIOR FILLING DATE: 1999-09-15
PRIOR PILLING DATE: 1999-09-15
PRIOR PILLING DATE: 1999-09-15
PRIOR PILLING DATE: 1999-10-05
PRIOR PILLING DATE: 1999-11-00
PRIOR FILLING DATE: 1999-11-29
PRIOR FILLING DATE: 1999-11-30
PRIOR FILLING DATE: 1999-11-30
PRIOR PILLING DATE: 1999-11-30
PRIOR PILLING DATE: 1999-12-02
PRIOR PILLING DATE: 1999-12-02
PRIOR PILLING DATE: 1999-12-02
PRIOR FILLING DATE: 1999-12-02
PRIOR FILLING DATE: 1999-12-03
PRIOR FILLING DATE: 1999-12-03
PRIOR FILLING DATE: 1999-12-03
PRIOR PILLING DATE: 1999-12-03
PRIOR PILLING DATE: 1999-12-03
PRIOR FILLING DATE: 1999-12-03
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              PCT/US99/21090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 229, Application US/09902572A Publication No. US20030108983A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Williams, P. Mickey
Wood, William, I.
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerritsen, Mary B
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Mather, Jennie P.
Pan, James
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Botstein, David
Desnoyers, Luc
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Gao, Wei-Qiang
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-903-823-229
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CURRENT APPLICATION NUMBER: US/09/907,652
CURRENT FILING DATE: 2002-01-16
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1099-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 229, Application US/09907652
Publication No. US20030104469A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerritsen, Mary E
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Mather, Jennie P.
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Gao, Wei-Qiang
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US-09-907-652-229
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic Oligonucleotide Probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 229, Application US/09905125 Publication No. US20030113719A1 GENERAL INFORMATION:
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Ferrara, Napoleone
Filvaroff, Ellen
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Best Local Similarity 93.83
Matches 15; Conservative
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Botstein, David
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US-09-905-125-229
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US-09-902-572A-229
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                                    FILE REFERENT APPLICATION NUMBER: US/09/902,572A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 1099-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-01-15
PRIOR PLING DATE: 1999-11-29
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Publication No. US20030113718A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Bllen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Wood, William, I.
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Tumas, Daniel
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APPLICANT: Ashkenzi, Avi
APPLICANT: Botstein, David
APPLICANT: Baton, Dan L.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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CURRENT PEDLICATION NUMBER: US/09/906,815A

CURRENT PILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: US/09/906,414

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20949

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/2094

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
                                Sequence 229, Application US/09906815A Publication No. US20030113838A1 GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Grimaldi, Christopher
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Mather, Jennie P.
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Eaton, Dan L.
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APPLICANT: Thumse, Denited
APPLICANT: Thumse, Denited
APPLICANT: Thumse, Denited
APPLICANT: Wood, William, I.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF THE 2000-09-18
CURRENT APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-28
PRIOR PELING DATE: 2000-00-22
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-00-08
PRIOR PELING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: PCT/US99/2031
PRIOR PELING DATE: 1999-10-12
PRIOR PELING DATE: 1999-11-00
PRIOR PELING DATE: 1999-12-00
PRIOR PELING DATE: 1999-10-00-00-00
PRIOR PELING DATE: 1999-10-00-00-00
PRIOR PELING DATE: 1999-10-00-00-00
PRIOR PELING DATE: 1999-10-00-00-00
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Godowski, Paul J.
Grimaldi, Christopher J.
                                                                Gurney, Austin L.
Hillan, Kenneth, J.
Kijavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas P.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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PRIOR APPLICATION NUMBER: PCI/0399/23099
PRIOR PLINING DATE: 1999-10-05
PRIOR PLINING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/0599/28114
PRIOR PLINING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR PLINING DATE: 1999-12-02
PRIOR PLINING DATE: 1999-12-02
PRIOR PLINING DATE: 1999-12-02
PRIOR PLINING DATE: 1999-12-10
PRIOR PLINING DATE: 1999-12-10
PRIOR PLINING DATE: 1999-12-00
PRIOR PLINING DATE: 1999-12-05

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GCTGTCCACAGGGGAG 18

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: 09/665,350
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                     PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PLICATION NUMBER: PCT/US99/30095
PRIOR PLICATION NUMBER: PCT/US99/30911
PRIOR PLICATION NUMBER: PCT/US99/30911
PRIOR PLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PLICATION NUMBER: PCT/US00/00219
PRIOR PLICATION NUMBER: PCT/US00/00219
PRIOR PLICATION NUMBER: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 229, Application US/09903806
Publication No. US20030130489A1
GENERAL INFORMATION:
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Godowski, Paul J.
Grimaldi, Christopher J.
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Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
FEATURE:
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Filvaroff, Ellen
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Gerritsen, Mary E
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Roy, Margaret Ann
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
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PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                Gaps
ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic;
OTHER INFORMATION: oligonucleotide probe
US-09-906-815A-229
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                                                                                                                                                                    Query Match
0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US/09/905,449

CURRENT PELLING DATE: 2000-09-18

REIOR PELLING DATE: 2000-09-18

PRIOR PELLING DATE: 1090-07-22

PRIOR PELLING DATE: 1999-07-07

PRIOR PELLING DATE: 1999-07-07

PRIOR PELLING DATE: 1999-07-28

PRIOR PELLING DATE: 1999-07-28

PRIOR PELLING DATE: 1999-07-28

PRIOR PELLING DATE: 1999-09-08

PRIOR PELLING DATE: 1999-09-13

PRIOR PELLING DATE: 1999-09-15

PRIOR PELLING DATE: 1999-10-15

PRIOR PELLING DATE: 1999-10-15

PRIOR PELLING DATE: 1999-11-29

PRIOR PELLING DATE: 1999-11-29

PRIOR PELLING DATE: 1999-11-30

PRIOR PELLING DATE: 1999-11-30
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
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Paoni, Nicholas F.
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Mather, Jennie P.
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APPLICANT: Abkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
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Pred. No. 7.7e+02;
0; Mismatches 1; Indels
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
                                     PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
              APPLICATION NUMBER: PCT/US99/30095
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5. US20030148370A1
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Grimaldi, Christopher J.
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Tumas, Daniel
                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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Hillan, Kenneth, J
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Gerritsen, Mary E.
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Mather, Jennie P.
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Best Local Similarity 93.83
Matches 15; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Gao, Wei-Qiang
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APPLICANY: Stewart, Timothy A.
APPLICANY: Stewart, Timothy A.
APPLICANY: Stewart, Timothy A.
APPLICANY: Stewart, Timothy A.
APPLICANY: William, P. Mickey
APPLICANY: Wood, William, P. Mickey
APPLICANY: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/904,992
RIOR FILING DATE: 1000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR PELIOR DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US99/21690
PRIOR APPLICATION NUMBER: PCT/US99/21690
PRIOR APPLICATION NUMBER: PCT/US99/21690
PRIOR APPLICATION NUMBER: PCT/US99/21690
PRIOR APPLICATION NUMBER: PCT/US99/2869
PRIOR APPLICATION NUMBER: PCT/US99/2869
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PRIOR APPLICATION NUMBER: PCT/US99/2869
PRIOR APPLICATION NUMBER: PCT/US99/28669
PRIOR APPLICATION NUMBER: PCT/US99/28669
PRIOR APPLICATION NUMBER: PCT/US99/28669
PRIOR PILING DATE: 1999-110-05
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                                                                                        Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-903-806-229
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 229, Application US/09904992
Publication No. US20030135025A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Paoni, Nicholas F.
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Eaton, Dan L.
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Length 18;
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CURRENT PEDLICATION NUMBER: 0200-07-16
CURRENT PELLING DATE: 2000-07-16
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1090-07-2
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-20
PRIOR FILING DATE: 1999-12-00
PRIOR PILING DATE: 1999-12-00
PRIOR FILING DATE: 1999-12-00
PRIOR PILING DATE: 1999-12-00
PRIOR PILING DATE: 1999-12-00
Acids Encoding the Same
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; Publication No. US20030148419A1
; GENERAL INFORMATION:
; APPLICANT: Generhech, Inc.
; APPLICANT: Botterin, David
; APPLICANT: Desnoyers, Luc
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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ORGANISM: Artificial Sequence
FEATURE:
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Eaton, Dan L
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Matches 15; Conserva
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APPLICANT:
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
       PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
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Publication No. US20030148371A1
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Grimaldi, Christopher J.
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Stewart, Timothy A
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Filvaroff, Ellen
Fong, Sherman
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ORGANISM: Artificial Sequence
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Gerber, Hanspeter
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Mather, Jennie P.
Pan, James
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Hillan, Kenneth,
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Eaton, Dan L.
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CURRENT APPLICATION NUMBER: US/09/904,532 PRIOR ADPLICATION DATE: 2001-07-13
                                                       Sequence 229, Application US/09904532
Publication No. US20030152922A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Numas, Daniel
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Filvaroff, Ellen
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Mather, Jennie P.
                                                                                                                                               APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botterin, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Sao, Wei-Qiang
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APPLICAWY: Williams, Daniel
APPLICAWY: Williams, D. Mickey
APPLICAWY: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT PILING DATE: 2001-07-11
PRIOR PELING DATE: 2001-07-11
PRIOR PELING DATE: 1999-07-07-12
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-38
PRIOR PILING DATE: 1999-07-38
PRIOR PILING DATE: 1999-07-18
PRIOR PILING DATE: 1999-07-18
PRIOR PILING DATE: 1999-07-18
PRIOR PILING DATE: 1999-07-18
PRIOR PILING DATE: 1999-10-06
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-
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                                                    Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artíficial Sequence
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Paoni, Nicholas F.
Gerritsen, Mary E.
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Best Local Similarity
Matches 15; Conserva
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same FRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR PRIOR DATE: 1999-12-16

PRIOR PLING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/3091

PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 1999-12-20

PRIOR PLING DATE: 2000-01-05

WINDBER OF SEQ ID NOS: 423 CURRENT FILING DATE: 2001-07-37

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR PLILING DATE: 2000-02-22

PRIOR PLLING DATE: 1900-02-22

PRIOR PLLING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

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PRIOR APPLICATION NUMBER: PCT/US99/28564
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PPLICANT: Tumas, Daniel
PPLICANT: Williams, P. Mickey
PPLICANT: Wood, William, I.
TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
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                                                                                                                   Query Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                ; OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-904-532-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/904,766
CURRENT FILING DATE: 2001-07-12
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RIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
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                                                                                                                                                                                                                                                                                                Sequence 229, Application US/09904766 Publication No. US20030152999A1 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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ilvaroff, Ellen
                           TYPE: DNA
ORGANISM: Artificial Sequence
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Beton, Dan L.
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           LENGIH: 18
                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
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Pred. No. 7.7e+02;
0; Mismatches 1;
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CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-05
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LEDITH: 18
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Wood, William, I.
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 gererecacacadas 18
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Best Local Similarity 93.8%;
Matches 15; Conservative
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Gerritsen, Mary E
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Mather, Jennie P.
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Botstein, David
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Eaton, Dan L.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,877A
CURRENT APPLICATION NUMBER: US/09/904,877A
CURRENT APPLICATION NUMBER: US/01/43,048
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 2000-02-08-08
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-18
PRIOR PLING DATE: 1999-07-18
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-15
PRIOR PLING DATE: 1999-10-15
PRIOR PLING DATE: 1999-10-15
PRIOR PLING DATE: 1999-11-29
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; Sequence 229, Application US/09903562
; Publication No. US20030187238A1
; GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Gerber, Hanspeter
Gerritsen, Mary E.
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ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Paoni, Nicholas F
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICANT:
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                                                            PRIOR APPLICATION NUMBER: PCT/US99/2039, PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-13

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-30

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-04

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 1999-12-07

PRIOR PLING DATE: 1999-12-07
APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
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; Sequence 229, Application US/09904877A
; Publication No. US20030186358A1
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wel-Ciang
Gerber, Hanspeter
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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SEQ ID NO 229
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APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,618
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PCT/US00/04414
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PRIOR PELLING DATE: 2000-02-22
PRIOR PELLING DATE: 1999-07-06
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-18
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: PCT/US99/21040
PRIOR PELLING DATE: 1999-10-29
PRIOR PELLING DATE: 1999-11-30
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-20
PRIOR PELLING DATE: 1999-11-20
PRIOR PELLING DATE: 1999-12-06
PRIOR PELLING DATE: 1999-12-02
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
                                                                                                                                                                                                     Godowski, Paul J.
Grimaldi, Christopher J.
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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ORGANISM: Artificial Sequence
FEATURE:
                                    Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Roy, Margaret Ann
Filvaroff, Ellen
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                                        APPLICANT: SUBJECTANT: SUBJECTANT: SUBJECTANT: SUBJECTANT: SUBJECTANT: THOUGH A APPLICANT: THOUGH A APPLICANT: THOUGH A APPLICANT: THIRSE, DATIO, SUBJECTANT: WAILIAME, P. MICKEY APPLICANT: THIRSE, DATIO: MILLIAME, P. MICKEY APPLICANTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICANTON NUMBER: US/09/66.350
PRIOR PELINKO DATE: 1000-09-18
PRIOR APPLICATION NUMBER: US/09/66.350
PRIOR APPLICATION NUMBER: US/09/66.350
PRIOR APPLICATION NUMBER: US/09/66.350
PRIOR APPLICATION NUMBER: US/09/66.350
PRIOR APPLICATION NUMBER: PCT/US9/2094
PRIOR APPLICATION NUMBER: PCT/US9/2094
PRIOR APPLICATION NUMBER: PCT/US9/2094
PRIOR APPLICATION NUMBER: PCT/US9/2094
PRIOR PLINKO DATE: 1939-09-13
PRIOR PLINKO DATE: 1939-10-12
PRIOR PLINKO DATE: 1939-10-12
PRIOR APPLICATION NUMBER: PCT/US9/2094
PRIOR APPLICATION NUMBER: PCT/US9/2099
PRIOR APPLICATION NUMBER: PCT/US9/2099
PRIOR APPLICATION NUMBER: PCT/US9/2099
PRIOR PRINKO DATE: 1939-10-20
PRIOR APPLICATION NUMBER: PCT/US9/3099
PRIOR PRINKO DATE: 1939-10-20
PRIOR PRILING DATE: 1939-12-20
PRIOR PRILICATION NUMBER: PCT/US9/30999
PRIOR PLICATION NUMBER: PCT/US9/30999
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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Sequence 229, Application US/09906618
Publication No. US20030190610A1
GENERAL INFORMATION:
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                  Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Ferrara, Napoleone

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/907,728

CURRENT APPLICATION NUMBER: US/09/907,728

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: US/05/350

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-07
                                                                                                                                                                                                    Sequence 229, Application US/09907728
Publication No. US20030190611A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Destean, David
APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
3 GCTGTCCACAGGGGAG 18
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Filvaroff, Ellen
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Gerritsen, Mary E
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APPLICANT: Pan, James
APPLICANT: Pan, Vicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,805
CURRENT PILING DATE: 2001-09-18
FRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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                                                                                                                                                                FEATURE:
, OTHER INFORMATION: Synthetic Oligonucleotide Probe US-09-907-728-229
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER 00 SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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Publication No. US20030211568A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
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                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity 93.8
Matches 15; Conservative
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Eaton, Dan L.
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APPLICATION NUMBER: US 60/143,048
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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// OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-805-229
                                              FRIOR FILING DATE: 1999-10-05

PRIOR PELICATION NUMBER: PCT/US99/28214

PRIOR PELICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-20

PRIOR PILING DATE: 1999-12-30

PRIOR PILING DATE: 1999-12-30
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   APPLICATION NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 229, Application US/09904938A Publication No. US20030211569A1
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Godowski, Paul J.
Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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ilvaroff, Ellen
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Hillan, Kenneth, J
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICANT
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PRIOR PILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
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Grimaldi, Christopher J.
Gurney, Austin L.
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ORGANISM: Artificial Sequence
PEATURE:
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Filvaroff, Ellen
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Gerritsen, Mary E
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Kljavin, Ivar J.
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Matches 15; Conservative
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Botstein, David
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Gao, Wei-Qiang
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APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT PALLICATION NUMBER: US/09/08,576
CURRENT PILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PC7/US00/0414
PRIOR PILING DATE: 1090-00-05
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-06
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DAT
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COTHER INFORMATION: Description of Artificial Sequence: Synthetic;
COTHER INFORMATION: Oligonucleotide probe
7. OTHER 1876-229
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Grimaldi, Christopher
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Artificial Sequence
                                                                                                                    Ferrara, Napoleone
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Mather, Jennie P.
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APPLICANT: Tunas, Daniel
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/906,722A
CURRENT FILING DATE: 2001-07-16
PRIOR PELICATION NUMBER: US/09/906,722A
CURRENT FILING DATE: 2000-02-27
PRIOR PELING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-03
PRIOR FI
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                                                                                                                              Roy, Margaret Ann
Mather, Jennie P.
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Gaps
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Ouery Match 0.4%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 7.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                   ; Sequence 24, Application US/10282958
; Publication No. US20030110519A1
                                                                                              1101 GCTGTCCTCAGGGGAG 1116
                                                                                                                                         GCTGTCCACAGGGGAG 18
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                           RESULT 1203
US-10-282-958-24
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Gaps

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1101 GCTGTCCTCAGGGGAG 1116

ò a Sequence 229, Application US/09908576
Publication No. US20040005553A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi

US-09-908-576-229

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APPLICANT: KOY, MAIGATE AND
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
FILE REFRENCE: P1618P2C85
CURRENT FILING DATE: 2002-11-18
FRIOR APPLICATION NUMBER: US 60/143,048
FRIOR FILING DATE: 1999-07-07
FRIOR FILING DATE: 1999-07-07
FRIOR FILING DATE: 1999-07-28
FRIOR FILING DATE: 1999-07-28
FRIOR FILING DATE: 1999-07-28
FRIOR FILING DATE: 1999-09-13
FRIOR FILING DATE: 1999-09-13
FRIOR FILING DATE: 1999-09-13
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-10-05
FRIOR FILING DATE: 1999-10-05
FRIOR FILING DATE: 1999-10-05
FRIOR FILING DATE: 1999-10-05
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 229, Application US/10299937
Publication No. US20030185846A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dererecacadedad 18
                                                                                                                                  Nicholas F.
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Gerritsen, Mary E.
                                                      lather, Jennie P.
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Botstein, David
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Eaton, Dan L.
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                            COUNTER: USA

COUNTER READABLE FORM:

MEDIUM TYPER: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/282,958

FILING DATE: 28-Oct-2002

CLASSIFICATION: CUNKNOWN>

PRIOR APPLICATION: CUNKNOWN>

PRILING DATE: 08-Jul-1999

APPLICATION NUMBER: US/09/042,780

FILING DATE: 08-Jul-1999

APPLICATION NUMBER: US/09/042,780

FILING DATE: CUNKNOWN

ATTORNEY/AGENT INFORMATION:

NAME: Elizabeth A: Hanley

REGISTRATION NUMBER: 33,505

REFERENCE/DOCKET NUMBER: MNI-032CP

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION FOR SEQ. OF TELECOMMUNICATION:

TELECOMMUNICATION FOR SEQ. OF TELECOMMUNICATION FOR SEQ.
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-282-958-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 229, Application US/10299976
Publication No. US20030180312A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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                                                                                                                                                                                                                                                       CITY: Boston
STATE: Massachusetts
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Filvaroff, Ellen
Fong, Sherman
Gao, Mei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Best Local Similarity 93.83
Matches 15; Conservative
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US-10-299-976-229
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                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 7.7e+02;
0; Mismatches 1; Indels
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PRIOR PEDICATION NUMBER: PCT/USO/04414
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 1000-00-02-02
PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-8
PRIOR PELING DATE: 1999-07-8
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20949
PRIOR APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/298,993
CURRENT FILING DATE: 2002-11-18
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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FILING DATE: 1999-09-15
                                            PRIOR FILING DATE: 1995-07-07
PRIOR PAPLICATION NUMBER: US 09/038,073
PRIOR FILING DATE: 1998-03-11
NUMBER OF SEQ ID NOS: 2285
SEQ ID NO 1134
LENGTH: 18
FILING DATE: 1996-01-12
APPLICATION NUMBER: US 60/000,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/10298993
o. US20030211576A1
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Grimaldi, Christopher
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Stewart, Timothy A.
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Kljavin, Ivar J.
Mather, Jennie P.
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Best Local Similarity 93.8%;
Matches 15; Conservative
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerber, Hanspeter
Gerritsen, Mary E
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                                                                                                                                                                                                                                                                CRGANISM: Mus musculus US-10-440-850-1134
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                                                                                                                                                                                                                                          TYPE: RNA
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Publication No. US20030207837A1

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: MSCANGGEN, Jim
ITILE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Rever
                                                                                                                                                                                                                                       APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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SEQ ID NO 229
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: oligonucleotide probe
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                                                                                                                                                                                                                                                                                                                                           THE REPERENCE: 1961892086

CURRENT APPLICATION NUMBER: US/10/299, 937

CURRENT PILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: PCT/USOO/04414

PRIOR FILING DATE: 2000-02-2

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146, 222

PRIOR PELING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15
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THE REFERENCE: 250/130 (MRHBOD-900-A)
CURRENT APPLICATION NUMBER: US/10/440,850
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: US/9/650,012
PRIOR PILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 08/585,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
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                           Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                                                                                       Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGTCCACAGGGAG 18
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Stewart, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 93.88
Matches 15; Conservative
                                                                                                                                                                                                                      Tumas, Daniel
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PCT/US99/21547

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FEATURE:
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
FILE REFERENCE: 10466-14
FILE REPERENCE: 10466-14
FRICH RELING DATE: 2003-05-29
FRICH FILING DATE: 2000-02-22
FRICH FILING DATE: 1999-07-07
FRICH FILING DATE: 1999-07-07
FRICH FILING DATE: 1999-07-06
FRICH FILING DATE: 1999-07-26
FRICH FILING DATE: 1999-07-28
FRICH FILING DATE: 1999-09-08
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                       PRIOR FILING DATE: 1999-10-05, PRIOR FILING DATE: 1999-10-05, PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Oligonucleotide probe
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PRIOR APPLICATION NUMBER: PCT/US99/23089
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Publication No. US20030225253A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
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Stewart, Timothy A.
                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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Matches 15; Conservative
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
IIIIE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IIIIE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 1;
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CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCIVUS99/20594
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APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
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Publication No. US20040005665A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Eaton, Dan L.
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1101 GCTGTCCTCAGGGGAG 1116
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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ORGANISM: Artificial Sequence
FEATURE:
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Botstein, David
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Eaton, Dan L.
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APPLICANT: Generach, Avi
APPLICANT: Botstein, Davi
APPLICANT: Desnoyers, Luc
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Matches 15; Conserv
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US-10-425-447-229
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APPLICANT:
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                               PRIOR APPLICATION NUMBER: PCT/US99/2154/
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
REMAINING PATE: 1999-11-29
REMAINING PATE: 423
SEQ ID NO 229
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CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: PT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/21090
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Wood, William, I.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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                  LING DATE: 1999-09-15
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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TITLE OF INVENTION: HUMAN OBESITY LIPIN3 POLYNUCLEOTIDE AND
TITLE OF INVENTION: HOLYPEPTIDE SEQUENCES AND METHODS OF USE THEREOF
FILE REFERENCE: 220002064100
CURRENT APPLICATION WUMBER: US/10/206,618
CURRENT FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 18
                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
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PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PLING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
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Publication No. US20040023331A1
GENERAL INFORMATION:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 39780-1618P2C78C1
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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                                          TITLE OF INVENTAGES

TITLE REFERENCE: P16182C83

CURRENT APPLICATION NUMBER: US/10/215,371

CURRENT PILIOR DATE: 2002-08-08

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 1998-09-10

PRIOR PILING DATE: 1997-10-17

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 229
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CURRENT FILING DATE: 2004-02-02
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PRIOR APPLICATION NUMBER: 09/909,064
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04114
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Grimaldi, Christopher
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desnoyers, Luc
Baton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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APPLICANT: Tumas, Daniel

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT PILING DATE: 2003-04-28

REIOR APPLICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 229
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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; Sequence 229, Application US/10215371
; Publication No. US20040137561A1
                                                          Godowski, Paul J.
Grimaldi, Christopher J.
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                                                                                                                                                                                                                                                                                                                     Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                              Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                      Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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   Gerritsen, Mary E.
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APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin I
APPLICANT: Hillan, Kenneth I
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Wood, William I
Yuan, Jean
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US-10-251-117-712
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APPLICANT: Egeland, Janice A.
APPLICANT: Belland, Janice A.
APPLICANT: Ball. Steven
APPLICANT: Paul. Steven
APPLICANT: The Government of the United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Susceptibility and Resistance Genes for
TITLE OF INVENTION: Bipolar Affective Disorder
FILE REFERENCE: 015280-24811005
CURRENT APPLICATION NUMBER: US/09/881,012
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US/09/175,158
PRIOR APPLICATION NUMBER: US 60/062,924
PRIOR FILING DATE: 1997-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.4%; Score 14.4; DB 1; Length 18; ilarity 93.8%; Pred. No. 7.7e+02; Conservative 0; Mismatches 1; Indels
                                            PRIOR FILING DATE: 1998-09-17
PRIOR PELING DATE: 1998-09-17
PRIOR PELING DATE: 1998-09-16
PRIOR PILING DATE: 1998-09-16
PRIOR PILING DATE: 1998-06-04
PRIOR PILING DATE: 1999-06-04
PRIOR PILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/066,770
PRIOR APPLICATION NUMBER: 60/065,186
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
SEQ ID NO 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 240
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 230
LENGTH: 19
FILING DATE: 2000-02-22
APPLICATION NUMBER: PCT/US98/19437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 230, Application US/09881012
Publication No. US20020192655A1
GENERAL INFORMATION:
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; Publication No. US20030013669A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: UT1585 primer US-09-881-012-230
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                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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hes 15; Conserva
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US-09-754-066-6/c
                                                                                                                                                                                                                                                                                                                                    LENGTH: 18
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Matches
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                                    METHOD OF TREATING HIV INFECTION AND RELATED SECONDARY INFECTIONS THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 14.4; DB 1; Length 19; 93.8%; Pred. No. 8.1e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ_for Windows Version 2.0
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/754,066
FILING DATE: 05-Jan-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/848,013
APPLICATION NUMBER: 07/830,886
FILING DATE: 2001-05-07
APPLICATION NUMBER: 07/830,886
FILING DATE: 04-FEB-1992
APPLICATION NUMBER: 07/84,277
FILING DATE: 21-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 02939.04541 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                       ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
GENERAL INFORMATION:
APPLICANT: BURCOGLU, ARSINUR
TITLE OF INVENTION: METHOD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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LENGTH: 19 base pairs
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                                                                                                                                                                                             ZIP: 20001
COMPUTER READABLE FORM:
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                         NUMBER OF SEQUENCES:
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r:
US-10-244-647-370
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APPLICANT: Ribozyme Pharmaceutical, Inc.

APPLICANT: Ribozyme Pharmaceutical, Inc.

APPLICANT: Morrissey, David

APPLICANT: Morrissey, David

APPLICANT: Morrissey, David

APPLICANT: Beigelman, Leonid

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U

TITLE OF INVENTION: BOART: 2003-04-14

FRICH APPLICATION NUMBER: US 60/358,580

PRIOR PILING DATE: 2002-02-0

PRIOR PILING DATE: 2002-07-03

PRIOR PILING DATE: 2002-07-03

PRIOR PILING DATE: 2002-03-26

PRIOR PILING DATE: 2001-06-08

PRIOR PILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 1524

SEQ ID NO 380

LENGTH: 19
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TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA); FILE REFERENCE: 400/060 (MBHB02-1000); CURRENT APPLICATION NUMBER: US/10/244,647; CURRENT FILING DATE: 2003-04-14; PRIOR APPLICATION NUMBER: US 60/358,580; PRIOR FILING DATE: 2002-02-20; PRIOR APPLICATION NUMBER: US 60/393,924; PRIOR PILING DATE: 2002-07-03; PRIOR PILING DATE: 2002-07-03; PRIOR FILING DATE: 2002-07-03; PRIOR FILING DATE: 2002-07-04; PRIOR FILING DATE: 2002-07-05; PRIOR PILING DATE: 2002-07-06; PRIOR FILING DATE: 2001-06-08; NUMBER: US 60/296,876; NUMBER: OF SEQ ID NOS: 1524; SORTWARE: PATENTIN VERSION 3.0; SEQ ID NO 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%; Score 14.4; DB 1; Length 19; 62.5%; Pred. No. 8.1e+02; tive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 14.4; DB 1; Length 19; 62.5%; Pred. No. 8.1e+02; tive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 380, Application US/10244647; Publication No. US20030206887A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 62.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 370, Application US/10244647
Publication No. US20030206887A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: Moswigaph, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
                                                                                                                                                                                                                                                     Target sequence/siNA sense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region US-10-251-117-1019
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                                                                                                                                                                                                                        FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-10-251-117-712
            PRIOR FILING DATE: 2001-07-25
PRIOR PEDICATION NUMBER: US 60/296,249
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 1213
SECTWARE: Patentin version 3.0
SEQ ID NO 712
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1019, Application US/10251117
Publication No. US20030170891A1
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                                                                                                                                                                            TYPE: RNA
ORGANISM: Artificial Sequence
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Best Local Similarity 93.8
Matches 15; Conservative
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US-10-251-117-1019/c
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Gaps

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GARKEAL INFORMATION:

APPLICANT: Ribozyme Pharmaceutical, Inc.

APPLICANT: Ribozyme Pharmaceutical, Inc.

APPLICANT: Mozriggen, James

APPLICANT: Mozriggen, James

APPLICANT: Mozriggen, James

APPLICANT: Beigelman, Leonid

TITLE OF INVENTION: RNA Interfering Nucleic Acid (siNA)

TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)

TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)

TITLE OF INVENTION WHBER: US/10/244,647

CURRENT APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR PILING DATE: 2002-07-03

PRIOR PELING DATE: 2002-07-03

PRIOR PELING DATE: 2002-03-26

PRIOR PILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 1524

SEQ ID NOS: 1524

SEQ ID NOS: 1524

SEQ ID NOS: 1524

SEQ ID NOS: 1524
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; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-244-647-1016
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Pred. No. 8.1e+02;
0; Mismatches 1; Indels
Best Local Similarity 62.5%; Pred. No. 8.1e+02; Matches 10; Conservative 5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1016, Application US/10244647; Publication No. US20030206887A1; GENERAL INFORMATION:
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; Sequence 1026, Application US/10244647
; Publication No. US20030206887A1
                                                                                                                            2776 TTCCGGAAACTAGTGT 2791
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Best Local Similarity 93.8
Matches 15; Conservative
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US-10-244-647-1016/c
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APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: McSuiggen, Javid
APPLICANT: McSuiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)
TITLE OF INVENTION NUMBER: US 60/358,580
PRIOR PILING DATE: 2002-02-26
PRIOR PILING DATE: 2002-03-26
PRIOR FILING DATE: 2002-03-26
PRIOR FILING DATE: 2002-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
LENGTH: 19
                                                                                                                                                 APPLICANT: Nicoration:
APPLICANT: Morrissey, David
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: SEADOR Interfering Nucleic Acid (sinA)
FILE REFERENCE: 400/060 (MBHB02-1000)
CURRENT PILING DATE: 2003-04-14
FRIOR FILING DATE: 2002-02-20
FRIOR FILING DATE: 2002-02-20
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2002-03-26
FRIOR FILING DATE: 2001-06-08
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0.4%; Score 14.4; DB 1;
Best Local Similarity 62.5%; Pred. No. 8.1e+02;
Matches 10; Conservative 5; Mismatches 1;
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Sequence 415, Application US/10244647
Publication No. US20030206887A1
                                     Application US/10244647
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APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrisey, David
APPLICANT: Morrisey, David
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)
FILE OF INVENTION: Short Interfering Nucleic Acid (siNA)
FILE OF INVENTION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/359,580
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR PELING DATE: 2002-07-03
PRIOR PELING DATE: 2002-03-26
PRIOR FILING DATE: 2002-03-26
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-06-08
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Length 19; 1; Indels

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, OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r US-10-665-951-1042
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US-10-244-647-1061
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0.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 1;
               PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR PILING DATE: 2002-03-26
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR APPLICATION NUMBER: US 60/296,876
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: Patentin version 3.0
SEQ ID NO 1061
LENGTH: 19
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; Sequence 1057, Application US/10244647
; Publication No. U52003206887AI
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: McSviggen, James
APPLICANTON: Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/606 (MEHBOZ-1000)
CURRENT FILING DATE: 2003-04-14
PRIOR PLILING DATE: 2003-04-14
PRIOR PLILING DATE: 2002-07-03
PRIOR PLILING DATE: 2002-07-03
PRIOR PLILING DATE: 2002-05-26
PRIOR FILING DATE: 2002-05-26
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SSC ID NO 1057
LENGTH: 19
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Sequence 1061, Application US/10244647

Sequence 1061, Application US/10244647

Sequence 1061, Application US/10244647

Sequence 1061, Application US/10244647

GENERAL INFORMATION:

APPLICANT: Rosaviggen, James

APPLICANT: McSwiggen, James

APPLICANT: Beigelman, Leonid

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)

TITLE OF INVENTION: Short Interference Mediated Inhibition of Hepatitis B Virus (HBV)

TITLE REFERENCE: 400/060 (WBHB02-1000)

CURRENT APPLICATION NUMBER: US/10/244,647

CURRENT FILING DATE: 2000-04-14
                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region US-10-244-647-1026
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0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                       2776 TTCCGGAAACTAGTGT 2791
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                                         TYPE: RNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-244-647-1057/c
SEQ ID NO 1026
                                                                                 FEATURE:
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TYPE: RNA
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APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: McSwiggen, James

APPLICANT: Beigelman, Leonid

TITLE OF INVENTION: Growth Factor and Vascular Endothelial

TITLE OF INVENTION WINBER: US /10/665,951

CURRENT PAPLICATION WINBER: US /0/665,951

CURRENT PAPLICATION WINBER: US /0/399,348

PRIOR FILING DATE: 2003-09-18

PRIOR FILING DATE: 2003-07-29

PRIOR FILING DATE: 2002-07-03

PRIOR FILING DATE: 2002-07-03

PRIOR PAPLICATION WINBER: US /0/399,348

PRIOR PELICATION WINBER: US /0/399,49

PRIOR FILING DATE: 2002-11-04

PRIOR FILING DATE: 2002-01-10-07

PRIOR PELICATION WINBER: PCT/US 02/17674

PRIOR FILING DATE: 2002-02-20

PRIOR FILING DATE: 2002-02-20

PRIOR FILING DATE: 2002-02-20

PRIOR FILING DATE: 2002-02-20

PRIOR PELICATION WINBER: PCT/US 06/389,580

PRIOR PELICATION WINBER: US 60/389,782

PRIOR PELICATION WINBER: US 60/386,782

PRIOR PELICATION WINBER: US 60/386,782
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Publication No. US20040138163A1
GENERAL INFORMATION
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Beigelman, James
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
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                                         Indels
Best Local Similarity 81.2%; Pred. No. 8.1e+02; Matches 13; Conservative 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1366, Application US/10665951; Publication No. US20040138163A1; GENERAL INFORMATION:
                                                                                                                1609 AAGTGCATCCACAGGG 1624
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US-10-665-951-1366/c
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N: Methods for Detecting, Grading or Monitoring an H. pylori Infec
EXT-048
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                                                                                                               Query Match 0.4%; Score 14.4; DB 1; Length 19; Best Local Similarity 93.8%; Pred. No. 8.1e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gallaches, Brian
APPLICANT: Salmons, Brian
APPLICANT: Salmons, Brian
APPLICANT: Gallar, Sabine
APPLICANT: Klein, Dieter
ITLE OF INVENTION: Targeted Integration Into Chromosomes
ITLE OF INVENTION: Using Retroviral Vectors
FILE REFERENCE: 2316.2005-000
CURRENT APPLICATION NUMBER: US/09/752,110A
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: PCT/EP99/04521
PRIOR APPLICATION NUMBER: PA 1998 01016
PRIOR APPLICATION NUMBER: PA 1998 01016
PRIOR FILING DATE: 1998-07-01
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.4%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 8.5e+02; tive 0; Mismatches 1; Indels
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Pred. No. 8.5e+02;
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Patent No. US20020110810A1
GENERAL INFORMATION:
PAPPLICANT: Shuber, Anthony
TITLE OF INVENTION: Methods for Detecting,
FILE REPRENCE: EXT-048
CURRENT APPLICATION NUMBER: US/09/755,004
CURRENT FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
LENGTH: 20
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial sequence
                      TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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; OTHER INFORMATION: APC forward primer
US-09-755-004-10
                                                                                                                                                                                                                                                                                                                                                       US-09-752-110A-20/c
; Sequence 20, Application US/09752110A
; Patent No. US20010043921A1
                                                                                                                                                                                                                2814 TGTATATGGTATATT 2829
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: PCR Primer US-09-752-110A-20
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Matches 15; Conservative
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Best Local Similarity
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US-09-755-004-10/c
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US-10-768-089-6
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                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region US-10-665-951-1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
            PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-03-11
PRIOR PILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
SOFTWARE: ParentIn version 3.2
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10768089
Publication No. US20040138167A1
GENERAL INFORMATION:
APPLICANT: BURCOGLU, ARSINUR
TITLE OF INVENTION:
AND RELATED SECONDARY INFECTION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.4%; Score 14.4; DB 1; Length 19; Best Local Similarity 93.8%; Pred. No. 8.1e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
CORRUTTR: IBM Compatible
CORRUTTR: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/768,089
FILING DATE: 02-Feb-2004
CLASSIFICATION NUMBER: US/09/754,066
FILING DATE: 05-Jan-2001
APPLICATION NUMBER: 08/848,013
FILING DATE: 05-Jan-2001
APPLICATION NUMBER: 07/830,886
FILING DATE: 04-FEB-1992
APPLICATION NUMBER: 07/48,277
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REPERENCE/DOCKET NUMBER: 02939.04541
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1998 CAAGCAGCTGGTGGAG 2013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202-508-9299
                                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS
FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 CAAGAAGCTGGTGGAG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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US-10-768-089-6/c
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; OTHER INFORMATION: Antisense Oligonucleotide US-09-920-671-14
                                                                                                                                                                                      ; Sequence 389, Application US/09232785; Publication No. US20030049612A1
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; Sequence 88, Application US/09967669
; Publication No. US20030092650A1
; GENERAL INFORMATION:
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                      1060 GCGTCCATGAGCTCCA 1075
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                                                  5 GCATCCATGAGCTCCA 20
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Best Local Similarity 93.8%;
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
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                                                                                                                                                                    US-09-232-785-389/c
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| Sequence 17, Application US/09774809
| Publication No. US20030004120A1
| GENERAL INFORMATION:
| APPLICANT: MoKAY, Robert A. |
| APPLICANT: Dean, Nicholas M. |
| APPLICANT: Mero, Brett A. |
| TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS |
| TITLE OF INVENTION: MOTHER: US/09/774,809 |
| CURRENT APPLICATION NUMBER: 09/196,902 |
| PRIOR FILING DATE: 1998-09-15 |
| PRIOR FILING DATE: 1998-09-15 |
| PRIOR FILING DATE: 1999-09-15 |
| PRIOR FILING DATE: 1999-08-07 |
| PRIOR FILING DATE: 1999-08-07 |
| SEQ ID NO 17 |
| LENGTH: 20 |
| LENGTH: 20 |
  Gaps
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WESOUR 1234

WESOUR 1234

Sequence 3262, Application US/09969373

Patent No. US2002013382A1

GENERAL INFORMATION:

APPLICANT: Effertz, Roger J.

APPLICANT: Effertz, Roger J.

APPLICANT: Bauge, Brian M.

IILE OF INVENTION: Soybean SSRB and Methods of Genotyping FILE REPERENCE: 38-10(52679)A

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR PLING DATE: 2001-01-13

NUMBER OF SEQ ID NOS: 4593

LENGTH: 20
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  1; Indels
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2338 TGTGTGTGTGTGCA 2353
                                                856 GAGGAGCTGGTGGAGG 871
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15; Conservative
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; ORGANISM: Glycine max
US-09-969-373-3262
  Matches
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; Sequence 14, Application US/09920671
; Publication No. US2001083283A1
; GENERAL INFORMATION:
; APPLICANT; C. Frank Bennett
; APPLICANT; C. Frank Bennett
; APPLICANT; C. STRANK BENNET
; TITLE OF INVENTION: ANTISENSE MODULATION OF COREST EXPRESSION
; FILE REPERENCE: RTS-0297
; CURRENT APPLICATION NUMBER: US/09/920,671
; CURRENT FILING DATE: 2001-08-01
; SEQ ID NOS: 91
; SEQ ID NO 14
; LENGTH: 20
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GENERAL INFORMATION:
APPLICANT: International Paper Co.
APPLICANT: Echt, Craig. S
APPLICANT: Echt, Craig. S
APPLICANT: Becht, Craig. S
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: MICROSATELITE DNA MARKERS AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
THERE REFERENCE: 4481/1E188US1
CURRENT FILING DATE: 1999-01-13
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 397
SOFUTANE: FastSEQ for Windows Version 3.0
SEQ ID NO 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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Pred. No. 8.5e+02;
0; Mismatches 1;
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Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1;
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Sequence 12, Application US/10374932
; Sequence 12, Application US/10374932
; Publication No. US20030235S86A1
; GENERAL INFORMATION:
; APPLICANT: van Dijk, Marcus Antonius
APPLICANT: van Dijk, Marcus Antonius
APPLICANT: Schuurman, Janine
APPLICANT: Schuurman, Jorgen
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Baadsgaard, Ole
; TITLE REPERENCE: GMI-024CP
; CURRENT FILING DATE: 2003-02-26
; CURRENT FILING DATE: 2001-08-23
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 10/226615
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 31
; NUMBER OF SEQ ID NOS: 31
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               CURRENT PELLING DATE: 2002-10-25
PRIOR PELLING DATE: 2002-10-25
PRIOR PELLING DATE: 2002-10-25
PRIOR FILING DATE: 2001-10-25
PRIOR FILING DATE: 2001-11-08
PRIOR PLING DATE: 2001-11-08
PRIOR PLING DATE: 2001-11-08
PRIOR PLING DATE: 2001-11-08
PRIOR PELLING DATE: 2001-11-08
PRIOR PELLING DATE: 2001-11-09
PRIOR PELLING DATE: 2001-11-09
PRIOR PELLING DATE: 2001-11-09
PRIOR PELLING DATE: 2001-12-04
PRIOR PELLING DATE: 2001-12-04
PRIOR PELLING DATE: 2001-12-04
PRIOR PELLING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR PELLING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 564
SOFTWARE: PERSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 363
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Primer US-10-282-174-363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens
US-10-374-932-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-345-444B-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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TITLE OF INVENTION: ALTSENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION FILE REFERENCE: RTS-0259
CURRENT APPLICATION NUMBER: US/09/967,669
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 90
LENGTH: 20
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| Sequence 38, Application US/10090011
| Publication No. US2030082810A1
| Publication No. US2030082810A1
| GENERAL INFORMATION:
| APPLICANT: Serup, Palle
| APPLICANT: Gradwohl Gerard
| TITLE OF INVENTION: Methods For Generating Insulin-Secreting
| TITLE OF INVENTION: Cells Suitable for Transplantation
| FILE REFERENCE: 6246-2200-US
| CURRENT APPLICATION NUMBER: US/10/090,011
| CURRENT FILING DATE: 2002-02-26
| PRIOR PILING DATE: 2001-02-26
| PRIOR FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-967-669-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 363, Application US/10282174
Publication No. US20030224380A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3007 TIGITITAAAACTGGA 3022
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                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Homo Sapien
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LENGTH: 20
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Sequence 1, Application US/10425037

Publication No. US20040054162A1

Publication No. US20040054162A1

GENERAL INFORMATION:

APPLICANY: Hanna, Midchelle M.

TITLE OF INVENTION: Synthesis

TITLE OF INVENTION: Synthesis

TITLE OF INVENTION: Synthesis

FILE REPERENCE: 2072.0010006

FILE REPERENCE: 2072.0010006

FILE REPERENCE: 2003-04-29

FRIOR FILING DATE: 2003-10-29

FRIOR FILING DATE: 2002-10-29

FRIOR FILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PARENTIN VERSION 3.2
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; Sequence 65, Application US/10380124;
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: 18is Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Preier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REPERENCE: RTS-0156
; CURRENT PILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 65
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Antisense Oligonucleotide US-10-380-124-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/10379741
; Publication No. US20040071702A1
; Publication No. US20040071702A1
; APPLICANT: van de Winkel, Jan G.J.
; APPLICANT: van Dijk, Marcus Antonius
; APPLICANT: Schuurman, Janine
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Petersen, Jorgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: P16DF2 Primer US-10-425-037-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1209 TGGGGAGGCTGCTTC 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2407 CTGGGTGTCCCCGCTG 2422
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ORGANISM: Artificial
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Sequence 18, Application US/10264958B
Sequence 18, Application US/20441
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Hoffman, Hal
APPLICANT: Kolodner, Richard
TITLE OF INVENTION: Thered Cryopyrins, Nucleic Acid Molecules Encoding These, and I
TITLE OF INVENTION: Thered Cryopyrins, Nucleic Acid Molecules Encoding These, and I
TITLE OF INVENTION: Thered Cryopyrins, Nucleic Acid Molecules Encoding These, and I
TITLE OF INVENTION: Thered: 2046 (10209575)
CURRENT FILING DATE: 2002-10-04
FRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 18
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.4%; Score 14.4; DB 1; Length 20; 93.8%; Pred. No. 8.5e+02; ive 0; Mismatches 1; Indels
                                                          GENEKAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Monia, Brett
APPLICANT: Gaarde, William A.
ITLE OF INVENTION: OF UNK PROTEINS
FILE REPERENCE: ISPH-0726
CURRENT APPLICATION NUMBER: US/10/345,444B
CURRENT APPLICATION NUMBER: US 09/395,404B
PRIOR APPLICATION NUMBER: US 09/396,902
PRIOR APPLICATION NUMBER: US 09/396,902
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: US 09/306,616
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: US 09/130,616
PRIOR FILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-07
PRIOR PILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 17
LENGTH: 20
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ORGANISM: Artificial Sequence
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                   Publication No. US20040029823A1
GENERAL INFORMATION:
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Best Local Similarity 93.8<sup>†</sup>
Matches 15; Conservative
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US-10-380-124-65/c
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US-10-264-958B-18
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                                                                                              Conservative
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                                               Query Match
Best Local Similarity
Matches 15; Conserv
           US-10-303-266-130
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TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (1L-15) FILE REPERENCE: GMI-024CP2
CURRENT APPLICATION NUMBER: US/10/379,741
CURRENT FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: US 60/314,731
PRIOR PILING DATE: 2001-08-23
PRIOR PILING DATE: 2001-08-23
PRIOR PILING DATE: 2002-08-23
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 54, Application US/10303266

Sequence 54, Application Wollo101848A1

GENERAL INFORMATION:

APPLICANT: Donna T. Ward

APPLICANT: Donna T. Ward

APPLICANT: Remeth W. Dobie

TITLE OF INVENTION: WODULATION OF GLUCOSE TRANSPORTER-4 EXPRESSION

FILE REPERBNCE: RTS-0426

CURRENT APPLICATION NUMBER: US/10/303,266

CURRENT PILING DATE: 2002-11-23

WUMBER OF SEQ ID NOS: 157

LENGTH: 20
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US-10-203-266-130
US-10-203-266-130
Sequence 130, Application US/10303266
Publication No. US20040101848A1
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Alexander H. Borchers
APPLICANT: Kenneth W. Doble
TITLE OF INVENTION: MODILATION OF GLUCOSE TRANSPORTER-4 EXPRESSION
FILE REFERENCE: RTS-0426
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                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 14.4; DB 1; Length 20;
illarity 75.0%; Pred. No. 8.5e+02;
Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Score 14.4; DB 1; Length 20; Best Local Similarity 93.8%; Pred. No. 8.5e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Antisense Oligonucleotide US-10-303-266-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/303,266
CURRENT FILING DATE: 2002-11-23
NUMBER OF SEQ ID NOS: 157
SEQ ID NO 130
LENGTH: 20
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                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
US-10-379-741-12
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                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-303-266-54/c
                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                 Query Match
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  Length 20;
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                                           Indels
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Sequence 155, Application US/10316243

Publication No. US20040110147A1

GENERAL INFORMATION:

APPLICANT: Ravi Jain

TITLE REFERENCE: RTS-0462

CURRENT APPLICATION NUMBER: US/10/316,243

CURRENT FILING DATE: 2002-12-09

NUMBER OF SEQ ID NOS: 168

SEQ ID NO 155

LENGTH: 20
                                                                                                                                                                                                                 US-10-316-243-82
; Sequence 82, Application US/10316243
; Publication No. US20040110147A1
; Publication No. US20040110147A1
; GENERAL INCORMATION:
; APPLICANT: Renneth W. Dobie
; APPLICANT: Ravi Jain
; TITLE OF INVENTION: MODULATION OF BAF53 EXPRESSION
; FILE REFERENCE: RTS-0462
; CURRENT APPLICATION NUMBER: US/10/316,243
; CURRENT FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 82
; LENGTH: 20
0.4%; Score 14.4; DB 1;
93.8%; Pred. No. 8.5e+02;
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Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
0.4%; Score 14:4; DB 1;
Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
FEATURE:
1 OTHER INFORMATION: Antisense Oligonucleotide
US-10-316-243-82
                                           Mismatches
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; Sequence 22, Application US/10317279
; Publication No. US20040110703A1
; GENERAL INFORMATION:
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                                                                                      2107 CCCAGCTCCAGCTCCT 2122
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Gaps

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Sequence 1086, Application US/10671395
Publication No. US2004013206341
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Gleres, James K
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
CURRENT APPLICATION UNMERS: US/10/671,395
CURRENT FILING DATE: 2003-09-25
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
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APPLICANT: Baadsgaard, Ole
APPLICANT: Baadsgaard, Ole
APPLICANT: Huang, Haichun
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD20
FILE REFERENCE: GMI-055
CURRENT APPLICATION NUMBER: US/10/687,799
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: US 60/419,163
PRIOR FILING DATE: 2002-10-17
PRIOR FILING DATE: 2002-04-02
NUMBER OF SEQ ID NOSE: 57
SOFTWARE: PSELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
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       93.8%; Pred. No. 8.5e+02;
tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ), OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/10687799
Publication No. US20040167319A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2316 TCTGTGTGTGTGTG 2331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Teeling, Jessica
APPLICANT: Rulls, Sigrid
APPLICANT: Glennie, Martin
APPLICANT: van de Winkel, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                           18 GCTGCAGGTGCTGGA 3
                                                                             53 GGCTGCAGGTGCTGAA
                              15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parren, Paul
Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: artificial
                                                                                                                                                                                                RESULT 1254
US-10-671-395-1086/c
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LENGTH: 20
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LENGTH: 20
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APPLICANT: Ming-Yi Chiang
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF DR1-ASSOCIATED PROTEIN 1 EXPRESSION
FILE REFERENCE: HTS-0027
CURRENT APPLICATION NUMBER: US/10/317,279
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 59
LENGTH: 20
LENGTH: 20
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Sequence 51, Application US/10317279
Sequence 51, Application US/10317279
Sequence 51, Application US/10317279
GENERALI INFORMATION:
APPLICANT: Ming-Yi Chiang
TITLE OF INVENTION: MODULATION OF DR1-ASSOCIATED PROTEIN 1 EXPRESSION
FILE REPRENCE: HTS-0027
CURRENT APPLICATION NUMBER: US/10/317,279
CURRENT FILING DATE: 2002-12-10
WUMBER OF SEQ ID NOS: 59
SEQ ID NO 51
LENGTH: 20
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Fublication No. US20040115640A1
GENERAL INFORMATION:
APPLICANT: Kathleen Wyers
TITLE OF INVENTION: MODULATION OF ANGIOPOIETIN-2 EXPRESSION
FILE REFERENCE: RTS-0454
CURRENT APPLICATION NUMBER: US/10/317,803
CURRENT FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 244
SEQ ID NO 116
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.4%; Score 14.4; DB 1; Length 20; Best Local Similarity 93.8%; Pred. No. 8.5e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                      Length 20;
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O.4%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-317-279-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1545 CTTCAAGGACCTGGTG 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1545 CTTCAAGGACCTGGTG 1560
                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-317-803-116/c
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US-10-317-279-51
                                                                                                                                                                                                                         TYPE: DNA
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FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-11
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ORGANISM: ARTIFICIAL SEQUENCE
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CORGANISM: Homo sapiens
US-10-085-906-147
                                                                                                                              US-10-085-906-147
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PUBLICATION NO. US20030054371A1

GENERAL INFORMATION:

APPLICANT: Wu, Paul

APPLICANT: Wu, Paul

TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: UNMBER: US/10/085,906

CURRENT RAPLICATION NUMBER: US 60/126,215

PRIOR PELING DATE: 1999-03-25

PRIOR PELING DATE: 1999-03-24

PRIOR PELING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 545

SOFTWARER FREEKSQ for Windows Version 4.0

LENGTH: 27
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                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Description of Artificial Sequence; note OTHER INFORMATION: synthetic construct US-10-781-142-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                   3; Indels
Best Local Similarity 75.0%; Pred. No. 8.5e+02; Matches 15; Conservative 2; Mismatches 3
                                                        853 GAGGAGGAGCTGGTGGAGGC 872
                                                                           288 CGICCGCIICCGCIGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 CGTCCGCTTCCGCTAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-085-906-78
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us-uy-725-265-11

j Sequence 11, Application US/09725265

j Sequence 11, Application US/0901000015A1

j Publication No. US2001000015A1

j PublicanT: KURAMGAMA, TAKAHIRO

j APPLICANT: KURAMGAMA, TAKAHIRO

j APPLICANT: YAMAGAMA, TOYOKAZU

j APPLICANT: YAMAGAMA, TOYOKAZU

j APPLICANT: YAMAGAMA, TOYOKAZU

j APPLICANT: YAMAGAMA, OSAMU

j APPLICANT: WOYOMAKU, TOYOKAZU

j APPLICANT: WOYOMAKU, TOYOKAZU

j APPLICANT: WOYOMAKU, TOYOKAZU

j TITLE OF INVENTION: WUCLEIC ACID PROBES FOR THE METHOD FOR ANALYZING DAT:

j TITLE OF INVENTION: WUCLEIC ACID PROBES FOR THE METHOD FOR ANALYZING DAT:

j TITLE OF INVENTION NUMBER: US 09/556,127

j PRIOR APPLICATION NUMBER: US 09/556,127

j PRIOR PILING DATE: 1999-04-20

j PRIOR PILING D
                                                                                                                                                                                                                                                                                                                                            Sequence 147, Application US/10085906

Sequence 147, Application US/10085906

Publication No. US20030054371A1

GENERAL INFORMATION:

APPLICANT: Wing, Vincent

APPLICANT: Wing, Vincent

APPLICANT: Wing, Vincent

APPLICANT: Gray, Gary S.

TITLE OF INVENTION: COSTINULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTINULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTINULATORY RECEPTOR LOCUS

CURRENT APPLICATION NUMBER: US/10/085,906

CURRENT APPLICATION NUMBER: US 60/126,215

PRIOR PILING DATE: 1999-03-25

PRIOR PILING DATE: 1999-03-24

PRIOR APPLICATION NUMBER: BCT/US00/07938

PRIOR APPLICATION NUMBER: PCT/US00/07938

PRIOR APPLICATION NUMBER: PCT/US00/07938

NUMBER OF SEQ ID NOS: 545

SEQ ID NO 147

LEMBER OF SEQ ID NOS: 545

SEQ ID NO 147
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3310 TITITCTITAGGAGATITATTIT 3333
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APPLICANT: KAMAGANA, TAKAHIRO
APPLICANT: KAMAGANA, TAKAHIRO
APPLICANT: KAMAGANA, TAKAHIRO
APPLICANT: KAMAGANA, YOICHI
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOYAMA, OSAMU
APPLICANT: WOYAMA, OSAMU
APPLICANT: WOYAMA, OSAMU
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: HE METHOD
TITLE OF INVENTION: THE METHOD
TITLE OF INVENTION: THE METHOD
TITLE OF INVENTION: THE METHOD
FILE REFERENCE: 0163-0758-0X
CURRENT APPLICATION NUMBER: US/10/683,386
CURRENT FILING DATE: 2000-04-20
FRIOR FILING DATE: 1999-04-20
FRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PARENTIN VERBION 3.1
SEQ ID NO 11
LENGTH: 30
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APPLICANT: Fritz, Brett
APPLICANT: Herrmann, Mark
TITLE OF INVENTION: Real-Time Monitoring of PCR Amplification Using Nanoparticle Prob
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0.4%; Score 14.4; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels
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PRIOR APPLICATION NUMBER: US 09/556,127
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: UP 1999-111601
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SEQ ID NO 11
LENGTH: 30
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Publication No. US20040063137A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     FEATURE:

CTHER INFORMATION: SYNTHETIC DNA

US-10-209-608-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: SYNTHETIC DNA US-10-683-386-11
                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KURANE, RYUICHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-306-630-2/c
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APPLICANT: KURANE, RYUICHIRO
APPLICANT: KANAGAMA, TAKAHIRO
APPLICANT: KANAGAMA, TAKAHIRO
APPLICANT: KANAGAMA, TOGHI
APPLICANT: TORINURA, MASAKI
APPLICANT: TORINURA, SHINYA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
TITLE OF INVENTION: NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
TITLE OF INVENTION: NUCLEIC ACID PROBES, AND METHOD FOR ANALYZING DATA
TITLE OF INVENTION: NUMBER: USO00-193133
PRIOR PLILING DATE: 2000-06-27
PRIOR PLILING DATE: 2000-08-03
PRIOR PLILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PALCATION NUMBER: JESOO-09-26
NUMBER OF SEQ ID NOS: 108
SSEQ ID NO 11
LENGTH: 30
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APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAWA, YOICHI
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: KOYAMA, OSAMU
APPLICANT: FUNUSHO, KENTA
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
TITLE OF INVENTION: THE METHOD
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                                      Query Match 0.4%; Score 14.4; DB 1; Length 30; Best Local Similarity 75.0%; Pred. No. 1.2e+03; Matches 18; Conservative 0; Mismatches 6; Indels
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                                                                                                                                                                    3474 ATATATATATTTATTGAGTTTTT 3497
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PRIOR FILING DATE: 2000-11-29
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; Sequence 11, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09891517
Patent No. US20020106653A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic DNA US-09-891-517-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                     US-09-891-517-11
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Sequence 923, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:
APPLICANT: Hood, Lerry E.
APPLICANT: Rowen, Ler
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
                                                                                                                                                                                                                                                                                                                                                          0.4%; Score 14.2; DB 1; Length 19; 84.2%; Pred. No. 8.7e+02; tive 0; Mismatches 3; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4190, Application US/09969373
; Sequence 4190, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz. Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genu FILER REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US 09/754,853
; CURRENT APPLICATION NUMBER: US 09/754,853
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; RECORDER FILING DATE: 2001-01-13
; RECORDER FILING DATE: 2001-01-13
; SEQ ID NO 4190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 14.2; DB 1;
84.2%; Pred. No. 8.7e+02;
tive 0; Mismatches 3;
                 FRIOR APPLICATION NUMBER: 08/955,841
PRIOR FILING DATE: 1997-10-21
PRIOR PILING DATE: 1997-10-21
PRIOR PILING DATE: 1995-11-19
PRIOR PILING DATE: 1995-11-19
PRIOR FILING DATE: 1995-12-21
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FASELSEQ for Windows Version 4.0
SERGITH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2335 GTGTGTGTGTGTGTGCA 2353
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Best Local Similarity 84.2'
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 84.2
Matches 16, Conservative
                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-548-51
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CORGANISM: Glycine max
US-09-969-373-4190
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STATE: Washing
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                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: APC gene probe mutant
US-10-306-630-2
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Publication No. US20030165917A1
GENERAL INFORMATION:
APPLICANT: ULLMAN, EDWIN
APPLICANT: ULLY YEN PING
TITLE OF INVENTION: ISOTHERWAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
FILE REFERENCE: 3817.05-1
CURRENT FILING DATE: 2002-08-14
PRIOR PILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 34
LENGTH: 39
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65.6%; Pred. No. 1.4e+03;
tive 0; Mismatches 11; Indels
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CURRENT APPLICATION NUMBER: US/09/925,548
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 09/390,425
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3262 TATTTTTTTGTCTTTGTCCTTTTTCAGGAGAA 3293
              CURRENT APPLICATION NUMBER: US/10/306,630
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: US 60/334,644
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin vergion 3.0
SEQ ID NO. 2
LENGTH: 33
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Patent No. US20020107216A1
GENERAL INFORMATION:
APPLICANT: Dedhar, Shoukat
APPLICANT: Hannigan, Greg
APPLICANT: Yee, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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FILE REFERENCE: 01-1747-A
                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial
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Sequence 19, Application US/09835371

Sequence 19, Application US/09835371

Seneral INCORMATION:
Seneral INCORMATION:
APPLICANT: UHLMANN, Eugen
APPLICANT: UHLMANN, Eugen
APPLICANT: WILL, David W
ITILE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES, AND AGENTS AND
TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
FILE REFERENCE: 02401.1743 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/09/835,371
CURRENT FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 19
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Publication No. US20030022172A1

GENERAL INPORMATION:

GENERAL INPORMATION:

APPLICANT: UHLMANN, GERHARD

APPLICANT: WILL, DAVID W

TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND

TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND

TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND

TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND

CURRENT APPLICATION NUMBER: US/09/835,370

CURRENT APPLICATION NUMBER: US/09/835,370

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 19
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                                                                                                                                                                                                                 Gaps
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OTHER INFORMATION: Description of Artificial Sequence: base sequence;
OTHER INFORMATION: of PNA targeting CMV
US-09-835-371-19
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CTHER INFORMATION: Description of Artificial Sequence: nucleotide
CTHER INFORMATION: base sequence of PNA derivatives that bind to
CTHER INFORMATION: viral and cellular targets
US-09-835-370-19
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                                                                                                                                                        0.4%; Score 14.2; DB 1; Length 19;
84.2%; Pred. No. 8.7e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels
TYPE: nucleic acid
STRANDEDRES: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                               184 GGGGAGGACGAGGCTGAGG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 GGGGAGGACGAGGCTGAGG 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                   Best Local Similarity 84.2
Matches 16; Conservative
                                                                                    ;
US-09-860-784-18
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US-09-835-371-19
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US-09-835-370-19
                                                                                                                                                          Query Match
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UHLMANN, Eugen
TITLE OF INVENTION: G CAP-STABILIZED OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
          COMPUTER: BADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 33,963
FELEPAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: 923:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
ITPE: INCORMATION SEQ ID NO: 923:
STRANDEDNESS: single
TOPPOLOGY: linear
US-09-263-959-923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/860,784
FILING DATE: 21-May-2001
CLASSIFTCATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/594,452
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COlin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18748/264/HOCE
TELECOMMUNICATION:
TELEPHONE: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 14.2; DB 1;
84.2%; Pred. No. 8.7e+02;
live 0; Mismatches 3;
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STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2924 GGGGGGTGGGGGGGTGG 2942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/09860784 Patent No. US20020151512A1 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 84.2*
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA US-09-793-146-17
                GENERAL INFORMATION:
APPLICANT: ULIMANN. EUGEN
APPLICANT: HILANDHL, GERHARD
TITLE OF INVENTION: POLYANIDB-OLIGONUCLEOTIDE DERIVATIVES, THEIR
TITLE OF INVENTION: PREPARATION AND USE
FILE REPRENCE: 02481.1437-02.
CURRENT APPLICATION NUMBER: US/09/793,146
CURRENT PILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: P4 08 528.1
PRIOR APPLICATION NUMBER: P4 08 528.1
PRIOR APPLICATION NUMBER: P4 08 528.1
PRIOR FILING DATE: 1994-03-14
PRIOR FILING DATE: 1995-03-13
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.4%; Score 14.2; DB 1; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3;
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Best Local Similarity 84.2%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
  US20030203359A1
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0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
Score 14.2; DB 1; Length 19;
Pred. No. 8.7e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                       Sequence 10. Application US/09880313A
| Publication No. US20030044791A1
| GENERAL INFORMATION:
| APPLICANT: Flemington, Erik K
| TILLE OF INVENTION: Adaptors and Methods of Use
| FILE REFERENCE: 9397/1000
| CURRENT APPLICATION NUMBER: US/09/880,313A
| CURRENT PILING DATE: 2001-06-13
| NUMBER OF SEQ ID NOS: 276
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 47
| LENGTH: 19
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Publication No. US20030104378A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Allwai, Hatim
APPLICANT: Bartholomay, Christian
APPLICANT: Chehak, LuAnne
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS.04944

CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 2640

SEQ ID NOS: 2640

SEQ ID NO 1955

LENGTH: 19
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US-09-793-146-17
; Sequence 17, Application US/09793146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: Oligonucleotide US-09-880-313A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3200 AGCTGGAGGATCCCCTCCA 3218
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    0.4%;
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    Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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US-09-864-636A-1955
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Length 19; Indels

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| Sequence 1955, Application US/09864426A |
| Sequence 1955, Application US/09864426A |
| Publication No. US20040018489A1 |
| GENERAL INFORMATION: |
| APPLICANT: Third Wave Technologies |
| APPLICANT: Lyamichev, Victor |
| APPLICANT: Lyamichev, Victor |
| APPLICANT: Saiser, Michael |
| TITLE OF INVENTION: Braymes for the Detection of RNA Sequences |
| TITLE OF INVENTION: Braymes for the Detection of RNA Sequences |
| TITLE REFERENCE: FORS-04946 |
| CURRENT FILING DATE: 2001-05-24 |
| NUMBER OF SEQ ID NOS: 2640 |
| SEQ ID NO 1955 |
| LENGTH: 19
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Pred. No. 8.7e+02;
0; Mismatches 3; Indels
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17. Application US/10005338B
18. Publication No. US20030044895A1
18. Publication No. US20030044895A1
18. PAPLICANT: DENEFLE, Patrice
18. APPLICANT: ROSIER-MONTUS, Marie-Francoise
18. APPLICANT: RABES, Catherine
18. APPLICANT: ARNOULD-REGUIGNE, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2485 GTGCAGAATGTAAGTGGGC 2503
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1 gegaageaageareage 19
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; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-226-992-24
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US-10-226-992-107
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Publication No. US20030170691A1
GENERAL INFORMATION:
APPLICANT: Gimeno, Ruth
APPLICANT: Wu, Zhidan
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Hubbard, Brian K.
TITLE OF INVENTION: (DGAT2) FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: MP101-265P2RM
                                                                                                                                                                                                                                                                                                                           Length 19;
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Pred. No. 8.7e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                         Ouery Match 0.4%; Score 14.2; DB 1; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3;
FILE REPERENCE: 400/055 (MBHB01-1110-B)
CURRENT APPLICATION NUMBER: US/10/226, 992
CURRENT FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: US 60/315,315
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 184
SOFTWARE: Patentin version 3.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/324,618
CURRENT FILING DATE: 2002-12-19
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Best Local Similarity 73.7%;
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                                                                                                                                                                                                 TYPE: RNA
                                                                                                                                                                             LENGTH:
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                                      APPLICANT: DEAN, Michael
TITLE OF INVENTION: OCCURAINING SUCH HUMAN ABCAS, ABCA6, ABCA9, AND ABCA10 GENES
TITLE OF INVENTION: CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF
FILE REPERBNCE: ABCA5, 6, 9, 10
CURRENT APPLICATION NUMBER: US,10/005,338B
CURRENT FILING DATE: 2001-12-07
PRIOR PAPLICATION NUMBER: US 60/263,231
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PATENTION OF 217
SOFTWARE: ABCA11 Ver. 2.1
LENGTH: 19
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Sequence 24, Application US/10226992
Publication No. US20030148507A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Posnaugh, Kathy
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Prostaglandin D2 Receptor TITLE OF INVENTION: and Prostaglandin D2 Synthetase (PTGDS) Gene Expression Using Sh TITLE OF INVENTION: RNA
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| Publication No. US20030113726A1
| GENERAL INPORMATION:
| APPLICANT: Bristol-Wyers Squibb Company
| TITLE OF INVENTION: HUMAN SINGLE NUCLECTIDE POLYMORPHISMS;
| FILE REFRERENCE: D0053NP
| CURRENT APPLICATION NUMBER: US/10/005,956
| CURRENT FILING DATE: 2001-12-03
| PRIOR APPLICATION NUMBER: 60/251,015
| PRIOR APPLICATION NUMBER: 60/263,678
| PRIOR PILING DATE: 2001-01-23
| PRIOR PILING DATE: 2001-01-33
| PRIOR PILING DATE: 2001-01-33
| PRIOR PILING DATE: 2001-03-02
| NUMBER OF SEQ ID NOS: 1579
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 596
| LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 14.2; DB 1; Length 19; Best Local Similarity .84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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  DUVERGER, Nicolas
ALLIKMETS, Rando
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-005-956-596
                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-005-338B-177
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US-10-005-956-596/c
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US-10-226-992-24/c
  APPLICANT:
APPLICANT:
APPLICANT:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaccuticals, Inc.

APPLICANT: Ribozyme Pharmaccuticals, Inc.

APPLICANT: Ribozyme Pharmaccuticals, Inc.

APPLICANT: Roswiggen, James

TITLE OF INVENTION: RAM Interference Mediated Inhibition of Epidermal Growth Factor R

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

FILE REFERENCE: 900/042 (MBHB02-468-A)

CURRENT APPLICATION NUMBER: US 60/293,924

PRIOR FILING DATE: 2002-07-03

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-02-20

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-06-06

WHORE FILING DATE: 2001-06-06

WHORE FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-06-06

WHORE FILING DATE: 2001-07-25

WHUBER OF SEQ ID NOS: 1213

SEQ ID NO 650
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; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-251-117-400
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84.2%; Pred. No. 8.7e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 19;
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                        CURRENT APPLICATION NUMBER: US/10/251,117
CURRENT FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR PELING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR PELING DATE: 2002-07-25
PRIOR PELING DATE: 2002-07-25
PRIOR PELING DATE: 2001-07-25
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
NUMBER: PRIOR PILING DATE: 2001-06-06
NUMBER: PRIOR PILING DATE: 2001-06-06
SEQ ID NO 400
      900/042 (MBHB02-468-A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 650, Application US/10251117
Publication No. US20030170891A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 16; Conservative
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Sequence 1-1. Application US/10251117

Publication No. US20030170891A1

SERNEAL INPORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
FILE REFERENCE: 900/042 (MBHB02-468-A)
CURRENT APPLICATION NUMBER: US f0/393,924
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR PILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 1213
SSOFTWARE: Patentin version 3.0
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US-10-221-117-400/c.
Sequence 400, Application US/10251117
Sequence 400, Application US/2030170891A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Rossiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
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0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 8.7e+02;
Matches 15; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: 60/341,947
PRIOR FILING DATE: 2002-12-19
PRIOR PILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 151, Application US/10251117
Publication No. US20030170891A1
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                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: hDC2 probe US-10-324-618-33
                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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LENGTH: 19
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Thu Oct 28

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JULY SEQUENCE 957, Application US/10251117

Publication No. US20030170891A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaccuticals, Inc.

TITLE OF INVENTION: Gene Expression using Short Interfering RNA

FILE REFERENCE: 900/042 (MBHB02-468-A)

CURRENT APPLICATION NUMBER: US 60/393,924

PRIOR FILING DATE: 2002-00-03

PRIOR FILING DATE: 2002-06-06

PRIOR PILING DATE: 2002-06-06

PRIOR PILING DATE: 2002-06-06

PRIOR PILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-06-06

PRIOR FILING DATE: 2001-06-06
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Sequence 972, Application US/10251117

SERVERAL INFORMATION:

APPLICANT: Microsward Name Pharmaceuticals, Inc.

APPLICANT: Microsward Name Pharmaceuticals, Inc.

APPLICANT: Microsward Name Pharmaceuticals, Inc.

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

TITLE OF INVENTION UNMER: US/10/251,117

CURRENT APPLICATION NUMBER: US 60/393,924

PRIOR PILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/393,520

PRIOR PILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 69/316,466

PRIOR PILING DATE: 2001-07-25

PRIOR PILING DATE: 2001-07-25
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; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-251-117-957
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    Length 19;
                                                                                          Indels
1 0.4%; Score 14.2; DB 1;
Similarity 57.9%; Pred. No. 8.7e+02;
11; Conservative 5; Mismatches 3;
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                                                                                                                                                                        1938 CGACCTGTACATGATCATG 1956
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SOFTWARE: PatentIn version
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    Query Match
Best Local S
Matches 11
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| Sequence 720, Application US/10251117
| Publication No. US20030170891A1
| CENERAL INFORMATION:
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: Ribozyme Pharmaceuticals, Inc.
| APPLICANT: McSwiggen, James
| APPLICANT: McSwiggen, James
| APPLICANT: McSwiggen, James
| APPLICANT: McSwiggen, James
| TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
| FILE REPERENCE: 900/042 (MBH002-468-A)
| TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
| FILE REPERENCE: 900/042 (MBH002-468-A)
| FILE REPERENCE: 900/042 (MBH002-468-A)
| FRIOR PILICATION NUMBER: US 60/393,924
| PRIOR PILICATION NUMBER: US 60/398,580
| PRIOR PILING DATE: 2002-05-06
| PRIOR PILING DATE: 2002-02-20
| PRIOR PILING DATE: 2001-06-06
| PRIOR PILING DATE: 2001-06-06
| PRIOR PILING DATE: 2001-06-06
| WUMBER OF SEQ ID NOS: 1213
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 720
| LEADTH: 19
                                                                                                                                                   ## PERIOR FILING DATE: 2002-02-20
## PRIOR FILING DATE: 2002-02-24
## PRIOR FILING DATE: 2002-02-26
## PRIOR FILING DATE: 2002-02-06
## PRIOR FILING DATE: 2001-06-06
## PRIOR PRIOR
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; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-251-117-720
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                                                                                          Sequence 665, Application US/10251117
Publication No. US20030170891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3414 AGGGCCCGCCCTGTGTGC 3432
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Artificial Sequence
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APPLICANT: McSwiggen, James
TILLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using
TITLE OF INVENTION: Interfering RNA
FILE REFERENCE: 900/033
FILE REFERENCE: 900/033
FURENT APPLICATION UNDER: US/10/205,309
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 674
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US-10-205-309-18
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                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/084,839
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: Patentin version 3.1
SEQ ID NO 1955
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/10205309; Publication No. US20030190635A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Thompson, Lisa C.
PEPLICANT: Ved'Yk, Kevin L.
TITLE OF INVENTION: RNA Detection Assays
FILE REFERENCE: FORS-06666
                                                  Kwiatkowski, Jr., Robert W.
Lukowiak, Andrew A.
                                                                                                                                                                            Neri, Bruce P.
Olson, Sarah M.
Olson-Munoz, Marilyn C.
Schaefer, James J.
Skrzypczynski, Zbigniew
Takova, Tsetska Y.
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; Publication No. US20030190635A1
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                                                                                                       Lyamichev, Victor
Lymaicheva, Natalie E.
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2'
Matches 16; Conservative
                          Caiser, Michael
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US-10-205-309-343
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                                                                                                                               APPLICANT
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TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor I
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor I
TITLE OF INVENTION: RNA Interference Mediated Interfering RNA
FILE REFERENCE: 900/042 (MBHB02-468-A)
CURRENT APPLICATION NUMBER: US/10/251,117
RIGHOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR PILING DATE: 2002-02-20
PRIOR PLING DATE: 2001-02-30
PRIOR PLING DATE: 2001-02-30
PRIOR PLING DATE: 2001-02-30
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-06-06
                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region US-10-251-117-972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-251-117-1027
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0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                 Ouery Match 0.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1027, Application US/10251117
Publication No. US20030170891A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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Argue, Brad T.
Bartholomay, Christian T.
Chehak, LuAnne
Curtis, Michelle L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gequence 1955, Application US/10084839 Publication No. US20030186238A1 GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
                                                                                                                                                                                                                                                                                                                                         3414 AGGGCCGGCCCTGTGTGC 3432
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SOFTWARE: Patentin version 3.0
SEQ ID NO 972
LENGTH: 19
                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1027
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ORGANISM: Artificial Sequence
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Hall, Jeff G.
Ip, Hon S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-251-117-1027/c
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APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U
TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/060 (MBHB02-100/244,647
CURRENT APPLICATION NUMBER: US 60/358,580
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR PILING DATE: 2002-02-20
PRIOR PILING DATE: 2002-07-06
PRIOR APPLICATION NUMBER: DCT US 60/393,924
PRIOR FILING DATE: 2002-07-06
PRIOR PILING DATE: 2002-07-06
PRIOR FILING DATE: 2002-07-06
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
NUMBER OF SEQ ID NOS: 1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1293
US-10-454-323-3/c
i Sequence 3, Application US/10454323
i Sequence 3, Application No. US20040001833A1
i GENERAL INFORMATION:
i APPLICARTA Agus David B.
i TITLE OF INVENTION: Method of Treating Cancer Using Kinase Inhibitors
i TITLE OF INVENTION WHERE: US/10/454,323
i CURRENT FILING DATE: 2003-06-05
i PRIOR FILING DATE: 2003-06-05
i RAPLICATION NUMBER: 60/386,622
i RAPLICATION NUMBER: 60/386,622
i RAPLICATION NUMBER: 0003-06-05
i NUMBER OF SEQ ID NOS: 9
i SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 14.2; DB 1; Length 19; 84.2%; Pred. No. 8.7e+02; tive 0; Mismatches 3; Indels
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Publication No. US20040005584A1
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ORGANISM: Artificial Sequence
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APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 84.2
Matches 16, Conservative
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ORGANISM: Homo sapiens
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Matches 16, Conserv
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US-10-349-143-4702/c
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Publication No. US20030206887A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceutical, Inc.

APPLICANT: McSwiggen, James

APPLICANT: McSwiggen, James

APPLICANT: McSwiggen, James

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV) U

TITLE OF INVENTION: Short Interfering Nucleic Acid (sina)

FILE REFERENCE: 400/060 (MBHB02-1000)

CURRENT APPLICATION NUMBER: US/10/244,647

CURRENT FILING DATE: 2002-02-20

PRIOR FILING DATE: 2002-07-03

PRIOR FILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: US 60/398,580

PRIOR FILING DATE: 2002-07-03

PRIOR PAPLICATION NUMBER: US 60/398,680

PRIOR APPLICATION NUMBER: US 60/296,876

PRIOR PILING DATE: 2001-06-08
                                                             APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Alzheimer's Disease Using
TITLE OF INVENTION: Interfering RNA
FILE REFERENCE: 900/033
CURRENT APPLICATION NUMBER: US/10/205,309
CURRENT FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 674
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-205-309-343
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0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 8.7e+02;
Matches 14; Conservative 2; Mismatches 3; Indels
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Pred. No. 8.7e+02;
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                                       Ribozyme Pharmaceuticals, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3659 CCTGCAGGGCCATGGCTCA 3677
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SOFTWARE: Patentin version 3.0
SEQ ID NO 511
LENCTH: 19
                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
             GENERAL INFORMATION:
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US-10-244-647-1157/c
                                                                                                                                                                                                                                                                               SEQ ID NO 343
LENGTH: 19
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| Sequence 322, Application No. US20040009946A1
| GENERAL INFORMATION:
| APPLICANT: Klinghoffer, Richard
| APPLICANT: Wilson, Linda K.
| TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION |
| TITLE OF INVENTION: BY RNA INTERFERENCE |
| TITLE OF INVENTION: BY RNA INTERFERENCE |
| CURRENT APPLICATION NUMBER: US/10/444,925 |
| CURRENT FILING DATE: 2003-05-23 |
| NUMBER OF SEQ ID NOS: 599 |
| SOFTWARE: PSECSEQ for Windows Version 4.0 |
| LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                                                    APPLICANT: Lewis, Stephen Patrick
APPLICANT: Lewis, Stephen Patrick
APPLICANT: Klinghoffer, Richard
APPLICANT: Wilson, Linda K.
TITLE OF INVENTION: MODULATION OF PTPIB SIGNAL TRANSDUCTION
TITLE OF INVENTION: BY RNA INTERFERENCE
FILLE REFERENCE: 200125.441
FILLE REPERENCE: 200125.441
CURRENT APPLICATION NUMBER: US/10/444,925
CURRENT FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 486, Application US/10444925
Publication No. US20040009946A1
CENERAL INFORMATION:
APPLICANT: Lewis, Stephen Patrick
APPLICANT: Klinghoffer, Richard
TITLE OF INVENTION: MODULATION OF PTPIB SIGNAL TRANSDUCTION
TITLE OF INVENTION: BY RNA INTERFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Small interfering RNA
US-10-444-925-392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Small interfering RNA
                       Sequence 372, Application US/1044925
Publication No. US20040009946A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: Artificial Sequence
US-10-444-925-372/c
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Publication No. US20040005584A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
ITILE OF INVENTION: Blallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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          FILE REFERENCE: GENEET.020CPI
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
FRIOR APPLICATION NUMBER: US/09/422,978
FRIOR APPLICATION NUMBER: US/09/422,978
FRIOR PILING DATE: 1999-10-021
FRIOR PILING DATE: EARLIER FILING DATE: 1999-04-21
FRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
FRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
FRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
FRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
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; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-11075 for SEQ 2449,
US-10-349-143-6383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , LOCATION: 1..19 -
, OTHER INFORMATION: upstream amplification primer 99-17134 for SEQ 768,
US-10-349-143-4702
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CURRENT PILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/09/422,978

PRIOR FILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20

PRIOR FILING DATE: EARLIER PELICATION NUMBER: US 60/109,732

PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/109,732

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/082,614

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 6383

LENGTH: 19
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Pred. No. 8.7e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 84.2%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapiens
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US-10-349-143-6383/c
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RESULT 1296

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105-10-182-644A-6/c

| Sequence 6, Application US/10182644A
| Publication No. US20040115788A1
| GENERAL INFORMATION:
| APPLICAMT: The Government of the United States of America
| TITLE OF INVENTION: Hybrid adeno-retroviral vector for the transfection
| TITLE OF INVENTION: of cells.
| FILE REFERENCE: 56873
| CURRENT APPLICATION NUMBER: US/10/182,644A
| CURRENT PILING DATE: 2003-06-26
| PRIOR APPLICATION NUMBER: 60/179,327
| PRIOR PILING DATE: 2000-01-31
| NUMBER OF SEQ ID NOS: 12
| SOSTWARE: Patentin Ver. 2.1
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FEATURE:
CHER INFORMATION: Description of Artificial Sequence: PCR primer
05-10-182-544A-6
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APPLICANT: Dhallan, Ravinder S.
TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 543312000420
CURRENT APPLICATION NUMBER: US/10/661,165
CURRENT APPLICATION NUMBER: US/10/661,165
CURRENT PILING DATE: 2003-09-11
PRIOR PILING DATE: 2003-09-13
PRIOR PILING DATE: 2002-05-08
PRIOR PILING DATE: 2002-05-08
PRIOR PILING DATE: 2002-03-11
PRIOR PILING DATE: 2002-03-11
PRIOR PILING DATE: 2002-03-11
PRIOR PILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR PILING DATE: 2003-08-29
PRIOR FILING DATE: 2003-08-29
PRIOR PILING DATE: 2003-08-29
PRIOR PILING DATE: 2003-08-29
PRIOR PILING DATE: 2003-08-29
PRIOR PILING DATE: 2003-08-28
                                                                             NAME/KEX: misc_feature; LOCATION: 5, 6, 7, 8, 9; OTHER INFORMATION: These nucleotides may be absent US-10-376-770-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.4%; Score 14.2; DB 1; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                              Query Match 0.4%; Score 14.2; DB 1; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3;
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Publication No. US20040137470A1
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     TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 19
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US-10-376-770-89/C

TILE REPERENCE: 543112000120

TILE REPERENCE: 543112000120

CURRENT APPLICATION NUMBER: US/10/376,770

CURRENT APPLICATION NUMBER: US/093,618

PRIOR FILING DATE: 2002-02-8

PRIOR FILING DATE: 2002-03-11

PRIOR FILING DATE: 2002-03-01

SROPTWARE PESCE FOR WINDER: US 60/378,354

NUMBER OF SEQ ID NOS: 262

SOFTWARE: PSELSEQ for Windows Version 4.0

SEQ ID NO 89

LENGTH: 19
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TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
TITLE OF INVENTION: TRANSDUCTION BY RNA INTERPERENCE
FILE REPERENCE: 200125.49
CURRENT APPLICATION NUMBER: 0310/444,795B
CURRENT FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 842
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 372
LENGTH: 19
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FILE REFERENCE: 200125.441
CURRENT PEPLICATION NUMBER: US/10/444,925
CURRENT FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Mindows Version 4.0
SEQ ID NO 486
LENGTH: 19
                                                                                                                                                                                                                                                  FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-925-486
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; OTHER INFORMATION: Small interfering RNA
US-10-444-7958-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 372, Application US/1044795B
Publication No. US20040077574A1
GENERAL INFORMATION:
APPLICANT: Klinghoffer, Richard
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ORGANISM: Artificial Sequence
                                                                                                                                                                                           TYPE: RNA
ORGANISM: Artificial Sequence
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SOFTWARE: FastSEQ for Windows Version 4.0

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GREALL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Mosayigen, James
APPLICANT: Mosayigen, James
APPLICANT: Mosayigen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Beigelman, Leonid
APPLICANT: Beigelman, Leonid
APPLICANT: Pavo, Pamela
ITTLE OF INVENTION: Rowth Factor and Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sINA)
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sINA)
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sINA)
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sINA)
TITLE OF INVENTION: UNMER: US/10/66,951
CURRENT APPLICATION NUMBER: US 10/664,668
PRIOR PLING DATE: 2003-09-18
PRIOR PLING DATE: 2003-07-29
PRIOR PLING DATE: 2003-07-29
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-02-20
PRIOR PLING DATE: 2002-02-20
PRIOR PLING DATE: 2002-02-20
PRIOR PLING DATE: 2002-03-20
PRIOR PLING DATE: 2002-03-65
PRIOR PLING DATE: 2002-03-20
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Publication No. US20040138163A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Beigelman, Leonid
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/131 (MBHB02-742-F)
CURRENT APPLICATION NUMBER: US/0/665,951
CURRENT FILING DATE: 2003-09-18
FRIOR APPLICATION NUMBER: US 10/664,668
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                                                                                                 Sequence 815, Application US/10665951
Publication No. US20040138163A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 815
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 84.2
Matches 16; Conservative
                                                                     JS-10-665-951-815/c
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US-10-665-951-1041
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VS-10-665-991-89

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US-10-665-951-388
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                   NAME/KEY: misc_feature

LOCATION: (5)...(9)

; OTHER INFORMATION: These nucleotides may be absent

US-10-661-165-89
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ORGANISM: Artificial Sequence
                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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SEQ ID NO 89
LENGIH: 19
                                                                                                                                                          FEATURE
                                    LENGTH
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, OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r US-10-665-951-1046
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APPLICANT: Situa Theorapeutics, Inc.
APPLICANT: Situa Theorapeutics, Inc.
APPLICANT: Beigelman, Leonid
APPLICANT: ROWENTION: Growth Factor and Vascular Endothelial
TITLE OF INVENTION: GROWTH Factor and Vascular Endothelial
FILE REFERENCE: 400/131 (MEMBER: US 10/665,951
CURRENT FILING DATE: 2003-09-18
FRIOR APPLICATION NUMBER: US 60/399,348
FRIOR PELING DATE: 2002-07-09
FRIOR APPLICATION NUMBER: US 10/287,949
FRIOR APPLICATION NUMBER: US 10/287,949
FRIOR APPLICATION NUMBER: US 60/389,580
FRIOR APPLICATION NUMBER: US 60/389,580
FRIOR PELING DATE: 2002-05-09
FRIOR APPLICATION NUMBER: US 60/386,580
FRIOR APPLICATION NUMBER: US 60/386,580
FRIOR APPLICATION NUMBER: US 60/386,782
FRIOR PELING DATE: 2002-03-01
FRIOR APPLICATION NUMBER: US 60/386,782
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US-10-665-951-1052
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PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
SOFTWARE: Patentin version 3.2
SEQ ID NO 1046
LENGTH: 19
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Publication No. US20040138163A1
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                               TYPE: RNA
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APPLICANT: Sitra Therapeutics, Inc.
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Grow Expression Using Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/131 (MEHBO2-742-F)
FILE REFERENCE: 400/131 (MEHBO2-742-F)
FILE REPERENCE: 2003-09-18
FRICK PILING DATE: 2003-09-18
FRICK PILING DATE: 2003-00-20
FRICK APPLICATION NUMBER: DG (0/399, 348
FRICK FILING DATE: 2002-07-29
FRICK FILING DATE: 2002-07-29
FRICK FILING DATE: 2002-07-29
FRICK FILING DATE: 2002-11-04
FRICK FILING DATE: 2002-11-04
FRICK FILING DATE: 2002-11-04
FRICK FILING DATE: 2002-11-07
FRICK FILING DATE: 2002-02-19
FRICK FILING DATE: 2002-03-19
FRICK FILING DATE: 2002-03-11
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US-10-665-951-1041
                                          PRIOR APPLICATION NUMBER: PCT/US 03/05022
PRIOR APPLICATION NUMBER: US 60/399,348
PRIOR FILING DATE: 2002-02-20
PRIOR PILING DATE: 2002-07-29
PRIOR PILING DATE: 2002-07-29
PRIOR PPLICATION NUMBER: US 60/393,796
PRIOR PPLICATION NUMBER: US 10/287,949
PRIOR PILING DATE: 2002-11-04
PRIOR PPLICATION NUMBER: US 10/306,747
PRIOR PILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: PCT/US 02/17674
PRIOR APPLICATION NUMBER: PCT/US 02/17674
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR PILING DATE: 2002-02-20
PRIOR PLING DATE: 2002-02-20
PRIOR PILING DATE: 2002-06-06
PRIOR PILING PATE: 2002-06-06
PRIOR PILING P
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Pred. No. 8.7e+02;
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Best Local Similarity 57.9%; Pred. No. 8.7e
Matches 11; Conservative 5; Mismatches
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Publication No. US20040138163A1
GENERAL INFORMATION:
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LENGTH: 19
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; OTHER INFORMATION; Description of Artificial Sequence: sinA antisense region
US-10-665-951-1370
                         PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: PCT/US 03/05022
PRIOR APPLICATION NUMBER: PCT/US 03/05022
PRIOR FILING DATE: 2002-02-02
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-03
PRIOR PLING DATE: 2002-07-03
PRIOR PLING DATE: 2002-07-03
PRIOR PLING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: US 10/287,949
PRIOR APPLICATION NUMBER: US 10/306,747
PRIOR PLING DATE: 2002-11-27
PRIOR PLING DATE: 2002-05-09-09
PRIOR PLING DATE: 2002-05-09
PRIOR PLING DATE: 2002-05-09
PRIOR PLING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR PLING DATE: 2002-03-11
PRIOR PLING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
APPLICATION NUMBER: US 10/664,668
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin version 3.2
SEQ ID NO 1370
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Sequence 1365, Application US/10665951
Sequence 1365, Application US/10665951
Sequence 1365, Application US/10665951
Sequence 1365, Application US/10665951
Sequence 1365, Application No. US2004013816341
Sequence 1365, Application No. US2004013816341
APPLICANT: Serve Teavo. Pamela
APPLICANT: Baigelman, Leonid
APPLICANT: Revense Teach and Vascular Endothelial
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: 800-10-10-10
FILE REFERENCE: 2003-09-18
PRIOR FILING DATE: 2003-09-18
PRIOR PILING DATE: 2003-00-20
PRIOR PILING DATE: 2002-00-20
PRIOR APPLICATION NUMBER: US 60/393,796
PRIOR APPLICATION NUMBER: US 60/393,796
PRIOR PILING DATE: 2002-11-27
PRIOR FILING DATE: 2002-01-20
PRIOR FILING DATE: 2002-01-20
PRIOR FILING DATE: 2002-11-27
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-03-20
PRIOR PILING DATE: 2002-03-20
PRIOR PILING DATE: 2002-03-20
PRIOR PILING DATE: 2002-03-20
PRIOR PAPLICATION NUMBER: US 60/356,580
PRIOR PILING DATE: 2002-03-11
PRIOR PILING DATE: 2003-03-11
PRIOR PILING 
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Sequence 1370, Application US/10665951
Publication No. US20040138163A1
Publication No. US20040138163A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Bayco, Pamela
TITLE OF INVENTION: RNA Interference Wediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sina)
FILE REPERENCE: 400/131 (MRHB02-742-F)
CURRENT APPLICANTON NUMBER: US/10/665,951
CURRENT FILING DATE: 2003-09-18
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    UACACAAUCCAGAGUGACG 19
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GENERAL INVCRMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Beisgelman, Leonid
APPLICANT: Beisgelman, Leonid
APPLICANT: Beisgelman, Leonid
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Growth Factor and Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial
TITLE OF INVENTION: BOADE: 2003-09-18
PRIOR FILING DATE: 2003-09-18
PRIOR PELING DATE: 2003-07-29
PRIOR PELING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: US 60/399,348
PRIOR PELING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/399,348
PRIOR PELING DATE: 2002-07-03
PRIOR PELING DATE: 2002-11-27
PRIOR PELING DATE: 2002-05-29
PRIOR FILING DATE: 2002-05-29
PRIOR FILING DATE: 2002-05-29
PRIOR FILING DATE: 2002-06-29
PRIOR FILING DATE: 2002-06-39
PRIOR FILING DATE: 2002-03-11
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Length 19;
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    Ouery Match 0.4%; Score 14.2; DB 1; Best Local Similarity 84.2%; Pred. No. 8.7e+02; Matches 16; Conservative 0; Mismatches 3;
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Publication No. US20040138163A1
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Sequence 1683, Application US/10665951
Publication No. US20040138163A1
GENERAL INFORMATION:
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APPLICANT: Based and Interference Mediated Inhibition of Vascular Endothelial
APPLICANT: Begins James
APPLICANT: Begins James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Gene Expression Using Short Interfering Mucleic Acid (sinA)
TITLE OF INVENTION: Gene Expression Using Short Interfering Mucleic Acid (sinA)
TITLE OF INVENTION Gene Expression Using Short Interfering Mucleic Acid (sinA)
TITLE OF INVENTION NUMBER: US/10/665,951
CURRENT FILING DATE: 2003-09-18
FRIOR PELING DATE: 2003-09-28
FRIOR PELING DATE: 2003-07-29
FRIOR PELING DATE: 2003-07-29
FRIOR PELING DATE: 2003-07-29
FRIOR PELING DATE: 2003-07-29
FRIOR APPLICATION NUMBER: US 60/399,348
FRIOR APPLICATION NUMBER: US 60/399,349
FRIOR PELING DATE: 2002-11-07
FRIOR PELING DATE: 2002-03-03
FRIOR APPLICATION NUMBER: US 60/363,124
FRIOR PELING DATE: 2002-60-06
FRIOR FRIENG DATE: 2002-60-06
FRIOR FRIENG DATE: 2002-06-06
FRIOR FRIENG DATE: PARTICATION NUMBER: US 60/363,124
FRIOR FRIENG DATE: 2002-06-06
FRIOR FRIENG DATE: PARTICATION NUMBER: US 60/363,124
FRIOR FRIENG DATE: 2002-06-06
FRIOR FRIENG DATE: PARTICATION NUMBER: US 60/363,124
FRIENG PERIOR PERIOR DATE: 2002-06-06
FRIENG PERIOR PERIOR DATE: PARTICATION NUMBER: US 60/363,124
FRIEND PERIOR PERIOR DATE: PARTICATION NUMBER: PARTENT DATE PARTICATION NUMBER: PARTENT DATE PARTENT
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                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region US-10-665-951-1376
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PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
SOFTWARE: Patentin version 3.2
SEQ ID NO 1376
LENGTH: 19
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Publication No. US20040138163A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-665-951-1674
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LENGTH: 19
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GURREAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Meswiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Beavo, Pamela
TTILE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TTILE OF INVENTION: Growth Factor and Vascular Endothelial
TTILE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
TITLE OF INVENTION WINDER: US/10/665,951
CURRENT APPLICATION NUMBER: US/10/665,951
CURRENT FILING DATE: 2003-09-18
PRIOR PLING DATE: 2003-09-18
PRIOR FILING DATE: 2003-07-29
PRIOR PLING DATE: 2002-07-29
PRIOR PLING DATE: 2002-05-29
PRIOR PLING DATE: 2002-05-29
PRIOR PLING DATE: 2002-05-29
PRIOR PLING DATE: 2002-05-29
PRIOR PLING DATE: 2002-06-29
PRIOR PLING DATE: 2002-06-26
PRIOR PLING DATE: 2002-06-36
PRIOR
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US-10-665-951-1683
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GENERAL INFORMATION:
APPLICANT: Since Therapeutics, Inc.
APPLICANT: Beigelman, Leonid
APPLICANT: British Beigelman, Leonid
APPLICANT: British Beigelman, Leonid
APPLICANT: British Briti
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ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/sinA sense r US-10-665-951-2263
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APPLICANT: Beigelman, Leonid
APPLICANT: Beigelman, Leonid
APPLICANT: Beigelman, Leonid
APPLICANT: Beigelman, Leonid
APPLICANT: Bavo, Pamela
TITLE De INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE DE INVENTION: Gene Expression Using Short Interfering Nucleic Acid (sinA)
FILE EMPERSNCE: 400/131 (MHHB02-742-P)
CURRENT APPLICATION NUMBER: US/10/665,951
CURRENT FILING DAFE: 2003-09-18
PRIOR FILING DATE: 2003-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
US-10-665-951-1930
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PRIOR PLILING JUNES. PCT/US 03/05022
PRIOR PLILING JUNES. PCT/US 03/05022
PRIOR PLILING DATE: 2003-02-20
PRIOR FLIING DATE: 2003-07-29
PRIOR FLIING DATE: 2002-07-03
PRIOR PLILING DATE: 2002-07-03
PRIOR PLILING DATE: 2002-11-04
PRIOR PLILING DATE: 2002-11-27
PRIOR PLILING DATE: 2002-11-27
PRIOR PLILING DATE: 2002-11-27
PRIOR PLILING DATE: 2002-05-29
PRIOR PLILING DATE: 2002-02-20
PRIOR PLILING DATE: 2002-03-11
PRIOR PLILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
SOFTWARE: PRECENTIN VERSION 3.2
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2455
SOFTWARE: Patentin version 3.2
SEQ ID NO 1930
LENGTH: 19
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0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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Sequence 2263, Application US/10665951
Publication No. US20040138163A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1735 GGCCGCTCCCCGTGAGT 1753
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ORGANISM: Artificial Sequence
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Best Local Similarity 68.4
Matches 13; Conservative
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APPLICANT: Beigelman, Leonid
APPLICANT: Beigelman, Leonid
APPLICANT: Beigelman, Leonid
APPLICANT: Beroco, Pamela
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
FILE REPRENCE: 400/131 (MBHBD2-742-F)
CURRENT APPLICATION NUMBER: US/10/665,951
CURRENT PILING DATE: 2003-09-18
PRIOR PHILOR DATE: 2003-09-18
PRIOR PELICATION NUMBER: US 60/399,348
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR PELICATION NUMBER: US 60/399,348
PRIOR PELICATION NUMBER: US 60/399,348
PRIOR APPLICATION NUMBER: US 10/287,949
PRIOR APPLICATION NUMBER: US 10/287,949
PRIOR APPLICATION NUMBER: US 10/287,949
PRIOR PILING DATE: 2002-11-04
PRIOR FILING DATE: 2002-11-04
PRIOR FILING DATE: 2002-11-04
PRIOR FILING DATE: 2002-11-04
PRIOR FILING DATE: 2002-11-07
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                                                                                                                  PRIOR APPLICATION UNMBER: PCT/US 03/05022
PRIOR FILING DATE: 2003-02-16
PRIOR FILING DATE: 2003-02-20
PRIOR PILING DATE: 2003-02-20
PRIOR PLING DATE: 2002-07-29
PRIOR PLING DATE: 2002-07-29
PRIOR PLING DATE: 2002-07-03
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-11-04
PRIOR PLING DATE: 2002-12-20
PRIOR PLING DATE: 2002-05-29
PRIOR PLING DATE: 2002-05-29
PRIOR PLING DATE: 2002-05-20
PRIOR PLING DATE: 2002-02-06
PRIOR PLING DATE: 2002-02-06
PRIOR PLING DATE: 2002-02-06
PRIOR PLING DATE: 2002-03-01
PRIOR PLING DATE: 2002-03-03-01
PRIOR PLING PAPELCATION NUMBER: US 60/386, 782
PRIOR PLING DATE: 2002-03-03-01
PRIOR PLING DATE: 2002-03-03-01
PRIOR PLING PAPELCATION NUMBER: US 60/386, 782
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        CURRENT FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: US 10/664,668
PRIOR FILING DATE: 2003-09-18
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PEDLICATION NUMBER: US 60/358,580
FILING DATE: 2002-02-20
APPLICATION NUMBER: US 60/363,124
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Publication No. US20040138163A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1573 CAGGTGGCCCGGGGCATGG 1591
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ORGANISM: Artificial Sequence
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LENGTH: 19
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                                                                                                                                                                                                                                                                                                                         Length 19;
                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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Sequence 14, Application US/10715117

Publication No. US20040171037A1

GENERAL INPORMATION:

APPLICANT: L1 JUNG

APPLICANT: L1 JUNG

APPLICANT: SIN, WUN CHEY

APPLICANT: YANG, JIANXIN

TITLE OF INVENTY AMELIFIED GENES INVOLVED IN CANCER

FILE REFERENCE: 38002-0062

CURRENT PPLICATION NUMBER: US/10/715,117

CURRENT FILING DATE: 2003-11-19

PRIOR FILING DATE: 2002-11-19

PRIOR FILING DATE: 2002-11-19

PRIOR FILING DATE: 2002-11-19

PRIOR FILING DATE: 2002-12-19

PRIOR FILING DATE: 2002-12-19
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APPLICANT: LI, JUNG
APPLICANT: SIN, WIN CHEY
APPLICANT: SIN, WIN CHEY
APPLICANT: SIN, WIN CHEY
APPLICANT: YANG, JIANXIN
TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANCER
FILE REFERENCE: 38002-0062
CURRENT APPLICATION NUMBER: US/10/715,117
CURRENT PILING DATE: 2003-11-18
PRIOR FILING DATE: 2002-11-19
PRIOR PILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 13
LENGTH: 19
                                                                                                                                                                                                                                                                                                                            Score 14.2; DB 1;
Pred. No. 8.7e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 978 CCCCAAGAAAGGCCTGGGC 996
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      2003-06-20
CURRENT FILING DATE: 2003-06-2
NUMBER OF SEQ ID NOS: 206
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 37
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                  0.4%;
                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                              FEATURE:
COTHER INFORMATION: Synthetic
US-10-600-070-37
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.21
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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US-10-715-117-14
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Publication No. US20040139500A1
GENERAL INFORMATION:
APPLICANT: Oitha, Stanislav
APPLICANT: Kokharova, Olga A.
APPLICANT: Gao, Hongo
TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-665-951-2264
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CURRENT APPLICATION NUMBER: US/10/600,070
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         1950 GATCATGCGGGAGTGCTGG 1968
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                                           1 GACCAUGCUGGACUGCUGG 19
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
tes 13; Conservé
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RESULT 1323
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                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: SIRNA sequence
US-10-715-117-14
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0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 8.7e+02;
Matches 15; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 95, Application US/10385163
; Publication No. US20040180844A1
; GENERAL INFORMATION:
; APPLICANT: Fesik, Stephen W.
; APPLICANT: Halbert, Donald N.
; APPLICANT: McDowell, Jeffrey A.
; APPLICANT: Schurdak, Mark E.
; APPLICANT: Sarthy, Aparna V.
; TITLE OF INVENTION: Method Of Killing Cancer Cells
; FILE REFERENCE: 7046.US.01
; CURRENT APPLICATION NUMBER: US/10/385,163
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Realk, Stephen W.
APPLICANT: Halbert, Donald N.
APPLICANT: Halbert, Donald N.
APPLICANT: Schurdak, Mark E.
APPLICANT: Schurdak, Mark E.
APPLICANT: Sarthy, Aparna V.
ITLE OF INVENTION: Method Of Killing Cancer Cells
FILE REFERENCE: 7046.02.21
CURRENT APPLICATION NUMBER: US/10/796,177
CURRENT PILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: US/60/453,420
PRIOR PLICHG DATE: 2006-03-10
NUMBER OF SEQ ID NOS: 121
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 19
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US-10-385-163-95
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Publication No. US20040180848A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            293 GCTTCCGCTGCCCAGCCGC 311
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                                                   TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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SEQ ID NO 14
LENGTH: 19
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; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense rous-10-683-990-22
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APPLICANT: Usman, Nassim
TITLE OF INVENTION: RA Interference Mediated Inhibition of Placental Growth Factor
TITLE OF INVENTION: Gene Expression Using SHort Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/134 (02-742-H)
CURRENT APPLICATION NUMBER: US/10/683,990
PRIOR APPLICATION NUMBER: PCT/US03/05022
PRIOR PILING DATE: 2003-10-10
PRIOR FILING DATE: 2003-02-20
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PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 256
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                                                                                                                                                                                              Length 19;
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                FEATURE:
; OTHER INFORMATION: antisense oligonucleotide US-10-796-177-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2002-02-20
PRIOR PELING DATE: 2002-02-20
PRIOR PELING DATE: 2002-02-20
PRIOR PELING DATE: 2002-03-11
PRIOR PELING DATE: 2002-03-11
PRIOR PELING DATE: 2002-03-11
PRIOR PELING DATE: 2002-05-06
PRIOR PELING DATE: 2002-07-03
PRIOR PELING DATE: 2002-07-03
PRIOR PELING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/399,348
PRIOR PELING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR PELING DATE: 2002-08-29
PRIOR PELING DATE: 2002-09-05
PRIOR PELING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR PELING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR PELING DATE: 2002-09-05
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; Publication No. US20040198682A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/10683990
Publication No. US20040198682A1
GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Artificial Sequence
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Gaps

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Sequence 138, Application US/09758881

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

CURRENT APPLICATION NUMBER: US/09/758,881

CURRENT FILING DATE: 2001-01-11

PRIOR PELLING DATE: 2000-04-06

PRIOR FILING DATE: 1999-04-06

PRIOR FILING DATE: 1999-04-06

NUMBER OF SEQ ID NOS: 152

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFERMATION: Description of Artificial Sequence: Synthetic
US-09-758-881-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.4%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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APPLICANT: THE RECENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: RAY, JASCAHARA
TITLE OF INVENTION: METHOD FOR PRODUCTION OF NEUROBLASTS
TITLE OF THE REFERENCE: REGENIAGO-5
CURRENT APPLICATION NUMBER: US/09/915,229
CURRENT FILING DATE: 2001-07-24
PRIOR PILING DATE: 1997-06-27
PRIOR PILING DATE: 1997-06-19
PRIOR PILING DATE: 1995-06-19
PRIOR PILING DATE: 1993-11-03
PRIOR PILING DATE: 1993-11-03
PRIOR PILING DATE: 1993-01-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 20
                     Score 14.2; DB 1;
Pred. No. 9.1e+02;
0; Mismatches 3;
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US-09-915-229-3
                                                                                                                                                             2850 TATGGAAGAGGAAAAGGCT 2868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1006 GIGCACAAGAICICCCGCT 1024
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Publication No. US20020039789A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                1 TGTGGCAGAGCCAAAGGCCT 19
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ORGANISM: Artificial Sequence
                     Query Match 0.4%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Matches 16; Conserva
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: Uses, James
APPLICANT: Wesign
APPLICANT: Wesign
APPLICANT: Uses, Sension
APPLICANT: Uses, Sension
APPLICANT: Uses, Sension
APPLICANT: Uses, Sension
TITLE OF INVENTION: Gene Expression Using SHort Interfering Nucleic Acid (sina)
FILE REPERENCE: 400/134 (02-142-18)
CURRENT FILING DATE: 2003-10-10
FRIOR APPLICATION NUMBER: US 60/358,580
FRIOR APPLICATION NUMBER: US 60/358,580
FRIOR APPLICATION NUMBER: US 60/358,782
FRIOR APPLICATION NUMBER: US 60/359,796
FRIOR APPLICATION NUMBER: US 60/393,796
FRIOR APPLICATION NUMBER: US 60/406,784
FRIOR FILING DATE: 2002-00-05
FRIOR APPLICATION NUMBER: US 60/406,784
FRIOR FILING DATE: 2002-00-05
FRIOR APPLICATION NUMBER: US 60/406,784
FRIOR FILING DATE: 2002-00-05
FRIOR APPLICATION NUMBER: US 60/406,784
FRIOR FILING DATE: 2002-00-05
FRIOR APPLICATION NUMBER: US 60/406,784
FRIOR FILING DATE: 2002-00-05
FRIOR APPLICATION NUMBER: US 60/406,784
FRIOR FILING DATE: 2002-00-05
FRIOR APPLICATION NUMBER: US 60/406,784
FRIOR A
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Sequence 243, Application US/09216393

Patent No. US20010014447A1

GRNERAL INFORMATION:

APPLICANT: Wilhausen, Michael James

TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

CURRENT APPLICATION NUMBER: US/09/216,393

CURRENT PILING DATE: 1998-12-18

EARLIER PILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 364

SEQ ID NO 243

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region US-10-683-990-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Primer US-09-216-393-243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 14.2; DB 1; Length 19;
84.2%; Pred. No. 8.7e+02;
tive 0; Mismatches 3; Indels
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
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Sequence 29, Application US/09416384A
Patent No. US20020081584A1
GENERAL INFORMATION:
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Query Match 0.4%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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APPLICANT: RACALLISTER, THOWAS W.
APPLICANT: SETHURAMAN, NATARAJAN
APPLICANT: SETHURAMAN, ABBIE G.
TITLE OF INVENTION: GENETICALLY ENGINEERED GLUTAMINASE AND ITS USE IN
TITLE OF INVENTION: AMTIVIRAL AND ANTICANCER THERAPY
TILL OF INVENTION NUMBER: US/09/842,628
CURRENT APPLICATION NUMBER: 08/050,482
PRIOR PILLING DATE: 1995-04-25
PRIOR PLILING DATE: 1995-04-25
PRIOR PLILING DATE: 1991-12-04
PRIOR PILLING DATE: 1991-12-04
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GENERAL INFORMATION:
GENERAL INFORMATION:
FAPFLICANT: Felinberg, Andrew
APPLICANT: Strichman-Almashanu, Liora
APPLICANT: Strichman-Almashanu, Liora
APPLICANT: Jiang, Shan
TITLE OF INVENTION: METHYLATED CPG ISLANDS
FILE REFERENCE: 01107.00128
CURRENT FAPPLICATION NUMBER: US/09/861,893
CURRENT FILING DATE: 2001-05-22
FRIOR APPLICATION NUMBER: 60/206,158
FRIOR FILING DATE: 2000-05-22
FRIOR APPLICATION NUMBER: 60/206,161
FRIOR APPLICATION NUMBER: 60/206,161
FRIOR PILING DATE: 2000-06-52
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
ENGTHAL 20
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  0.4%; Score 14.2; DB 1; Length 20; ilarity 84.2%; Pred. No. 9.1e+02; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.4%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09842628
Patent No. US20020064862A1
GENERAL INFORMATION:
                                                                                                            2385 TGCCTCCAGGTGCAGAGGT 2403
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Patent No. US20020045257A1
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ORGANISM: Artificial Sequence
FEATURE:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 20
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Best Local Similarity 84.2
Matches 16; Conservative
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  Query Match
Best Local Similarity
Matches 16; Conserva
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US-09-842-628-11/c
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APPLICANT: BLUMENFELD, Marta
APPLICANT: BLUMENFELD, Marta
APPLICANT: BUUMENFELD, Marta
APPLICANT: BUUMENFELD, Marta
APPLICANT: CHUMAKOV, Ilya
APPLICANT: COHEN, Daniel
APPLICANT: COHEN, Daniel
APPLICANT: COHEN, Daniel
APPLICANT: COHEN, Daniel
APPLICANT: ESSIOUX, Laurent
ITILE OF INVENTION: Genes, proteins and biallelic markers related to central...
FILE REPERENCE: GENSET.045AUS
CURRENT FILING DATE: 1999-10-12
FRIOR FILING DATE: 1999-10-30
FRIOR FILING DATE: 1998-10-12
FRIOR APPLICATION NUMBER: 60/103,955
FRIOR FILING DATE: 1998-10-12
FRIOR APPLICATION NUMBER: 60/132,277
FRIOR APPLICATION NUMBER: 60/132,277
FRIOR APPLICATION NUMBER: 60/132,277
FRIOR APPLICATION NUMBER: 60/132,277
FRIOR APPLICATION DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 71
SSQ ID NO 29
LENGTH: 20
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APPLICANT: McKay, Robert A.
APPLICANT: McAda Brett
APPLICANT: Monda Brett
APPLICANT: Monda Brett
APPLICANT: Monda Brett
APPLICANT: Monda Brett
TITLE OF INVENTION: POR THE MODULATION OF JNK PROTEINS
TITLE OF INVENTION: POR THE MODULATION OF JNK PROTEINS
TITLE OF INVENTION: POR 1912
CURRENT APPLICATION NUMBER: US/09/774,809
CURRENT APPLICATION NUMBER: 09/396,902
PRIOR FILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PAPLICATION NUMBER: 09/130,616
PRIOR PLING DATE: 1999-08-07
PRIOR PLING DATE: 1999-08-07
PRIOR PLING DATE: 1997-08-03
                                                                        Gaps
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Score 14.2; DB 1;
Pred. No. 9.1e+02;
0; Mismatches 3;
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US-09-416-384A-29
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Gaps
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'OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
'OTHER INFORMATION: primer
US-09-760-285-4
                                         RESULT 1333
US-09-982-262B-62
| Sequence 62, Application US/09982262B
| Sequence 62, Application US/09982262B
| Publication No. US20030077565A1
| GENERAL INFORMATION:
| APPLICANT: C. Frank Bennett
| APPLICANT: C. Frank Bennett
| TITLE OF INVENTION: OLGONUCLEOTIDE MODULATION OF CELL ADHESION FILE REFERENCE: 15PH-6612
| CURRENT APPLICATION NUMBER: US/09/982,262B
| PRIOR APPLICATION NUMBER: 09/659,288
| PRIOR PILING DATE: 2000-09-12
| PRIOR PRILING DATE: 1998-06-12
| PRIOR PILING DATE: 1998-06-12
| PRIOR FILING DATE: 1998-06-12
| PRIOR FILING DATE: 1993-06-17
| PRIOR PRILING DATE: 1993-06-10
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indel8
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APPLICANT: Sass, Luigi
APPLICANT: Sass, Philip M
TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
FILE REFERENCE: MOR-0017
CURRENT PAPLICATION WUMBER: US/09/760,285
CURRENT FILING DATE: 2001-01-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Antisense Oligonucleotide
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     2 GAAGGITICCAGGGAAGAG 20
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Matches 16; Conserva
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US-09-760-285-4/c
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APPLICANT: C. FIANK Bennett
APPLICANT: C. FIANK Bennett
APPLICANT: Jacqueline Wyatt
TIER COF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
FILE OF INVENTION: ANTISENSE: US/09/865,866
CURRENT APPLICATION NUMBER: US/09/865,866
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 68
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 160, Application US/09771933
Fublication No. US20030023387A1
GENERAL INFORMATION:
APPLICANT: Gill-Garrison, Rosalynn D
APPLICANT: Martin, Christopher J
APPLICANT: Martin, Christopher J
APPLICANT: Computer-assisted Means for Assessing Lifestyle Risk
TITLE OF INVENTION: Computer-assisted Means for Assessing Lifestyle Risk
TITLE OF INVENTION: Factors
FILE REFERENCE: 620-130
CURRENT APPLICATION NUMBER: US/09/771,933
CURRENT APPLIANG DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 205
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 160
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                                                                                                                                                                       Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                     ; OTHER INFORMATION: Synthetic Sequence US-09-774-809-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3400 GACGGTTTCCAGGGAGGGG 3418
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US-09-865-866-68
; Sequence 68, Application US/09865866
; Publication No. US20030045487A1
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TYPE: DNA ORGANISM: Artificial Sequence
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US-09-771-933-160/c
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. TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
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Sequence 2531, Application US/09864426A
Sequence 2531, Application US/09864426A
Sequence 2531, Application No. US2004018489A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Lyamichev, Victor
APPLICANT: Saiser, Michael
TITLE OF INVENTION: Barymes for the Detection of RNA Sequences
FILE REFERENCE: FORS-04946
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2531
LENGTH: 20
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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| Publication No. US20030022311A1
| Publication No. US20030022311A1
| GENERAL INFORMATION:
| APPLICANT: Dunnington, Damien D. Frantz, James D. Shoelson, Steven E. TITLE OF INVENTION: HUMAN CIS PROTEIN NUMBER OF SEQUENCES: 12
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: SMithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Antisense Oligonucleotide US-09-908-147-26
                                FILE REFERENCE: RTS-0185
CURRENT APPLICATION NUMBER: US/09/908,147
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 26
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                1844 TGGGGGCTCCCCGTACCC 1862
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 acaagrirgccagcgrece
                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                             Sequence 2, Application US/09899440
Publication No. US20030092158A1
GENERAL INFORMATION:
APPLICANT: Stein, CY
TITLE OF INVENTION:
PHOSPHOROTHIOATE ANTISENSE HEPARANASE OLIGONUCLEOTIDES
FILE REPERENCE: 0575/63180
CURRENT APPLICATION NUMBER: US/09/899,440
CURRENT FILING DATE: 2001-07-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
ENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2531, Application US/09864636A; Sequence 2531, Application US/09864636A; Publication No. US20030104378A1; GENERAL INFORMATION: US20030104378A1; GENERAL INFORMATION: Third Wave Technologies; APPLICANT: Third Wave Technologies; APPLICANT: Chehak, Ludane; APPLICANT: Chehak, Ludane; TITLE OF INVENTION: Detection of RNA Sequences; FILE REFERENCE: FORS-04944; CURRENT APPLICATION NUMBER, US/09/864,636A; CURRENT FILING DATE: 2002-10-15; SEQ ID NOS: 2640; SEQ ID NOS: 2640; SEQ ID NOS: 2640; SEQ ID NO 2531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc feature
; LOCATION: ()..()
; OTHER INFORMATION: antisense oligonucleotide LB62
US-09-899-440-2
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Publication No. US20030144221A1
GENERAL INFORMATION:
APPLICANT: Hong Zhang
APPLICANT: Andrew T. Watt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 ACAAGTTTGGCAGCATCCG 488
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             20 GACAGAGICTICACTAACC
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                                                                                        RESULT 1335
US-09-899-440-2/c
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US-09-908-147-26
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US-10-079-429-66
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INCORPATION:
GENERAL INCORPATION:
APPLICATUT: Heacline et al.
TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
FILE REFERENCE: PF106F91D
CURRENT APPLICATION NUMBER: US/10/079, 429
CURRENT FILING DATE: 2002-02-2
FRIOR APPLICATION NUMBER: PCT/US95/01035
PRIOR PELING DATE: 1995-01-25
PRIOR PELING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1994-03-12
PRIOR PLING DATE: 1994-03-16
PRIOR PLING DATE: 1994-03-16
PRIOR PLING DATE: 1994-03-16
PRIOR APPLICATION NUMBER: 08/210, 143
PRIOR PLING DATE: 1994-01-27
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PATCHIN VERSION 3.0
SOFTWARE: PATCHIN VERSION 3.0
SEC ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Haseltine et al.
TITLE OF INVENTION: Human DNA Mismatch Repair Proteins FIRE REFERENCE: PF106P3D1
Score 14.2; DB 1;
Pred. No. 9.1e+02;
0; Mismatches 3;
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CURRENT FILING DATE: 2002-02-2
PRIOR APPLICATION NUMBER: US/10/079,429
PRIOR FILING DATE: 1995-01-25
PRIOR PILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/468,024
PRIOR PILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/465,769
PRIOR FILING DATE: 1994-08-23
PRIOR PILING DATE: 1994-08-23
PRIOR FILING DATE: 1994-08-23
PRIOR FILING DATE: 1994-08-13
PRIOR FILING DATE: 1994-08-13
PRIOR FILING DATE: 1994-08-13
PRIOR FILING DATE: 1994-08-13
PRIOR FILING DATE: 1994-01-27
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; Sequence 69, Application US/10079429
; Publication No. US20030027177A1
                                                                                                                                                                                                                                                                             US-10-079-429-66/c

: Sequence 66, Application US/10079429

: Publication No. US20030027177A1

: GENERAL INFORMATION:
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  Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
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Sequence 55, Application US/10079429

Publication No. US203002717741

GENERAL INFORMATION:

APPLICANT: Haseltine et al.

TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
FILE REFERENCE: PF106F301

CURRENT APPLICATION NUMBER: US/10/079,429

CURRENT FILING DATE: 2002-02-22

PRIOR FILING DATE: 1995-06-06

PRIOR FILING DATE: 1995-06-06

PRIOR PLICATION NUMBER: 08/465,769

PRIOR PLICATION NUMBER: 08/465,769

PRIOR PLING DATE: 1995-06-06

PRIOR FILING DATE: 1995-06-06

PRIOR FILING DATE: 1995-06-06

PRIOR FILING DATE: 1994-01-27

PRIOR APPLICATION NUMBER: 08/210,143

PRIOR FILING DATE: 1994-01-27

NUMBER OF SEQ ID NOS: 78

SOFTWARE: Patentin version 3.0

SEQ ID NO 55

LENTH: 20
                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/262,130
FILING DATE: 01-0ct-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/655,327
FILING DATE: 21-MA-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: 950486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFRAX: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2965 CCATGCAAGCAGAGCACCA 2983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 20 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
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US-10-224-260-3
SEQ ID NO 195
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APPLICANT: Minna, John D.
APPLICANT: Minna, John D.
APPLICANT: Minna, John D.
APPLICANT: Minna, John D.
APPLICANT: Main, Ming-Hui
APPLICANT: Wei, Ming-Hui
APPLICANT: Sekido, Yoshitaka
APPLICANT: Gao, Boning
APPLICANT: Gao, Boning
APPLICANT: Gao, Boning
APPLICANT: OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
ITILE REFERENCE: NIH-05043
CURRENT PRILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: BARLIER PRILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-12-30
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-30
PRIOR FILING DATE: BARLIER FILING DATE: 1998-12-30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
LENGTH: 20
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                                                                                                                                                         ; OTHER INFORMATION: primer useful for amplifying codons 415 to 863 of hMLH3 US-10-079-429-69
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-116-949-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 195, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: BAKET, Brenda F.
; APPLICANT: BAKET, LEX M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT APPLICATION NUMBER: 09/167,109
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
                                                                                                                                                                                                                                0.4%; Score 14.2; DB 1; Length 20; ilarity 84.2%; Pred. No. 9.1e+02; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 38, Application US/10116949 Publication No. US20030044911A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             1777 GACCGAGTCTACACTCACC 1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3706 TGGTGGCCAGAGGTGTCAC 3724
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  SOFTWARE: PatentIn version 3.0
                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                 Best Local Similarity
Matches · 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-067-125-195
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                        SEQ ID NO 69
LENGTH: 20
                                                                                                                                                                                                                                           Query Match
                                                                                                                                   FEATURE:
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Sequence 3, Application US/10224260

Sequence 3, Application US/10224260

Sequence 3, Application Wo. US20030059845A1

GENERAL INFORMATION:

APPLICANT: Van Tol, Hubert H.M.

Civelil, Olivier

TITLE OF INVENTION: A No. US20030059845A1el Human Dopamine Receptor and Uses

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                               ò
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                                                                                                                                                                                                                                                                   Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/224,260
FILING DATE: 20-ANG-2002
CLASSIFICATION: <university control of the control o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /partiāl
/cons splice= (5'site: YES, 3'site: NO)
/evidence= EXPERIMENTAL
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FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: No. US20030059845Alnan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..20
IDENTIFICATION METHOD: experimental
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-10-067-125-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1998 CAAGCAGCTGGTGGAGGAC 2016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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TELEX: 810-221-8317
INFORMATION FOR SEQ ID NO: 3:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.2%
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APPLICANT: Steele, Fintan R
APPLICANT: Chader, Gerald J
APPLICANT: Chader, Gerald J
APPLICANT: Chader, Gerald J
APPLICANT: Chader, Gerald J
APPLICANT: Becerra, Sofia P
APPLICANT: Bonson, Lincoln V
APPLICANT: Rodriguez, Ignacio R
FILE OF INVENTY FILING PATE: 2026-4203051
CURRENT FILING DATE: 2026-4203051
CURRENT FILING DATE: 1995-08-29
PRIOR FILING DATE: 1995-08-29
PRIOR FILING DATE: 1995-01-25
PRIOR FILING DATE: 1994-07-25
PRIOR FILING DATE: 1994-07-25
PRIOR FILING DATE: 1992-06-04
PRIOR FILING DATE: 1992-09-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
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OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC OTHER INFORMATION: PRIMER PEATURE:
                                                                                                                                                                                                                                                                                                                     Sequence 77, Application US/10238443
; Sequence 75, Application US/10238443
; Publication No. US2003083302A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Wart
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQLS EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US/09/798,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.2; DB 1;
Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antisense Oligonucleotide
US-10-238-443-75
0; Mismatches
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Best Local Similarity 84.2%;
Matches 16; Conservative
       Conservative
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Matches 16;
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                                                                                       Gaps
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Publication No. US20030083296A1

GENERAL INFORMATION:

APPLICANT: Hong Independent of the property of th
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   Length 20;
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US-10-000-7734-3/C

Sequence 3, Application US/10000773A

Publication No. US20030069195A1

GENERAL INFORMATION:
APPLICANT: Farrar, Generth Jane
APPLICANT: Humphries, Peter
APPLICANT: Humphries, Peter
TITLE OF INVENTION: Suppression of Polymorphic Alleles
FILE REFERENCE: MOR-001CP
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 09/142,125
PRIOR PILING DATE: 1999-04-12
PRIOR PILING DATE: 1999-04-12
PRIOR PILING DATE: 1999-04-12
PRIOR PILING DATE: 1996-03-03

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENTIN NUMBER: GB 9604449.0

PRIOR FILING DATE: 1996-03-01

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 3

LENGTH: 20

LENGTH: 20
                                                                                   3; Indels
                                           9.1e+02;
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Query Match 0.4%; Score 14.2; I
Best Local Similarity 84.2%; Pred. No. 9.16
Matches 16; Conservative 0; Mismatches
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                                                                                                                                                                                                                                  19 GCGGCCGGACGCGGCTCAC 1
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-001-844-11
                      Query Match
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Matches
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US-10-016-149-35/C
US-10-016-149-35/C
Publication No. US20030100524A1
Publication No. US20030100524A1
GENERAL INPORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: G. INVENTION: APPLICANTE Watt
TITLE OF INVENTION: DEPENDENT) EXPRESSION
FITE REFERENCE: RTS-0325
CURRENT APPLICATION NUMBER: US/10/016,149
CURRENT FILING DATE: 2001-11-01
NUMBER OF SQ ID NOS: 84
: LENGTH: 20
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APPLICANT: Berger, Nigel W.

APPLICANT: Fraser, Nigel W.

APPLICANT: Fraser, Nigel W.

APPLICANT: Leary, Jeffrey J.

TITLE OF INVENTION: Compounds And Methods For Treating And
TITLE OF INVENTION: Compounds And Methods For Treating And
TITLE OF INVENTION: Compounds And Methods For Treating And
FILE REFERENCE: PSC682C1

CURRENT APPLICATION NUMBER: US/10/108,164

PRIOR FILING DATE: 1999-07-01

PRIOR FILING DATE: 1999-07-01

PRIOR FILING DATE: 1999-07-01

PRIOR FILING DATE: 1997-07-03

PRIOR FILING DATE: 1997-09-03

PRIOR FILING DATE: 1997-09-01

PRIOR FILING DATE: 1997-09-01

PRIOR FILING DATE: 1997-09-01

PRIOR FILING DATE: 1997-09-01

PRIOR FILING DATE: 1998-04-01

NUMBER OF SOL ID NOS: 145

NUMBER OF SOL ID NOS: 145
                                                                  Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Antisense Oligonucleotide US-10-016-149-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 127, Application US/10108164
Publication No. US20030104356Al
GENERAL INFORMATION:
                                                                                                                                                                2585 GIGGGCTCGGCCCTCCCA 2603
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                                                                                                                                                                                                               20 GrrcGcrcGrccGcrcccA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
; OTHER INFORMATION: PRIMER 353
US-10-216-373-30
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;. ORGANISM: Mus musculus
US-10-108-164-127
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Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 20;
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lex M. COWSETT
TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
CURRENT APPLICATION NUMBER: US/10/001,844
CURRENT APPLICATION NUMBER: US/10/001,844
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 49
SEQ ID NO: 1
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQUENCE 13. Application US/10149352

SGUENCE 13. Application US/10149352

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/149,352

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: PCT/GB00/04741

PRIOR APPLICATION NUMBER: GB 9929487.8

PRIOR APPLICATION NUMBER: GB 9929487.8

PRIOR APLICATION NUMBER: GB 9929487.8

PRIOR FILING DATE: 1999-12-15

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 13

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3652 TIGCTIGCCTGCAGGGCCA 3670
                                                                                                  2000 AGCAGCTGGTGGAGGACCT 2018
                                                                                                                                                                                                                                         US-10-001-844-11; Sequence 11, Application US/10001844; Publication No. US20030105041A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2323 GTGTGTGTGTGTGTGTG 2341
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    0.4%;
Local Similarity 84.2%;
les 16; Conservative
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                                                                                                                                                                                                                                                                                                                      APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity
Matches 16; Conserv
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Sequence 32, Application US/10017621
Publication No. US20030138952A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Mark P. Roach
TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 1 EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Sequence 25, Application NS/10007010

Publication NO. US20030125275A1

GENERAL INFORMATION:

APPLICANT: Alexander H. Borchers

TITLE OP INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION

FILE REPERENCE: RTS-0345

CURRENT APPLICATION NUMBER: US/10/007,010

CURRENT FILING DATE: 2001-12-04

NUMBER OF SEQ ID NOS: 87

LENGTH: 20
                                                                                                                                                                                                           Sequence 11, Application US/10007010
; Bublication No. US20030125275A1
; GENERAL INFORMATION:
; APPLICANT: Alexander H. Borchers
; APPLICANT: Alexander H. Borchers
; TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
; FILE REFERENCE: RTS-0345
; CURRENT APPLICATION NUMBER: US/10/007,010
; CURRENT PILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 87
; LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.4%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 9.1e+02; tive 0; Mismatches 3; Indel8
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Mismatches
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                                                                                1 CCCCATCGCCTGCAGATGC 19
                                                 46 CCCCAGCGGCTGCAGGTGC 64
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Matches 16; Conservative
  16; Conservative
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Matches 16; Conserv
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  Matches
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                               Sequence 20. Application US/10269501
Publication No. US20030113347A1
GENERAL INFORMATION:
APPLICANT: Schweiz. Serum. & Impfinstitut Bern
APPLICANT: Guat, Maria, Grazia
APPLICANT: Gluck, Reinhard
APPLICANT: Gluck, Reinhard
APPLICANT: Malti, Ernst Manuostimulating and Immunopotentiating Reconstituted Influenza TITLE OF INVENTION: Uirosomes and Vaccines Containing Them
FILE REFERENCE: 009848-0290188
CURRENT FILING DATE: 2003-02-28
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i Sequence 75, Application US/10309362

j Sequence 75, Application US/10309362

j CENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: DOING T. Ward
    APPLICANT: AND T. Ward
    TITLE OF INVENTION: ANTISENSE MODULATION OF RECQLS EXPRESSION
    TITLE OF INVENTION: ANTISENSE US/10/309,362
    CURRENT APPLICATION NUMBER: US/10/309,362
    CURRENT FILING DATE: 2002-12-03
    PRIOR FILING DATE: 2001-03-01
    NUMBER OF SEQ ID NOS: 92
    NUMBER OF SEQ ID NOS: 92
    LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                      CURKENT FILING DAIE: 2003-002-28

PRIOR APPLICATION NUMBER: 09/264,551

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1994-04-11

PRIOR FILING DATE: 1994-04-11

PRIOR FILING DATE: 1993-03-03

PRIOR FILING DATE: 1998-05-03-03

PRIOR FILING DATE: 1998-05-22

PRIOR FILING DATE: 1998-05-23

PRIOR FILING DATE: 1997-05-08

PRIOR FILING DATE: 1997-05-08

PRIOR FILING DATE: 1997-05-08

PRIOR FILING DATE: 1991-05-08

PRIOR FILING DATE: 1991-05-10

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PARLENT NEWBER: PEBILOTETT OF SEQ ID NOS: 20

SOFTWARE: PARLENT NEWBER: PARLENT DATE: 1991-05-10
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2<sup>3</sup>
Matches 16; Conservative
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Best Local Similarity
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Sequence 76, Application US/10029517
Publication No. US20030148969A1
CENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
APPLICANT: Susan J. Myers
TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
FILE REFERENCE: RTS-0352
CURRENT APPLICATION NUMBER: US/10/029,517
CURRENT PILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No. US20030147864A1

Publication No. US20030147864A1

Publication No. US20030147864A1

APPLICANT: Remeth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION

TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION

TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION

CURRENT APPLICATION NUMBER: US/10/024,396

CURRENT PILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 91

LENGTH: 20
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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US-10-024-396-52
                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/187,049
FILING DATE: 28-Jun-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                               APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Leith, Debra K
REGISTRATION NUMBER: 32,619
REFERENCE/DOCKET NUMBER: 98-10
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-442-6674
TELEFAX: 206-442-6674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
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STRANDEDNESS: single
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78-10-017-621-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10-018-10
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 14.2; DB 1; Length 20; 84.2%; Pred. No. 9.1e+02; tive 0; Mismatches 3; Indels
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TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR
PAR4 (ZCHEMR2)
                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Antisense Oligonucleotide US-10-017-621-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE;
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-017-621-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                         CURRENT APPLICATION NUMBER: US/10/017,621
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 32
LENGTH: 20
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US-10-187-049-10/C
Sequence 10, Application US/10187049
Publication No. US20030143218A1
GENERAL INFORMATION:
PRESPLICANT: Xu, Wenfeng
PRESPLICANT: Xu, Wenfeng
PRESPLICANT: Xu, Wenfeng
Yee, David P.
Yee, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2729 ACGGGTACCTGAAGATGGG 2747
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.29
Matches 16; Conservative
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STATE: WA
FILE REFERENCE: RTS-0350
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FastSEQ for Windows Version 2.0
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Sequence 67, Application US/10376566
| Publication No. US20030158144A1
| GENERAL INFORMATION:
| APPLICANT: Kenneth W. Dobie
| APPLICANT: Kenneth W. Dobie
| APPLICANT: Brick Koller
| APPLICANT: Brick Koller
| TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR BETA EXPRESSION
| CURRENT APPLICATION NUMBER: US/10/376,566
| CURRENT PELLING DATE: 2003-02-27
| FRIOR PELLOATION NUMBER: US/10/005,058
| PRIOR FILING DATE: 2001-12-07
| NUMBER OF SEQ ID NOS: 96
| SEQ ID NO 67
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Publication No. US20030166138A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kinsella . Todd
APPLICANT: Ohashi, Cara
APPLICANT: Anderson, Dave
TITLE OF INVENTION: Cyclic Peptides and Analogs Useful to Treat Allergies
FILE REFERENCE: RIGL-002/01US
CURRENT APPLICATION NUMBER: US/10/197,927
CURRENT FILING DATE: 2003-01-23
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                                                                                                     PRIOR PELICATION NUMBER: US/09/722,319
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 1996-12-06
PRIOR PELING DATE: 1996-09-09
PRIOR PELING DATE: 1995-06-09
PRIOR PELING DATE: 1995-06-09
PRIOR PELING DATE: 1994-06-09
PRIOR PELING DATE: 1994-06-09
NUMBER: PRESIDENTIAL NUMBER: EP 94870093.5
NUMBER: PRESIDENTIAL NU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: Primer
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US-10-197-927-53/c
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| Sequence 66, Application US/10339604
| Sequence 66, Application US/10339604
| Sequence 66, Application Occupance 66, Application US/20030152982A1
| Sequence 66, Application US/20030152982A1
| Sequence 66, Application US/20030152982A1
| APPLICANT: DESTRICTORY OCCUPANCE OCCUP
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US-LIG-348-9-83/Application US/10348485

FUBLICATION NO. US20030148989A1

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

APPLICANT: Dean, Nicholas M.

APPLICANT: Holmlund, Jon T.

APPLICANT: OF INVENTION: Oligonuclectide Modulation Of Protein Kinase C
FILE REFERENCE: ISIS4954

CURRENT PELING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/10/25,139

PRIOR FILING DATE: 1997-03-31

PRIOR PILING DATE: 1997-03-31

PRIOR PILING DATE: 1993-07-09

PRIOR PILING DATE: 1993-07-09

PRIOR APPLICATION NUMBER: US 08/089,996

PRIOR PILING DATE: 1993-07-09

PRIOR APPLICATION NUMBER: US 07/852,852

PRIOR APPLICATION NUMBER: US 07/852,852

PRIOR PILING DATE: 1993-07-09

PRIOR PILING DATE: 1993-07-09
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                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Antisense Oligonucleotide US-10-029-517-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-485-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2380 CATCTTGCCTCCAGGTGCA 2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1812 CTTTGGGGTCCTGCTCTGG 1830
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                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 107
SEQ ID NO 76
                                                                                                                                                                                                                                                                                                          FEATURE:
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Gaps

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US-10-032-585-4348

Sequence 4348, Application US/10032585

Publication No. US20030180953A1

GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
TITLE OF INVENTION Gene Disruption Methodologies for Drug Target Discovery
CURRENT APPLICATION UNMERS: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4348

LENGTH: 20
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US-10-032-585-557, Application US/10032585
Sequence 5557, Application US/10032585
Sequence 5557, Application No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5557
LENGTH: 20
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APPLICANT: Shepard, Peter J.
TITLE OF INVENTION: JAGGED 2 INHIBITORS FOR INDUCING APOPTOSIS
FILE REFERENCE: ISPH-0660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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Pred. No. 9.1e+02;
0; Mismatches 3;
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. Sequence 53, Application US/10096399A
. Publication No. US20030185829A1
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1638 CAATGTGCTGGTGACCGAG 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      829 GCGTGGCTGGTGCTGC 847
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  20 AGGGACCTGCCTGACAGCA
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Best Local Similarity 84.2%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA; Candida albicans US-10-032-585-5557
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Publication No. US20030170636A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF JAGGED 2 EXPRESSION FILE REFERENCE: RTS-244
CURRENT APPLICATION NUMBER: US/10/091,625
CURRENT FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 53
LENGTH: 20
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Publication No. US20030170636A1
GENERAL INFORMATION:
APPLICANT: SHERENCE:
TITLE OF INVENTION: ANTISENSE MODULATION OF JAGGED 2 EXPRESSION
CURRENT APPLICATION UNMER: US/10/091,625
CURRENT FILING DATE: 2002-03-05
SEQ ID NO 72
LENGTH: 20
                                                                                                                                                                                                                                                                                             Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Antisense Oligonucleotide US-10-091-625-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antisense Oligonucleotide US-10-091-625-72
PRIOR APPLICATION NUMBER: 60/358,827
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.1
SEQ ID NO 53
LENGTH: 20
                                                                                                                                                                                                                       ; OTHER INFORMATION: synthetic primer US-10-197-927-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3048 GGGCCCCTGGCACTCTTGT 3066
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                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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RESULT 1375
US-10-321-856-243
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LENGTH: 20
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LENGTH: 20
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| Sequence 72. Application US/10096399A |
| Sequence 72. Application No. US2030185829A1 |
| Publication No. US2030185829A1 |
| Publication No. US2030185829A1 |
| Publication No. US2030185829A1 |
| APPLICANT: Koller, Erich |
| APPLICANT: Shepard, Peter J. |
| TITLE OF INVENTION: JAGGED 2 INHIBITORS FOR INDUCING APOPTOSIS |
| TITLE OF INVENTION UNMERS: US/10/096,399A |
| CURRENT FILING DATE: 2002-03-12 |
| SOFUMARE: Patentin version 3.1 |
| SSEQ ID NO 72 |
| LENGTH: 20
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                            ; OTHER INFORMATION: Antisense oligonucleotide
US-10-096-399A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Antisense oligonucleotide
CURRENT APPLICATION NUMBER: US/10/096,399A
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 91
SEQ TWARE: PatentIn version 3.1
SEQ ID NO 53
LENGTH: 20
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Kwiatkowski, Jr., Robert W.
Lukowiak, Andrew A.
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Argue, Brad T.
Bartholomay, Christian T.
Chehak, LuAnne
Curtis, Michelle L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2531, Application US/10084839 Publication No. US20030186238A1 GENERAL INFORMATION: APPLICANT: Third Wave Technologies
                                                                                                                                                                                                                                                                                                                                               3048 GGCCCCTGCCACTCTTGT 3066
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                                                                                                                                                                                                                                                                                                                                                                                          1 GGGCTGCTGCACACTTGT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyamichev, Victor
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Matches 16; Conservative
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Hall, Jeff G.
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                                                                                                                                 TYPE: DNA
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APPLICANT:
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Sequence 243, Application US/10321856
Publication No. US20030194393A1
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
FILE REFERENCE: TX-1-C2-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MICHAELES, MICHAELS CAPPLICANT: APPLICANT: ASSES, Luigh
APPLICANT: Grasso, Luigh
APPLICANT: Grasso, Luigh
APPLICANT: Grass, Philip M
TITLE OF INVENTION: HYPERMUTABLE CELLS
FILE REFERENCE: MOR-0005
FILE REFERENCE: MOR-0005
CURRENT APPLICATION NUMBER: US/09/708,200
PRIOR PILING DATE: 2003-02-19
PRIOR PLING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                     APPLICANT: Skrzypczynski, zbigniew APPLICANT: Takova, Testska Y. APPLICANT: Takova, Testska Y. APPLICANT: Thompson, Lisa C. TUTLE OF INVENTION: RNA Detection Assays TILE OF INVENTION: RNA Detection Assays CURRENT FILING DATE: 2002-02-26
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: Patentin version 3.1
                             Schaefer, James J.
Skrzypczynski, Zbigniew
Takova, Tsetska Y.
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son-Munoz, Marilyn C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10369845
Publication No. US20030186441A1
GENERAL INFORMATION:
APPLICANT: Nicolaides, Nicholas C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 ACAAGTTTGGCAGCATCCG 488
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic US-10-084-839-2531
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Matches 16; Conservative
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: DOLYNUCLECTIDES ENCODING THREE NOVEL HUMAN CELL SURFACE PROTEINS V
TITLE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4, I
TITLE OF INVENTION: THEREOF
FILE REFERENCE: D0153 NP
CURRENT APPLICATION NUMBER: US/10/193,477
CURRENT FILING DATE: 2002-07-11
PRIOR PAPLICATION NUMBER: US 60/304,888
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR PILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patentin version 3.1
LENGTH: 20
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APPLICANT: Pamela Nero
APPLICANT: Pamela Nero
APPLICANT: Mark J. Graham
APPLICANT: Mark J. Graham
APPLICANT: Erich Koller
APPLICANT: Erich Koller
APPLICANT: Mano Manolaran
TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
FILE REPERENCE: ISPH-0623.
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 09/048,810
PRIOR APPLICATION NUMBER: US 09/048,810
PRIOR PILING DATE: 1999-03-26
NUMBER OF SED ID NOS: 379
SOFTWARE FEALSEQ for Windows Version 4.0
                                                                                                                                                    Ouery Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 113, Application US/10193477
Publication No. US20030195163A1
GENERAL INFORMATION:
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Publication No. US20030203862A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         2340 TGTGTGTGTGTGCACATCC 2358
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Best Local Similarity 84.2%;
Matches 16; Conservative
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-193-477-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-193-477-113 '
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Publication No. US20030195163A1

GENERAL INFORMATION:
APPLICANT BETISTOL—Myers Squibb Company

TITLE OF INVENTION: DEUCINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4,

TITLE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4,

TITLE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4,

TITLE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4,

TITLE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4,

FILE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4,

FILE OF INVENTION: THEREOF

FILE REFERENCE: D0153 NP

CURRENT FILING DATE: 2002-07-11

PRIOR PAPLICATION NUMBER: US 60/372,147

PRIOR PLING DATE: 2002-04-12

NUMBER OF SEQ ID NOS: 229

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer 10 US-10-311-886-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.4%; Score 14.2; DB 1; Length 20; ilarity 84.2%; Pred. No. 9.1e+02; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-311-886-45
; Sequence 45, Application US/10311886
; Publication No. US20030195151A1
; GENERAL INFORMATION:
; APPLICANT: K.U. LEUVEN Research and Development et al.
; TITLE OF INVENITION: Biocatalyst inhibitors
; FILE REFERENCE: PCT/BE 01/00106
; CURRENT APPLICATION NUMBER: US/10/311,886
; CURRENT FILING DATE: 2002-12-23
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 45
; SEQ ID NO 45
; LENGTH: 20
      CURRENT APPLICATION NUMBER: US/10/321,856
                           CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 09/216,393
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin version 3.1
SEQ ID NO 243
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                        ), OTHER INFORMATION: Synthetic Primer US-10-321-856-243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2850 TATGGAAGAGGAAAAGGCT 2868
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                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial sequence
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Best Local Similarity
Matches 16; Conserva
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Sequence 72, Application No. US20030207839A1

GENERAL INFORMATION:
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF JAGGED 2 EXPRESSION
FILE REFERENCE: RTS-024

CURRENT APPLICATION NUMBER: US/10/461,668

CURRENT APPLICATION NUMBER: US/10/091,625

PRIOR FILING DATE: 2002-03-05

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SUBJECT STREET APPLICANT: SUBJECT STREET STREET TITLE OF INVENTION: ANTISENSE MODULATION OF JAGGED 2 EXPRESSION FILE REPERENCE: RTG-0244
CURRENT APPLICATION NUMBER: US/10/461,668
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US/10/091,625
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 53
LENGTH: 20
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
                                                                                        Length 20;
                                                                                                                                 3; Indels
                                                                                   Query Match

0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                    , OTHER INFORMATION: Antisense Oligonucleotide US-10-005-344-338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                   RESULT 1380
US-10-461-668-53
Sequence 53, Application US/10461668
Publication No. US20030207839A1
GENERAL INFORMATION:
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                                                                                                                                                                           2305 CAGAGCTTTGGTCTGTGTG 2323
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-461-668-72/c
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Sequence 57, Application US/10144488
Publication No. US20030212017A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF FARNESYL TRANSFERASE BETA SUBUNIT EXPRESS
FILE REFERENCE: RTS-0363
CURRENT APPLICATION NUMBER: US/10/144,488
CURRENT FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 57
LENGTH: 20
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TITLE OF INVENTION: ANTISENSE MODULATION OF COT ONCOGENE EXPRESSION
FILE REPERENCE: RTSP-0346
CURRENT APPLICATION NUMBER: US/10/181,873A
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: PCT/US01/01417
PRIOR FILING DATE: 2000-01-16
PRIOR FILING DATE: 2000-01-16
PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 89
LENGTH: 20
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Antisense Oligonucleotide US-10-181-873A-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 78, Application US/10181873A Publication No. US20030212019A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3447 TTAGATGTTACAAGTTTAT 3465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 CCTTCTGGCAGGCGGGCT 1
                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Matches 16; Conservative
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-10-144-488-57/c
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US-10-181-873A-78
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APPLICANT: Becker, Kenneth David
APPLICANT: Becker, Kenneth David
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi, Gonul
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Bartram, Lars
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
APPLICANT: Mullin, Kristina M.
APPLICANT: Mullin, Kristina M.
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
TITLE OF INVENTION: NUMBER: US 60/339,525
PRIOR FILING DATE: 2001-110-25
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR PELING DATE: 2001-11-09
PRIOR PILING DATE: 2001-12-04
PRIOR PILING DATE: 2001-12-04
PRIOR PELING DATE: 2001-12-04
PRIOR PILING DATE: 2001-12-04
PRIOR PELING DATE: 2001-11-04
PRIOR PELING DATE: 2001-11-04
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PRIO
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Sequence 80, Application US/10159266
Sequence 80, Application US/10159266
Sequence 80, No. US20030224511A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF CATHEPSIN Z EXPRESSION
TITLE PEPERENCE: RTS-0398
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 158
SEQ ID NO 80
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
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                                                                                                                                                                                                                                         Sequence 292, Application US/10282174
Publication No. US20030224380A1
GENERAL INFORMATION:
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       573 GCTGGGCAGCGACGTGGAG
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: hairpin oligonucleotide
US-10-400-670-4
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Sequence 14, Application US/10438075

Publication No. US20030216345A1.

Publication No. US20030216345A1.

GENERAL INFORMATION:

APPLICANT: Schering Aktiengesellschaft

TILE OF INVENTION: Histone deacetylase inhibitor and use thereof

TILE REFERENCE: 1023370.

CURRENT APPLICATION NUMBER: US/10/438,075

CURRENT FILIKG DATE: 2003-05-15

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 14

LENGTH: 20
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Publication No. US20030219742A1
GENERAL INFORMATION:
APPLICANT: Sanjay Bhanot
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HMGI-C EXPRESSION
FILE REPERENCE: RTS-0296
CURRENT APPLICATION NUMBER: US/10/114,279
CURRENT FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                            Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
; OTHER INFORMATION: Antisense oligonucleotide no.12
US-10-438-075-14
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-279-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1193 CCCTGGGCAAGCCCCTTGG 1211
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                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
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                               SEQ ID NO 4
LENGTH: 20
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LENGTH: 20
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NAME/KEY:
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TITLE OF INVENTION: ANTISENSE MODULATION OF BETA-SITE APP-CLEAVING ENZYME EXPRESSION FILE REFERENCE: RTS-0383
CURRENT APPLICATION NUMBER: US/10/159,942
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 133
SEQ ID NO 100
LENGTH: 20
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APPLICANT: Wystt, Jacqueline R.
APPLICANT: Workers, Timothy A.
TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
TITLE OF INVENTION: MODULATION BY OLIGONUCLECTIDES AND
TITLE OF INVENTION: GENERALION OF OLICONUCLECTIDES FOR GENE MODULATION
FILE REFERENCE: ISIS-4503
CURRENT APPLICATION NUMBER: US/10/388,263
CURRENT FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 947
SEQ ID NO 423
LENGTH: 20
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84.2%; Pred. No. 9.1e+02;
.ive 0; Mismatches 3; Indels
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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Publication No. US20030228597A1
GENERAL INFORMATION:
APPLICANT: COWBERT, Lex M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 423, Application US/10388263
Publication No. US20030228597A1
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Henri M.
Douglas G.
Cara
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Sasmor, Henri M.
Brooks, Douglas G.
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McNeil, John
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                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                 TYPE: DNA
ORGANISM: H. sapiens
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US-10-388-263-442/c
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APPLICANT:
APPLICANT:
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Sequence 28, Application US/10159942

Publication No. US20030224512A1

GENERAL INFORMATION:

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF BETA-SITE APP-CLEAVING ENZYME EXPRESSION

TITLE OF INVENTION: ANTISENSE WODULATION OF BETA-SITE APP-CLEAVING ENZYME EXPRESSION

CURRENT PELING DATE: 2002-05-31

NUMBER OF SEQ ID NOS: 133

SEQ ID NO 28

LENGTH: 20
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                                                                                                                      Gaps
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Publication No. US20030224511A1

GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TILLE OF INVENTION ANTISENSE MODULATION OF CATHEPSIN Z EXPRESSION
FILE REFERENCE: RTS-0398
CURRENT APPLICATION NUMBER: US/10/159,266
CURRENT PILING DATE: 2002-05-31

NUMBER OF SEQ ID NOS: 158
SEQ ID NO 152
LENGTH: 20
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                                                                       Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indel8
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Pred. No. 9.1e+02;
0; Mismatches 3;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-159-266-80
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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ORGANISM: Artificial Sequence
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ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                               US-10-159-266-152/c
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APPLICANT: Susan M. Freier
APPLICANT: Susan M. Preier
APPLICANT: Susan M. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRES
FILE REFERENCE: RTS-0365
CURRENT APPLICATION NUMBER: US/10/159,856
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 130
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; Publication No. US20030232436A1
; Fublication No. US20030232436A1
; GENERAL INFORMATION:
; APPLICANT: Brett F. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF E2-EPF EXPRESSION
; TILE REFERENCE: HTS-0021
; CURRENT APPLICATION WHERE: US/10/173,240
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 28
; LENGTH: 20
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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Pred. No. 9.1e+02;
0; Mismatches 3;
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                            , OTHER INFORMATION: Antisense Oligonucleotide US-10-159-856-83
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Publication No. US20030228689A1
GENERAL INFORMATION:
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US-10-173-240-39/c
; Sequence 39, Application US/10173240
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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ORGANISM: Artificial Sequence
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ORGANISM: H. sapiens
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FEATURE:
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US-10-159-856-80, Application US/10159856
| Publication No. US20030228689A1
| Sequence 80, Application No. US20030228689A1
| GENERAL INFORMATION:
| APPLICANT: Susan M. Freier
| TITLE OF INVENTION: ANTIENEW MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRE FILE REFERENCE: RTS-0365
| CURRENT APPLICATION UNDER: US/10/159,856
| CURRENT FILING DATE: 2002-05-31
| NUMBER OF SEQ ID NOS: 134
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US-10-159-856-83/C

US-10-159-86-83/C

US-10-159-86-83/C

SQUENCE 83, Application US/10159856

Publication No. US20030228689A1

GENERAL INFORMATION:
APPLICANT: Susan M. Freier

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRE
FILE REFERENCE: RTS-036-85

CURRENT APPLICATION NUMBER: US/10/159,856

CURRENT FILING DATE: 2002-05-31

NUMBER OF SEQ ID NOS: 134

SEQ ID NO 83

LENGTH: 20

TUTLE OF THE OF 
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                            APPLICANT: Borchers, Alexander
APPLICANT: Vickers, Timochy A.
TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
TITLE OF INVENTION: MODULATION BY OLIGONUCLECTIDES AND
TITLE OF INVENTION: GENERATION OF OLIGONUCLECTIDES FOR GENE MODULATION
TITLE OF INVENTION: GENERATION OF OLIGONUCLECTIDES FOR GENE MODULATION
TITLE OF INVENTION: US/10/388,263
CURRENT APPLICATION NUMBER: US/10/388,263
CURRENT FILING DATE: 2003-03-12
SOFTWARE: Fast SEQ for Windows Version 4.0
SEQ ID NO 442
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-442
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Wyatt, Jacqueline R.
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 84.2
Matches 16; Conservative
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FEATURE:
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Publication No. US20030232436A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie
TITLE OP INVENTION: ANTISENSE MODULATION OF E2-EPF EXPRESSION
FILE REPERENCE: HTG-0021
CURRENT APPLICATION NUMBER: US/10/173,240
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 39
LENGTH: 20
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Publication No. US20030232436A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie
TITLE REFERENCE: HTS-0021
CURRENT APPLICATION UNMBER: US/10/173,240
CURRENT APPLICATION NUMBER: US/10/173,240
NUMBER OF SEQ ID NOS: 80
ILENGTH: 20
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APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF E2-EPF EXPRESSION
FILE REPRENCE: HTS-0021
CURRENT APPLICATION NUMBER: US/10/173,240
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 72
LENGTH: 20
                                                                                                                                                                                                                                                                                                                   Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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US-10-173-240-72
Sequence 72, Application US/10173240
Publication No. US20030232436A1
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ORGANISM: Artificial Sequence
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ORGANISM: H. sapiens
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ORGANISM: H. sapiens
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Sequence 29, Application US/10174465

Publication No. US20030232772A1

Publication No. US20030232772A1

APPLICANT: C. Frank Bennett

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF EXTRACELLULAR-SIGNAL-REGULATED KINASE-6 E)

TOTHE OF INVENTION: ANTISENSE WODULATION OF EXTRACELLULAR-SIGNAL-REGULATED KINASE-6 E)

CURRENT APPLICATION NUMBER: US/10/174,465

CURRENT FILING DATE: 2002-06-17

NUMBER OF SEQ ID NOS: 70

LENGTH: 20

LENGTH: 20
                                                                                                                                                                                                                                                   Sequence 61, Application US/10174460

| Sequence 61, Application No. US20030232441A1
| GENERAL INFORMATION:
| APPLICANT: Brett P. Monia
| APPLICANT: Kenneth W. Dobie
| TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 4 EXPRESSION FILE REFERENCE: PTS-0014
| CURRENT APPLICATION NUMBER: US/10/174,460
| CURRENT FILING DATE: 2002-06-17
| NUMBER OF SEQ ID NOS: 109
| LENGTH: 20
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  Length 20;
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Score 14.2; DB 1;
Pred. No. 9.1e+02;
0; Mismatches 3;
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                     1821 CCTGCTCTGGGAGATCTTC 1839
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0.4%;

Best Local Similarity 84.2%;

Matches 16; Conservative
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US-10-174-465-29/c
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US-10-289-762-1841/c

| Sequence 1841, Application US/10289762
| Sequence 1841, Application No. US20040006218A1
| Publication No. US20040006218A1
| GENERAL INFORMATION:
| APPLICANT: Griffais, R. | APPLICANTION: TITLE OF INVENTION: and treatment of infection | TITLE OF INVENTION: and treatment of infection | FILE REFERENCE: 9710-003-999 | FILE REFERENCE: 9710-003-999 | CURRENT APPLICATION NUMBER: US/10/289,762 | UNMBER OF SEQ ID NOS: 6849 | SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION: APPLICATION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION NUMBER OF SEQ ID NOS: 6849 | LEMICANTION NUMBER OF SEQ ID NOS: 6849 | LEMICA
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Sequence 11617, Application US/20040005584A1

Sequence 11617, Application No. US20040005584A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Chunakov, Ilya

FILE REPERBNCE: GENSET.020CP1

CURRENT APPLICATION WUMBER: US/10/349,143

CURRENT APPLICATION WUMBER: US/09/422,978

PRIOR APPLICATION NUMBER: US/09/422,978

PRIOR PILING DATE: BARLIER PILING DATE: 1999-04-21

PRIOR PILING DATE: EARLIER PILING DATE: 1999-04-21

PRIOR PILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR PILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR PILING DATE: EARLIER FILING DATE: 1998-11-23

NUMBER: OF SEQ ID NOS: 11796

SEQ ID NO 11617
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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Best Local Similarity 84.2%
Matches 16; Conservative
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US-10-349-143-11617
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**APPLICANT: C. Warcusson

**APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: EXTRACELULAR-SIGNAL-REGULATED KINASE-6 INHIBITING

TITLE OF INVENTION: ANGIOGENESIS

TITLE OF INVENTION: ANGIOGENESIS

CURRENT APPLICATION

NUMBER OF SEQ ID NOS: 71

LENGTH: 20

TYPE: N.**
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; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT FILING DATE: 2002-07-02
; SEQ ID NO 134
; LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1404
US-10-188-646-64/C
S-10-188-646-64/C
Sequence 64, Application US/10188646
Publication No. US20040005565A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
CURRENT FILING DATE: 2002-07-02
CURRENT FILING DATE: 2002-07-02
NOMBER OF SEQ ID NOS: 153
LENGTH: 20
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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US-10-348-431-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1679 ACTTCGGGCTGGCCCGGGA 1697
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-188-646-134
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US-10-188-646-134
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1644 GCTGGTGACCGAGGACAAC 1662
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                                                                                            ; ORGANISM: Chlamydia pneumoniae US-10-289-762-4798
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    TYPE: DNA
    ORGANISM: Chlamydia pneumoniae
US-10-289-762-5790

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NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 4798
LENGTH: 20
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Matches 16; Conserv
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                                                                           TYPE: DNA
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                                                                                                                                                           Sequence 3458, Application US/10289762

Sequence 3458, Application WS. 1020040006218A1

GENERAL INFORMATION:

APPLICANT: Griffals, R.

TITLE OF INVENTION: Thereof and uses thereof, in particular for the diagnosis, preverser APPLICATION WHORER: US/10/289,762

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION WHORER: US/10/289,762

CURRENT FILING DATE: 2003-03-27

WUMBER OF SEQ ID NOS: 6849
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| Publication No. US20040006218A1
| Publication No. US20040006218A1
| GENERAL INFORMATION:
| APPLICANT: Griffals, R. | TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
| FILE REPERENCE: 9710-003-999 | CURRENT APPLICATION NUMBER: US/10/289,762 | CURRENT PILING DATE: 2003-03-27 | NUMBER OF SEQ ID NOS: 6849 | SEQ ID NO 4668
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Sequence 4798, Application US/10289762

Sequence 4798, Application US/10289762

Sequence 4798, Application US/10289762

GENERAL INFORMATION:

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve

TITLE OF INVENTION: and treatment of infection

TITLE OF INVENTION: and treatment of infection

TITLE OF INVENTION: and treatment of infection

CURRENT PPLICATION NUMBER: US/10/289,762

CURRENT FILING DATE: 2003-03-27
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3;
  1208 TTGGGGAGGCTGCTTCGG 1226
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                                               19 Trgaagaagcrgcrrcgg 1
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; ORGANISM: Chlamydia pneumoniae
US-10-289-762-4668
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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Sequence 4885. Application US/10289762

Publication No. US20040006218A1

Publication No. US20040006218A1

RENERAL INFORMATION:

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever

TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/10/289,762

CURRENT APPLICATION DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 6849

SEQ ID NOS + 6849
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Publication No. US20040006218A1

RENERAL INFORMATION:

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever

TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/10/289,762

CURRENT APPLICATION NUMBER: US/10/289,762

CURRENT FILING DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 6849
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
Length 20;
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       Query Match

0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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US-10-199-199-107
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                                                                                    APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmente
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 6696
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Publication No. US20040014047A1
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. Cowsert
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIM DOMAIN KINASE 1 EXPRESSION
CURRENT APPLICATION NUMBER: US/10/199,199
CURRENT FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 148
SEQ ID NO 107
LENGTH: 20
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Publication No. US20040014047A1
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIM DOMAIN KINASE 1 EXPRESSION
FILE REFERENCE: RTS-0375
CURRENT APPLICATION NUMBER: US/10/199,199
CURRENT FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 148
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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              Sequence 6696, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2613 CTGAGCCTGCAGGGAAGCC 2631
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; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6696
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ORGANISM: H. sapiens
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  US-10-289-762-6696
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LENGTH: 20
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MASUBA, Todd M.
APPLICANT: WANDER, Justin E.
APPLICANT: MANUER, Justin E.
APPLICANT: APPLICANT: AIsei
APPLICANT: APPLICANT: MINGSHITA, Taisei
APPLICANT: APPLICANT: METHODS OF IDENTIFYING COMPOUNDS THAT MODULATE IL-4 RECEPTOR-MEDIJ
TITLE OF INVENTION: SYNTHESIS UTILIZING AN ADENOSINE KINASE
TITLE REFERENCE: RIGL-009/0002
CURRENT APPLICATION NUMBER: US/10/197,381
CURRENT PILING DATE: 2002-07-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PARENTIN VETBION 3.1
SEQ ID NO 7
LENGTH: 20
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APPLICANT: Wasuda, Ustin B
APPLICANT: Kinsella, Todd M
APPLICANT: Kinsella, Todd M
APPLICANT: Kinselita, Taisei
APPLICANT: Bennett, Mark K
APPLICANT: Anderson, David C
TITLE OF INVENTION: Methods of Identifying Compounds that Modulate IL-4 Recep
TITLE OF INVENTION: Synthesis Utilizing a Chloride Intracellular Channel I
FILE REFERENCE: RIGL-013/0005
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                                                      Gaps
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     Length 20;
                                                      Indels
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
     Score 14.2; DB 1;
Pred. No. 9.1e+02;
                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-197-945A-14/c; Sequence 14, Application US/10197945A; Publication No. US20040014148A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: synthetic primer US-10-197-381-7
                                                                                                      1874 TGGAGGAGCTCTTCAAGCT 1892
                                                                                                                                                                                                                                                                           Sequence 7, Application US/10197381
Publication No. US20040014147A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                866 TGGAGGCTGACGAGGCGGG 884
                                                                                                                                     2 TGGTGGAGCACTCCAAGCT 20
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0.4%;
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     Query Match 0.45
Best Local Similarity 84.25
Matches 16; Conservative
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APPLICANT: MASUDA, Esteban
APPLICANT: KINGSLLA, Todd M.
APPLICANT: KINGSLLA, Todd M.
APPLICANT: KINGSHITA, Taisei
APPLICANT: KINGSHITA, Taisei
APPLICANT: BENNETT, Mark
K.
APPLICANT: BENNETT, Mark
K.
APPLICANT: BENNETT, Mark
K.
APPLICANT: BENNETT, Mark
K.
TITLE OF INVENTION: SYNTHESIS UTILIZING A B-CELL ASSOCIATED PROTEIN
TITLE OF INVENTION: SYNTHESIS UTILIZING A B-CELL ASSOCIATED PROTEIN
TITLE OF INVENTION: WUMBER: US/10/197,919
CURRENT APPLICATION NUMBER: 2002-07-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 20
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Publication No. US20040023378A1

GENERAL INFORMATION:

APPLICANT: Ming-Yi Chiang

APPLICANT: Kenneth W. Dobie

TITLE OF INVERTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION

TITLE OF INVERTION: ANTISENSE WOULATION OF KIAA1531 PROTEIN EXPRESSION

FILE REFERENCE: RTS-0367

CURRENT PLING DATE: 2002-07-31

NUMBER OF SEQ ID NOS: 134

SEQ ID NO 47
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: synthetic primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 111, Application US/10210290
                                                                                                                                                                Sequence 8, Application US/10197919
Publication No. US20040014649A1
GENERAL INFORMATION:
       866 TGGAGGCTGACGAGGCGGG 884
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                                                    20 TGGAGGCTGAAGCGCCGGG
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Best Local Similarity 84.2
Matches 16; Conservative
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Publication No. US20040014638A1

GENERAL INFORMATION:
APPLICANT: MASUDA, Esteban
APPLICANT: WARNER, Justin E.
APPLICANT: WARNER, Justin E.
APPLICANT: WARNER, Justin E.
APPLICANT: MANDERSON, David C.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT MODULATE IL-4 RECEPTOR-MEDI
TITLE OF INVENTION: SYNTHESIS UTILIZING A CLLD8 PROTEIN
FILE REFERRINCE: RIGL-007/00US
CURRENT APPLICANTION NUMBER: US/10/197,368
CURRENT FILING DATE: 2002-07-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEG ID NO 13
LENGTH: 20
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Masuda, Esteban
APPLICANT: Masuda, Esteban
APPLICANT: Masuda, Esteban
APPLICANT: Warner, Jusin E
APPLICANT: Warner, Jusin E
APPLICANT: Warner, Jusin E
APPLICANT: Warner, Jusin E
APPLICANT: Mark K
APPLICANT: Anderson, David C
TITLE OF INVENTION: Synthesis Utilizing a Thioredoxin-related 32 kDa Protein
TITLE OF INVENTION: Synthesis Utilizing a Thioredoxin-related 32 kDa Protein
TITLE OF INVENTION: Synthesis US/10/197,962B
CURRENT APPLICATION UNDER: US/10/197,962B
CURRENT FILING DATE: 2003-01-21
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 9
LENGTH: 20
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                 Sequence 9, Application US/10197962B Publication No. US20040014149A1
                                                                       866 TGGAGGCTGACGAGGCGGG 884
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 16; Conservative
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US-10-197-368-13/c
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Gaps

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Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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US-10-211-908-55/c
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    ; FEATURE:
US-10-210-589-98
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Publication No. US20040023378A1
GENERAL INFORMATION:
APPLICANT: Minge Yi Chiang
APPLICANT: Minge Yi Chiang
APPLICANT: Exic G. Marcusson
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
FILE REFERENCE: RTS-0367
CURRENT APPLICATION NUMBER: US/10/210,290
CURRENT FILING DATE: 2002-07-31
SUMDER OF SEQ ID NOS: 134
SEQ ID NO 111
LENGTH: 20
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US-10-210-589-48/C

i Sequence 48, Application US/10210589
i Publication No. US20040023381A1
i GENERAL INFORMATION:
    APPLICANT: C. Frank Bennett
    APPLICANT: Nicholas M. Dean
    TILLE OF INVENTION: ANTISENSE MODULATION OF PPPZRIA EXPRESSION
    TILLE OF INVENTION: ANTISENSE WOULLATION OF PPPZRIA EXPRESSION
    CURRENT APPLICATION NUMBER: US/10/210,589
    CURRENT FILING DATE: 2002-07-30
    NUMBER OF SEQ ID NOS: 122
    SEQ ID NO 48
    LENGTH: 20
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Sequence 98, Application US/10210589

Publication No. US20040023381A1

GENERAL INFORMATION:
APPLICANT: Victolas M. Dean
APPLICANT: Kenneth W. Dean
APPLICANT: Kenneth W. Dean
APPLICANT: Natholas M. Dean
APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.4%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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ORGANISM: Artificial Sequence
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Matches 16; Conservative
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TYPE: DNA
ORGANISM: H. sapiens
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Sequence 55, Application US/10211908

Redunce 55, Application US/10211908

Redunce 55, Application No. US20040023384A1

Redunce 55, Application No. US20040023384A1

APPLICANT: Brett P. Monia

APPLICANT: Reneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 12 EXPRESSION

TITLE REPERENCE: RTS-0420

CURRENT APPLICATION NUMBER: US/10/211,908

CURRENT FILING DATE: 2002-07-31

NUMBER OF SEQ ID NOS: 121

SEQ ID NO 55

LENGTH: 20
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Sequence 67, Application US/10210833
; Sequence 67, Application No. US20040023383A1
; Publication No. US20040023383A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF RESISTIN EXPRESSION
; FILE REPREMENCE: RF2-0396
; CURRENT APPLICATION NUMBER: US/10/210,833
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 165
; SEGO ID NO 67
; LENGTH: 20
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Antisense Oligonucleotide US-10-210-833-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1396 CTGCTGGGCGCCTGCACGC 1414
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                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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HAPPLICANT: KINSELLA, TODD M

HAPPLICANT: WARNER, UJGTIN E

HAPPLICANT: WARNER, UJGTIN E

HAPPLICANT: BENNET, WARK K

HAPPLICANT: BENNET, MARK

HAPPLICANT: BENNET, MARK

HAPPLICANT: BENNET, MARK

HAPPLICANT: MARKEN

HAPPLICANT
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APPLICANT: Donna T. Ward
APPLICANT: Donna T. Ward
APPLICANT: Donna T. Ward
APPLICANT: William A.Gaarde
APPLICANT: William A.Gaarde
APPLICANT: Jacqueline R. Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK3 EXPRESSION
FILE REFERENCE: RYS-0.174
CURRENT APPLICATION NUMBER: US/10/380,127A
CURRENT APPLICATION NUMBER: 09/658,688
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SEQ ID NO 83
LENGTH: 20
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Sequence 62, Application US/10454663
Sequence 62, Application Wo. 102040033977A1
SEMERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Christopher K. Mirabelli
TITLE OF INVENTION: OLIGONUCLEOTIDE MODULATION OF CELL ADHESION
FILE REFERENCE: ISPH-0744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 14.2; DB 1; Length 20;
84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: synthetic primer
US-10-222-729-15
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'Sequence 83, Application US/10380127A

'Publication No. US20040033976A1

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 84.25
Matches 16; Conservative
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APPLICANT: Noria, Brett
APPLICANT: Nero, Pam
APPLICANT: Narisense OLICONUCLEOTIDE COMPOSITIONS AND METHODS FOR THE MODULA
TITLE OF INVENTION: OF JNK PROTEINS
FILE REFRENCE: 159H-075
FILE REFRENCE: 159F-03-01-15
FRICK APPLICATION NUMBER: US 09/774,809
FRICK APPLICATION NUMBER: US 09/396,902
FRICK APPLICATION NUMBER: US 09/396,902
FRICK APPLICATION NUMBER: US 09/287,796
FRICK APPLICATION NUMBER: US 09/287,796
FRICK FILING DATE: 1999-04-07
FRICK FILING DATE: 1999-04-07
FRICK FILING DATE: 1999-04-07
FRICK FILING DATE: 1999-08-03
FRICK FILING DATE: 1997-08-03
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0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                                                                Publication No. US20040029273A1
GENERAL INFORMATION:
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: WAITSENSE MODULATION OF EDG1 EXPRESSION
FILE REFERENCE: RTS-0179
CURRENT APPLICATION NUMBER: US/10/215,448
CURRENT FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 105
SEQ ID NO 55
LENGTH: 20
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), OTHER INFORMATION: Antisense Oligonucleotide US-10-215-448-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Synthetic Sequence US-10-345-444B-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 61, Application US/1034544B

Publication No. US20040029823Al

GENERAL INFORMATION:

APPLICANT: MCKAY, Robert A.

APPLICANT: Dean, Nicholas M.
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; Sequence 15, Application US/10222729
; Publication No. US20040033538A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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Sequence 11, Application US/10380195A

Publication No. 10220040072776A1

Publication No. 10220040072776A1

GENERAL INFORMATION:

APPLICANT: Gleave, Martin

APPLICANT: Gleave, Martin

APPLICANT: Rennie, Paul

FILE REFERENCE: USC. 10.0330, 195A

CURRENT PILING DATE: 2000-09-13

FRIOR APPLICATION NUMBER: US 60/232, 641

FRIOR APPLICATION NUMBER: US 60/232, 641

FRIOR PELING DATE: 2000-09-14

SOFTWARE: PatentIn version 3.2

SOFTWARE: PatentIn version 3.2

ERNORT: 2000-09-14

SEQ ID NO 11

ENNORT: 2000-09-14

ENNORT: 2000-09-14

SEQ ID NO 11

ENNORT: 2000-09-14
                                                                                                                                                                                             APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Brett P. Monia
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
FILE REPERRNCE RTS-01156
CURRENT APPLICATION NUMBER: US/10/380,124
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 40
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Antisense Oligonucleotide
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US-10-380-195A-54
Sequence 54, Application US/10380195A
Publication No. US20040072776A1
                                                                                                                         Sequence 40, Application US/10380124
Publication No. US20040053874A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-380-124-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gage, Fred
APPLICANT: Gage, Fred
APPLICANT: Gage, Fred
APPLICANT: Ray, Jasodhara
ITILE OF INVENTION: METHOD FOR PRODUCTION OF NEUROBLASTS
FILE REFERENCE: REGENIA 60-5
CURRENT APPLICATION NUMBER: US/10/622,206
CURRENT APPLICATION NUMBER: US/09/915,229
PRIOR APPLICATION NUMBER: US/09/915,229
PRIOR PILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 08/884,427
PRIOR PLILING DATE: 1997-06-27
PRIOR PLILING DATE: 1997-06-27
PRIOR FILING DATE: 1995-05-19
PRIOR FILING DATE: 1993-01-03
PRIOR FILING DATE: 1993-01-04
PRIOR FILING DATE: 1993-01-06
PRIOR PLILING DATE: 1993-01-06
PRIOR PLILING DATE: 1993-01-06
PRIOR PLILING DATE: 1993-01-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FeatSEQ for Windows Version 4.0
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is Sequence 3, Application US/10622206
is Publication No. US20040048373A1
is GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-454-663-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Forward primer for PCR US-10-622-206-3
CURRENT APPLICATION NUMBER: US/10/454,663
CURRENT FILING DATE: 2003-04-04
                             CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: 09/982,262
PRIOR APPLICATION NUMBER: 09/982,262
PRIOR PILING DATE: 2001-10-18
PRIOR PELLING DATE: 2000-09-12
PRIOR PELLING DATE: 1998-08-03
PRIOR PILING DATE: 1995-05-12
PRIOR APPLICATION NUMBER: 08/440,740
PRIOR PILING DATE: 1995-05-17
PRIOR PELLING DATE: 1993-06-17
PRIOR FILING DATE: 1993-06-17
PRIOR FILING DATE: 1993-06-17
PRIOR FILING DATE: 1993-06-17
PRIOR FILING DATE: 1993-01-07
PRIOR FILING DATE: 1993-01-01
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ORGANISM: Artificial Sequence
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SEQ ID NO 62
LENGTH: 20
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; Publication No. US20040077571A1
; Publication No. US20040077571A1
; Publication No. US20040077571A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Thomas McGonigal
; TILE OF INVENTION: ANTISENSE MODULATION OF CDC14A EXPRESSION
; FILE REFERENCE: RTS-0262
; CURRENT APPLICATION NUMBER: US/10/274,311
; CURRENT FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 14
; LENGTH: 20
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Publication No. US20040077085A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF CDC14A EXPRESSION FILE REPERBNCE: RTS-0172
CURRENT APPLICATION NUMBER: US/10/274,387
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 14
LENGTH: 20
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84.2%; Pred. No. 9.1e+02;
iive 0; Mismatches 3;
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3;
                                                                                                                                                                   ; OTHER INFORMATION: Antisense Oligonucleotide US-10-274-347-16
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US-10-274-311-14
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CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 16
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 84.2<sup>3</sup>
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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US-10-274-311-14/c
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                                                                                                                                                  FEATURE:
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                                                                                        TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2
TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2
TITLE OF INVENTION: Oligodeoxynucleotides for Prostate and Endocrine Tumor Therapy
FILE REFERENCE: UBC.P-023
CURRENT APPLICATION NUMBER: US/10/380,195A
CURRENT APPLICATION NUMBER: PCT/US01/28748
PRIOR APPLICATION NUMBER: PCT/US01/28748
PRIOR APPLICATION NUMBER: US 60/232,641
PRIOR PILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
NUMBER OF SEC ID NOS: 63
SOFTWARE: Patent In version 3.2
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Publication No. US20040077083A1
GENERAL INFORMATION:
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 4 EXPRESSION
FILE REPRENCE: RTS-0161
CURRENT APPLICATION NUMBER: US/10/273,826
CURRENT FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 87
LENGTH: 20
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US-10-274-347-16/c
Sequence 16, Application US/10274347
Publication No. US20040077084A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Andrew T. Watt
APPLICANT: Junling Li
APPLICANT: Junling Li
APPLICANT: Wath Glaser
TITLE OF INVERTION: ANTISENSE WODULATION OF HISTONE DEACETYLASE 4 EXPRESSION
FILE REFERENCE: RTS-0264
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Pred. No. 9.1e+02;
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Best Local Similarity 84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                               Kiyama, Satoshi
Nelson, Colleen
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LENGTH: 20
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Sequence 528, Application US/10280183A Publication No. US20040081964A1 GENERAL INFORMATION:
APPLICANT: Pfizer Inc. APPLICANT: Bachmanov, Alexander A
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                                                                                                                                                                                                                                                                                                                               Beauchamp, Gary K.
Chatterjee, Aurobindo
De Jong, Pieter J.
Li, Shanru
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Best Local Similarity 84.23
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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US-10-210-802-111/c
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ORGANISM: Mouse
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Sequence 26, Application US/10728509

Sequence 26, Application US/10728301

Sequence 26, Application US/10728301

PUBLICANT: NOW CONTROL OF THE CALL OF THE CALL
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APPLICANT: Read, Danielle R.
APPLICANT: Read, Danielle R.
APPLICANT: Ross, Davidle R.
APPLICANT: Ross, David
APPLICANT: Tordoff, Michael G.
TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
TITLE OF INVENTION: CARBOHYDRAIE COMPOUNDS AND OTHER SWEETNERS
FILE REFERENCE: PC18306A
CURRENT APPLICATION NUMBER: US/10/280,183A
CURRENT APPLICATION NUMBER: 60/200,794
PRIOR FILING DATE: 2000-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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US-10-280-183A-230/c
Sequence 230, Application US/10280183A
Sequence 130, Application US/10280183A
Publication No. US20040081964A1
GENERAL INFORMATION:
APPLICANT: Pitzer Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bachmanov, Alexander A
Beauchamp, Gary K.
Chatteriee, Aurobindo
De Jong, Pleter J.
Li, Shanru
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20 GCCGAGTCCAAATAGGAGC 2
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 230
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ORGANISM: Mouse
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APPLICANT: Li, Xia
APPLICANT: Chmen, Jeffrey D
APPLICANT: Rose, David
APPLICANT: Tordoff, Michael G.
TITLE OF INVENTION: GENE MN SEQUENCE VARIATION ASSOCIATED WITH SENSING
TITLE OF INVENTION: GENE MY SEQUENCE VARIATION ACREETHERS
FILE REFERENCE: PC18306A
CURRENT PTLING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: 60/200,794
PRIOR PLLING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PALENT OF SEQ ID NOS: 652
SOFTWARE: PALENT OF SEQ ID NOS: 652
SEQ ID NO 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47, Application US/10210802

Publication No. US20040087523A1

GENERAL INFORMATION:

APPLICANT: Ming-Yi Chiang

TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION

TITLE REFERENCE: RIS-0367

CURRENT APPLICATION UNDER: US/10/210,802

CURRENT FILING DATE: 2002-07-31

NUMBER OF SEQ ID NOS: 134

SEQ ID NO 47

LENGTH: 20
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84.2%; Pred. No. 9.1e+02;
iive 0; Mismatches 3; Indels
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84.2%; Pred. No. 9.1e+02;
ive 0; Mismatches 3; Indels
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0; Gaps

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Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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US-10-300-424-94

Sequence 94, Application US/10300424

Sequence 94, Application US/2030424

Publication No. US20040096835A1

GENERAL INFORMATION:

TITLE OF INVENTION: MODILATION OF TNFSF14 EXPRESSION

FILE REPERENCE: RTS-0437

CURRENT APPLICATION NUMBER: US/10/300,424

CURRENT FILING DATE: 2002-11-19

NUMBER OF SEQ ID NOS: 129

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1447
US-10-300-424-25/C
US-10-300-424-25/C
Sequence 25, Application US/10300424
Publication No. US20040096835A1
GENERAL INFORMATION:
APPLICAMT: Kenneth W. Dobie
ITILE OF INVENTION: MODULATION OF THESF14 EXPRESSION
FILE REFRERNCE: RTS-0437
CURRENT APPLICATION UNMER: US/10/300,424
CURRENT FILING DATE: 2002-11-19
NUMBER OF SEQ ID NOS: 129
: SEQ ID NO 25
: LENGTH: 20
                                                                                                                                                                                        Query Match

0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred..No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                              FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-864-81
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-300-424-25
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0.4%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 9.1e
Matches 16; Conservative 0; Mismatches
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  SEQ ID NO 81
LEMCTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: H. sapiens
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Publication No. US20040091920A1

GENERAL INFORMATION:

APPLICANT: TSUJI, Toru

APPLICANT: TSUJI, Toru

TITLE OF INVENTION: Method of Constructing DNA Library and Utilization Thereof

FILE REFERENCE: P24048

CURRENT APPLICATION NUMBER: US/10/637,009

CURRENT FILING DATE: 2003-08-08

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2003-03-26

PRIOR PLILING DATE: 2003-03-26

PRIOR PLILING DATE: 2001-02-06

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin version 3.2
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Publication No. US20040092465A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
FILE REFERENCE: RTS-0432
CURRENT APPLICATION VMBER: US/10/293,864
CURRENT PILING DATE: 2002-11-11
NUMBER OF SEQ ID NOS: 165
                                                                        APPLICANT: Ming-Yi Chiang
APPLICANT: Ming-Yi Chiang
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTIONS ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
FILE REPERENCE: RTS-0367
CURRENT APPLICATION UNMBER: US/10/210,802
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 134
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Pred. No. 9.1e+02;
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0.4%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 9.1e
Matches 16; Conservative 0; Mismatches
Sequence 111, Application US/10210802
Publication No. US20040087523A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: H. sapiens
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ORGANISM: Artificial
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US-10-293-864-81
                                                                                                                                                                                                                               SEQ ID NO 111
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LENGTH: 20
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CURRENT APPLICATION NUMBER: US/10/303,329 CURRENT FILING DATE: 2002-11-21 NUMBER OF SEQ ID NOS: 70 SEQ ID NO 59 LENGTH: 20
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; OTHER INFORMATION: human GFAT antisense
US-10-688-706-3049
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 73, Application US/10688706 Publication No. US20040102412A1 GENERAL INFORMATION: APPLICANT: Pharmacia Corp.
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                                                                                                                                                                                                                                                                                                             572 TGCTGGGCAGCGACGTGGA 590
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Best Local Similarity 84.2
Matches 16, Conservative
                                                                                                              TYPE: DNA
ORGANISM: H. sapiens
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US-10-688-706-73
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US-10-303-329-31
US-10-303-329-31
Sequence 31, Application US/10303329
Publication No. US20040101850A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Nicholas M. Dean
APPLICANT: Kenneth M. Dobie
TITLE OF INVENTION: MODULATION OF C-SRC TYROSINE KINASE EXPRESSION
FILE REPERENCE: HTS-0005
CURRENT APPLICATION NUMBER: US/10/303,329
CURRENT FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 70
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Publication No. US20040101850A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Nicholas M. Dean
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF C-SRC TYROSINE KINASE EXPRESSION
FILE REFERENCE: HTS-0005
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                                                                                                                                                                                      TITLE OF INVENTION OF FORKHEAD BOX OIA EXPRESSION FILE REPERENCE: MODULATION OF FORKHEAD BOX OIA EXPRESSION FILE REPERENCE: MOGNOO1-101
CURRENT APPLICATION NUMBER: US/10/671,074
CURRENT FILING DATE: 2003-09-25
PRIOR PILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 176
LENGTH: 20
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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Pred. No. 9.1e+02;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-671-074-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                APPLICANT: Bhanot, Sanjay
APPLICANT: Veniant-Ellison, Murielle
                        Sequence 36, Application US/10671074 Publication No. US20040097459A1 GENERAL INFORMATION: APPLICANT: Dobie, Kenneth W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          572 TGCTGGGCAGCGACGTGGA 590
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                                                                                                                                                         APPLICANT: Lindberg, Richard A. APPLICANT: Shutter, John R.
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2%;
Matches 16; Conservative
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         US-10-671-074-36
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LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                     CYPE: DNA
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TOTAL OF INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Broschat, Kay
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01393/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT APPLICATION NUMBER: 05/419,268
PRIOR PILING DATE: 2003-10-17
PRIOR PILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin version 3.2
SEQ ID NO 3049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                  Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Broschat, Kay
TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
FILE REFERENCE: 01399/1
CURRENT APPLICATION NUMBER: US/10/688,706
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/419,268
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 3071
SOFTWARE: Patentin version 3.2
SEQ ID NO 73
LENGTH: 20
0.4%; Scor.
84.2%; Pred. No. >--
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Sequence 109, Application US/10315474
Sequence 109, Application US/10315474
Publication No. US20040110139A1
GENERAL INFORMATION
APPLICANT: Brett P. Monia
TITLE OF INVENTION: MODULATION OF G PROTEIN-COUPLED RECEPTOR 3 EXPRESSION
FILE REPERENCE: RTS-0338
CURRENT APPLICATION NUMBER: US/10/315,474
CURRENT FILING DATE: 2002-12-10
SEQ ID NO 109
LENGTH: 20
                                                                                                                                                                                                                  APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Renneth W. Dobie
TITLE OF INVENTION: MOULATION OF G PROTEIN-COUPLED RECEPTOR 3 EXPRESSION
FILE REFERENCE: RTS-0338
CURRENT APPLICATION NUMBER: US/10/315,474
CURRENT FILING DATE: 2002-12-10
NUMBER OF EQ ID NOS: 156
SEQ ID NO 37
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Publication No. US20040110150A1
GENERAL INFORMATION:
APPLICANT: Erich Koller
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MOULATION OF EPHRIN-B2 EXPRESSION
FILE REFERENCE: PTS-0057
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Pred. No. 9.1e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/316,516
  1288 GTAGCCGTGAAGATGCTGA 1306
                                                                                                                                                        , Sequence 37, Application US/10315474 ; Publication No. US20040110139A1
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Best Local Similarity 84.2
Matches 16; Conservative
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ORGANISM: H. sapiens
FEATURE:
                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                  US-10-315-474-37/c
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Sequence 10, Application US/10332406A

Publication No. US20040103453A1

GENERAL INFORMATION:
APPLICANT: Robert Dudler
APPLICANT: Wirth Robert Dudler
APPLICANT: Way Ann Lawton
TITLE OF INVENTION: Lipoxygenase Genes, Promoters, Transit Peptides and Proteins Ther
CURRENT APPLICATION NUMBER: US/10/332,406A

CURRENT FILING DATE: 2000-07-13

PRIOR APPLICATION NUMBER: GB 001275.9

PRIOR PILING DATE: 2000-07-13

PRIOR PILING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 22

SOOTWARR: Patentin Ver. 2.1
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                                                                                                                                                                                               RESULT 1454
US-10-688-706-3054/C
; Sequence 3054, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: PARAMACIA COTP.
; APPLICANT: PERSCHAL: KAY
; TILLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; TILLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ 1D NOS: 3071
; NUMBER OF SEQ 1D NOS: 3071
; SOFTWARE: PatentIn version 3.2
Length 20;
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
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Pred. No. 9.1e+02;
0; Mismatches 3;
  Score 14.2; DB 1;
Pred. No. 9.1e+02;
                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-3054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1). .. (20)
; OTHER INFORMATION: oligonuclectide US-10-332-406A-10
                                                                                      3269 TTTGCTTTGTCCTTTTCA 3287
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Query Match 0.4%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 3054
LENGTH: 20
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LENGTH: 20
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US-10-671-395-122

Sequence 122, Application US/10671395

SEQUENCE 122, Application US/10671395

GENERAL INFORMATION:

PAPPLICANT: Pharmacia Corp.

APPLICANT: Gierae, James K

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT PILLNG DATE: 2003-09-25

PRIOR APPLICATION NUMBER: 60/413,549

PRIOR FILING DATE: 2002-09-25
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7 APPLICANT: Pharmacia Corp.
7 APPLICANT: Gieree, James K
7 TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                           Sequence 19, Application US/10317279
Publication No. US20040110703A1
GENERAL INFORMATION:
APPLICANT: Ming-Yi Chiang
APPLICANT: Ming-Yi Chiang
TITLE OF INVENTION: MODULATION OF DR1-ASSOCIATED PROTEIN 1 EXPRESSION
TITLE OF INVENTION: WOULD US: 10027
CURRENT APPLICATION UNMBER: US/10/317,279
CURRENT FILING DATE: 2002-12-10
SEQ ID NO.9: 59
LENGTH: 20
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Antisense Oligonucleotide US-10-317-279-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: Human PGE2 antisense US-10-671-395-122
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              2 CTGAGCCTGCCGGGGATCC 20
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SOFWHARB: Patentin version 3.2
SEQ ID NO 122
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                   RESULT 1461
US-10-317-279-19/c
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US-10-671-395-309
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Matches
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                                                                                                                                                                                                                                                       Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                   3; Indels
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US-10-317-270-12/c
US-10-317-270-12/c
Sequence 12, Application US/10317270
Publication No. US20040110701A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
APPLICANT: Tamara Balac Sipes
TITLE OF INVENTION: MODULATION OF ZINEDIN EXPRESSION
FILE REFERENCE: RTS-0479
CURRENT APPLICATION NUMBER: US/10/317,270
CURRENT FILING DATE: 2002-12-10
SEQ ID NO 12
LENGTH: 20
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Publication No. US20040110701A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
APPLICANT: Tamara Balac Sipes
TITLE OF INVENTION: MODULATION OF ZINEDIN EXPRESSION
FILE REFERENCE: RTS-0479
CURRENT APPLICATION UNDEER: US/10/317,270
CURRENT APPLICATION UNDEER: US/10/317,270
UNDMBER OF SEQ ID NOS: 160
                                                                                                                                                                                                                                                  Query Match

0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                           ), OTHER INFORMATION: Antisense Oligonucleotide US-10-316-516-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Antisense Oligonucleotide US-10-317-270-12
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NUMBER OF SEQ ID NOS: 134
SEQ ID NO 23
LENGTH: 20
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ORGANISM: Artificial Sequence
                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity 84.4*
Constructive 16; Conservative
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US-10-317-270-90
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                                                                                                           TYPE: DNA
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Sequence 966, Application US/10671395
; Sequence 966, Application US/20040132063A1
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/VB
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR APPLICATION NUMBER: 60/413,549
; RIOR APPLICATION NOS: 1809
; SOFTWARE PARENTIN VERSION 3.2
; SEQ ID NO 966
; LENGTH: 20
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Publication No. US20040132063A1

GENERAL INFORMATION:

APPLICANT: Pharmacia Corp.

APPLICANT: Gierse, James K

TITLE OF INVENTION: ARTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: ANTISENSE US/10/671,395

CURRENT PALLICATION NUMBER: US/10/671,395

CURRENT PALLICATION NUMBER: 2003-09-25

PRIOR APPLICATION NUMBER: 2002-09-25

NUMBER OF SEQ ID NOS: 1809

SEQ ID NO 117

LENGTH: 20
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                                                                                                                                                                                                                      Query Match 0.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 9.1e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                ; OTHER INFORMATION: Human PGE2 antisense US-10-671-395-574
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SOFTWARE: Patentin version 3.2
SEQ ID NO 574
LENGTH: 20
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                                                                          TYPE: DNA ORGANISM: artificial FEATURE:
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US-10-671-395-966
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US-10-671-395-501

Sequence 501, Application US/10671395

Publication No. US20040132063A1

GENERAL INFORMATION:
APPLICANT: Glerse, James K

TITLE OF INVENTION: ANTIENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: ANTIENSE NOT STAGE 1179/1/US

TITLE OF INVENTION: ANTIENSE NOT STAGE 1179/1/US

CURRENT FILING DATE: 2003-09-25

NUMBER OF SEQ ID NOS: 1809

SOFTWARE PATENTIN VERSION 3.2

LENGTH: 20

LENGTH: 20
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Sequence 574, Application US/10671395

Fublication No. US20040132063A1

GENERAL INFORMATION:

APPLICANT: Pharmacia Corp.

APPLICANT: Giarse, James K

TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: 1179/1/US

CURRENT PAPLICATION. NUMBER: US/10/671,395

CURRENT PILING DATE: 2003-09-25

FRIOR FILING DATE: 2002-09-25
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84.2%; Pred. No. 9.1e+02;
tive 0; Mismatches 3; Indels
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0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
               FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
FRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SQCTWARE: Patentin version 3.2
LENGTH: 20
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       EXPRESSION
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Best Local Similarity 84.2
Matches 16; Conservative
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     TITLE OF INVENTION:
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Sequence 1450, Application US/10671395

Sequence 1450, Application US/10671395

Publication No. US20040132063A1

GENERAL INFORMATION:

APPLICANT: Pharmacia Corp.

APPLICANT: Glerse, James K

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE;

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE;

TITLE OF INVENTION: 1179/1/US

CURRENT APPLICATION NUMBER: US/10/671,395

CURRENT PILING DATE: 2003-09-25

PRIOR FILING DATE: 2002-09-25

NUMBER OF SEQ ID NOS: 1809

SOFTWARE: Patentin version 3.2

LENGTH: 20
                                                                                                                                                                                                           APPLICANT: Pharmacia Corp.

APPLICANT: Bramacia Corp.

APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
PRIOR FILING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 1809
SEQ ID NO 1180
LENGTH: 20
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84.2%; Pred. No. 9.1e+02;
ive 0; Mismatches 3; Indels
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                                                                                                                                       Sequence 1180, Application US/10671395
Publication No. US20040132063A1
GENERAL INFORMATION:
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Best Local Similarity 84.2
Matches 16; Conservative
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US-10-671-395-1450/c
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## Sequence 1140, Application US/10671395

## Publication No. US20040132063A1

## GENERAL INFORMATION:

## APPLICANT: Pharmacia Corp.

## APPLICANT: Glerse, James K

## TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

## TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

## TITLE OF INVENTION: ANTISENSE NOVIONINGER: US/10/671,395

## CURRENT APPLICATION NUMBER: US/10/671,395

## RIDER PRICATION NUMBER: 2003-09-25

## RIDER OF SEQ ID NOS: 1809

## SOFTWARE: PatentIn version 3.2

## SEQ ID NO 1140

** LENGTH: 20
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US-10-671-395-1174/c
Sequence 1174, Application US/10671395
Sequence 1174, Application US/10671395
Publication No. US20040132063A1
SERREAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Gierse, James K
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
FILE SEFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT PILING DATE: 2003-09-25
CURRENT PILING DATE: 2003-09-25
PRIOR FILING DATE: 2002-09-25
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                                             Score 14.2; DB 1; Length 20;
Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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Pred. No. 9.1e+02;
0; Mismatches 3;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 1174
LENGTH: 20
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Best Local Similarity 84.2%;
Matches 16; Conservative
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ORGANISM: artificial
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                                                  Query Match
Best Local Similarity
Matches 16; Conserv
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US-10-671-395-1140/c
       US-10-671-395-1117
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; Sequence 1499, Application US/10671395

2362 TGTGCCTGTGTGCGTGCGC 2380

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Sequence 1788, Application US/10671395

Sequence 1788, Application US/10671395

Publication No. US20040132063A1

GENERAL INFORMATION:

APPLICANT: Pharmacia Corp.

TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: ANTISENSE WOULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: ANTISENSE NO MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

TITLE OF INVENTION: EXPRESSION

SOSTUMBER OF SEQ ID NOS: 1809

SOSTUMBER OF SEQ ID NOS: 1809

SOSTUMBER PATENTIN VERSION 3.2

SEQ ID NO 1788

LENGTH: 20
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Publication No. US20040132682A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: THE REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
APPLICANT: Klimman, Dennis M.
APPLICANT: Klimman, Dennis M.
APPLICANT: Yamada, Hiroshi
TITLE OF INVENTION: MGTHOD OF TREATING INFLAMMATORY LUNG DISEASE WITH SUPPRESSORS OF
TITLE OF INVENTION: CDG OLIGONUCLEOTIDES
FILE REFERENCE: 4239-66902
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Pred. No. 9.1e+02;
0; Mismatches 3;
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Pred. No. 9.1e+02;
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CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: Patentin version 3.2
SEQ ID NO 1769
LENGTH: 20
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CURRENT FILING DATE: 2003-10-07
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PRIOR FILING DATE: 2002-10-08
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Best Local Similarity 84.29
Matches 16; Conservative
                                                                                                                                                                                                              TYPE: DNA ORGANISM: artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1199/1/08
CURRENT APPLICATION NUMBER: US/10/671,395
PRIOR PILING DATE: 2003-09-25
PRIOR FILING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 1809
SSCPTWARE: Patentin version 3.2
LENGTH: 20
                                                                             APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOWAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
FILE REPERENCE: 1179/1/05
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT APPLICATION NUMBER: 60/413,549
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SGCTWARE: PatentIn version 3.2
LENGTH: 20
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Publication No. US20040132063A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Flaarmacia Corp.
APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
FILE REFERENCE: 1179/1/US
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PEATURE:
; OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1662, Application US/10671395
Publication No. US20040132063A1
GENERAL INFORMATION:
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     Publication No. US20040132063A1
GENERAL INFORMATION:
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                        APPLICANT: Pharmacia Corp
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: artificial
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US-10-671-395-1662/c
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US-10-671-395-1769
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US-10-476-962-104/c
; Sequence 104, Application US/10476962
; Sequence 104, Application US/10476962
; Sequence 104, Application US/10476962
; Publication No. US20040191904A1
; GENERAL INFORMATION:
    APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
FILE REFERENCE: RTS-022
; CURRENT APPLICATION NUMBER: US/10/476,962
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PRIOP APPLICATION NUMBER: US/09/860,473
; NUMBER OF SEQ ID NOS: 169
; SEQ ID NO 104
; LENGTH:: 20
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; Sequence 105, Application US/10476962
; Publication No. US20040191904A1
; GENERAL INFORMATION:
    APPLICANT: C. Frank Bennett
    APPLICANT: Andrew T. Watt
    ITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
    FILE REFERENCE: RTS-022
    CURRENT APPLICATION NUMBER: 200-11-05
    PRIOR APPLICATION NUMBER: PRIOP APPLICATION NUMBER: US/09/860,473
    PRIOR PILING DATE: 2001-05-18
    NUMBER OF SEQ ID NOS: 169
    SEQ ID NO 105

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84.2%; Pred. No. 9.1e+02;
iive 0; Mismatches 3; Indels
     3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Antisense Oligonucleotide US-10-476-962-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Antisense Oligonucleotide US-10-476-962-105
0; Mismatches
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                                                     2290 GGAGACAGCTACACAGA 2308
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                                                                                                  2 GAAGAACAGCTACCCAGA 20
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ORGANISM: Artificial Sequence
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Matches 16; Conservative
     Matches 16; Conservative
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US-10-476-962-150/c
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US-10-766-185-12/c
; Sequence 12, Application US/10766185
; Publication No. US2004012565A1
; GENERAL INFORMATION:
; APPLICANT: Yoro, Heeleong
; APPLICANT: Ahn, Chang Ho
; APPLICANT: Lee, Young Bok
; APPLICANT: Lee, Young Bok
; APPLICANT: Jiang, Xiaoming
; TITLE OF INVENTION: Antiense Oligonucleotides that inhibit expression of HIF-1
; FILE REFERENCE: REX 7034
; CURRENT APPLICATION NUMBER: US/10/766,185
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 130
; SOUTHARE: PatentIn version 3.1
; SEQ ID NO 12
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US-10-741-601-26226

Sequence 26226, Application US/10741601

Publication No. US20040166519A1

GRENEAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION:
CURRENT PLING DATE:
UNDER OF SEC 1203-12-22

NUMBER OF SEC 1D NOS: 26415

SOFTWARE: FastSEQ for Windows Version 4.0

SES IN 0. 26226

TENTION OF 26226

SERVING OF 10 NOS: 26415

SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                     Length 20;
                                                                                                                                                       , OTHER INFORMATION: Suppressive oligonucleotide sequence. US-10-682-130-23
                                                                                                                                                                                                                                                  Query Match

0.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 3;
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     NUMBER OF SEQ ID NOS: 36
SOFWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 20
                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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CORGANISM: Homo sapiens
US-10-741-601-26226
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Tenenbaum, Scott A.
APPLICANT: Mathod for Identifying Functionally Related Genes and Drug Targets.
TITLE OF INVENTION: Method for Identifying Functionally Related Genes and Drug Targets.
FILE REFERENCE: RBN-001CP
CURRENT FILING DATE: 2003-6-18
PRIOR APPLICATION NUMBER: US 60/173,338
PRIOR APPLICATION NUMBER: US 69/750,401
PRIOR PILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 23
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APPLICANT: Keene, Jack D.
APPLICANT: Keene, Jack D.
APPLICANT: Carson, Craig C.
TITLE OF INVENTION: complexes
FILE OF INVENTION: complexes
FILE REFERENCE: RBN-001CN
CURRENT APPLICATION NUMBER: US/10/238,306B
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: US 09/750,401
PRIOR PLING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 60/173,338
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US-10-309-788-20
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                                                                                                                                                                                                                              ; OTHER INFORMATION: 3'-UTR sequence of Neuronal-Cadherin US-09-750-401-20
                                                                                                                                                                                                                                                                                                     0.4%; Score 14.2; DB 1;
15.8%; Pred. No. 1e+03;
tive 13; Mismatches 3;
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PRIOR APPLICATION NUMBER: US 60/173,338 PRIOR FILING DATE: 1999-12-28 NUMBER OF SEQ ID NOS: 37 SOFTWARE: Patentin version 3.1 SOFTWARE: Patentin version 3.1 LENGTH: 23 TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-238-306B-20; Sequence 20, Application US/10238306B; Publication No. US20030235830A1
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Publication No. US20030211466A1
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                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 3; Conserva
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Best Local Similarity
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                                                                                                                                                                                                         FEATURE:
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US-09-750-401-20
S-09-750-401-20
S-09-750-401-20
S-09-750-401-20
Publication No. US20020004211A1
GENERAL INFORMATION:
APPLICANT: Keene, Jack D.
APPLICANT: Tenenbaum, Scott A.
TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
TITLE OF INVENTION: complexes
TITLE OF INVENTION: COMPLEXES
FILE REFERENCE: RBN-001
CURRENT APPLICATION NUMBER: US/09/750,401
CURRENT FILING DATE: 2000-12-28
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TITLE OF INVENTION: NOVEL FAB FRAGWENT LIBRARIES AND METHOD FOR THEIR USE
FILE REFERENCE: DX/003 CON
CURRENT PAPLICATION NUMBER: US/09/988,899
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: PCT/US00/13682
PRIOR APPLICATION NUMBER: 9201558.6
PRIOR APPLICATION NUMBER: 99201558.6
PRIOR APPLICATION NUMBER: 1999-05-18
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 17
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                               APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
FILE REFERENCE: RTS-0222
CURRENT APPLICATION NUMBER: US/10/476,962
CURRENT APPLICATION NUMBER: DIO 3-11-05
PRIOR APPLICATION NUMBER: PRIOP APPLICATION NUMBER: US/09/860,473
PRIOR FILING DATE: 2001-05-18
SPEC ID NO 150
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.2; DB 1;
Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                    FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-476-962-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 0.4%; Score 14.2; D
Best Local Similarity 84.2%; Pred. No. 9.1e
Matches 16; Conservative 0; Mismatches
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Patent No. US20020102613A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 AGGGTTGCTTCGGAGAGGT 1
                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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     GENERAL INFORMATION:
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US-09-988-899-17/c
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APPLICANT: KANAGANA, TAKAHIRO
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA (
TITLE OF INVENTION: MUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA (
TITLE OF INVENTION: NUMBER: US/09/091,517
CURRENT APPLICATION NUMBER: US/09/091,517
CURRENT APPLICATION NUMBER: US/09/091,517
FRIOR FILING DATE: 2000-08-27
PRIOR FILING DATE: 2000-08-27
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PALENTIN VARIBER: US/09/09-26
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 13
ENGRET PALENTIN ON 13.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.4%; Score 14.2; DB 1; Length 30; 70.4%; Pred. No. 1.3e+03; tive 0; Mismatches 8; Indels
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                             PRIOR APPLICATION NUMBER: US 09/556,127
PRIOR FILING DATE: 2000-04-20
PRIOR PPLICATION NUMBER: UP 1999-111601
PRIOR PLIING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SOFWARE: Patentin version 3.1
LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09891517
Patent No. US20020106653A1
GENERAL INFORMATION:
APPLICANT: KURANE, RYUICHIRO
                                                                                                                                                                                                                                                                                                                           TYPE: DNA
SOGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic DNA US-09-891-517-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 19; Conservative
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Best Local Similarity
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ses 19; Conserva
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US-09-891-517-13
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Best Local S:
Matches 19
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WENDERLY 1900

Sequence 20, Application US/10629453

Publication No. US20040096878A1

Sequence 20, Application US/10629453

Publication No. US20040096878A1

APPLICANT: Keene, Jack D.

APPLICANT: Carson, Craig C.

APPLICANT: Tenenbaum, Scott A.

TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein

FILE REFERENCE: RBN-001DV

CURRENT APPLICATION NUMBER: US/10/629,453

CURRENT FILING DATE: 2003-07-29

PRIOR APPLICATION NUMBER: US 60/173,338

PRIOR PILING DATE: 1090-12-28

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin version 3.1

SEQ ID NO 20

LENGTH: 23

FERENCE: REMEMBER PATENTIN NUMBER: US 09760,401

SEQ ID NO 20

LENGTH: 23
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Publication No. US20010000175A1
GENERAL INFORMATION:
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: YOKOMAKU, YENTA
APPLICANT: FUNUSHO, KENTA
APPLICANT: FUNUSHO, KENTA
APPLICANT: FUNUSHOR: NUCLEIC ACID PROBES FOR THE METHOD FOR ANALYZING DAT
TITLE OF INVENTION: THE METHOD
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TITLE OF THE METHOD FOR 
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 14.2; DB 1; Length 2
Best Local Similarity 15.8%; Pred. No. 1e+03;
Matches 3; Conservative 13; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: 3'-UTR sequence of Neuronal-Cadherin
US-10-238-306B-20
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PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 23
                                                                                                                                                                                         TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                Sequence 958, Application US/09801274
Patent No. US20020032319A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Ireland, James S.
TITLE OF INVENTION: HUMAN SINGLE NUCLECTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Human beta-actin reverse primer
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0.4%; Score 14.2; DB 1;
Best Local Similarity 70.4%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 958
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          486 CCGGCAGACGTACACGCTGGACGTGCTGG 514
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3259 AGATATTTTATTTGCTTTGTCCTTTTT 3285
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                                                                                        3 ATATATTTTTTTTTTTTTTTTTT 29
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Publication No. US20020182687A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-09-801-274-958
                                                                                                                                                                                                                                                                                                               US-09-801-274-958/c
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US-10-208-357-2/c
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| Sequence 13, Application US/10683386
| Publication No. US20040063137A1
| GENERAL INFORMATION:
| APPLICANT: KANGARA, TAKAHIRO
| APPLICANT: KANGARA, TAKAHIRO
| APPLICANT: KANGARA, TOICHI
| APPLICANT: KANGARA, TOICHI
| APPLICANT: KANGARA, CAZUTAKA
| APPLICANT: YOKOMALU, TOYOKAZU
| APPLICANT: YOKOMALU, TOYOKAZU
| APPLICANT: KOYAMA, OSAMU
| APPLICANT: KOYAMA, OSAMU
| APPLICANT: TOYOMALU, TRUB METHOD
| TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
| TITLE OF INVENTION: THE METHOD
| TAKENT APPLICATION NUMBER: US/10/683,386
| CURRENT APPLICATION NUMBER: US/09/556,127
| PRIOR PILING DATE: 1099-04-20
| WINMER OF SEQ ID NOS: 70
| SEOF ID NOS: 70
| SEOF ID NOS: 70
| SEOF ID NOS: 70
| NUMBER OF SEQ ID NOS: 70
| NUMBER OF SEQ ID NOS: 70
                                                                                  APPLICANT: YANDA, KAZUTAKA

APPLICANT: YANDA, KAZUTAKA

APPLICANT: YOKOWAKU, TOYOKAZU

APPLICANT: KOYAMA, OSAMU

APPLICANT: KOYAMA, OSAMU

APPLICANT: KOYAMA, OSAMU

TITLE OF INVENTION: MUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT

TITLE OF INVENTION: MUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT

TITLE OF INVENTION: MUMBER: US/10/209,608

TITLE OF INVENTION: WUMBER: US/09/725,265

PRIOR APPLICATION NUMBER: US/09/725,265

PRIOR FILING DATE: 2000-01-29

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 1999-04-20

PRIOR FILING DATE: 1999-04-20

NUMBER OF SEQ ID NOS: 70

SEQ ID NO 13

LENGTH: 30
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; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: SYNTHETIC DNA US-10-209-608-13
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LENGTH: 30
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Sequence 479, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leey B.
APPLICANT: Roop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 14;
                                                                                                                                                                                                                                                                                                                                                                                        Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
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Pred. No. 6.7e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                   0.4%; Score 14; DB 1; L. ilarity 100.0%; Pred. No. 6.7e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic Oligonucleotide US-09-735-363A-15
CURRENT APPLICATION NUMBER: US/09/735,363A
                 CURRENT FILING DATE: ZUUU-12.
PRIOR APPLICATION NUMBER: 60/170,325
PRIOR FILING DATE: 1999-12-13
PRIOR PILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASCETS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 479:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.4%; Scc
Best Local Similarity 100.0%; Pi
Matches 14; Conservative 0;
                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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STRANDEDNESS: single
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STATE: Washington
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Best Local Similarity
Matches 14, Conserva
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Matches
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Sequence 6, Application US/10289921

Sublication No. US20030113337A1

GENERAL INFORMATION:

APPLICANT: MERUELO. Daniel

APPLICANT: MERUELO. Daniel

APPLICANT: LEVIN, Brandi A.

TITLE OF INVENTION: HIGH EFFICIENCY TISSUE SPECIFIC COMPOUND

TITLE OF INVENTION: DELIVERY SYSTEM USING STREPTAVIDIN-PROTEIN A FUSION PROTEIN

FILE REFERENCE: 5986/11123-US1

CURRENT APPLICATION NUMBER: US/10/289,921

CURRENT FILING DATE: 1995-11-30

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FESESEQ for Windows Version 3.0

SEQ ID NO 6

LENTH: 39
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APPLICANT: Phillip, Nigel
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
FILE REPERENCE: 02811-0181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.4%; Score 14.2; DB 1; Length 38; Best Local Similarity 62.9%; Pred. No. 1.5e+03; Matches 22; Conservative 0; Mismatches 13; Indels
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0.4%; Score 14.2; DB 1; Length 39;
Best Local Similarity 70.4%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: biotinylated poly(dT) oligonucleotide US-10-289-921-6
                    APPLICANT: Lohe, Peter
APPLICANT: Magner, Richard
TILLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REPRENCE: 50036/031002
CURRENT APPLICATION NUMBER: US/10/208,357
CURRENT APPLICATION NUMBER: US/10/619,103
PRIOR APPLICATION NUMBER: 60/145,834
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: designed sequence to act as a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3307 GGATTTTTTAGGAGATTTATTTTTGGACTTC 3341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCAG 3288
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                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
     APPLICANT: Kurz, Markus
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US-09-735-363A-15
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                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
LENGTH: 38
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Gaps

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Sequence 562, Application US/09263959
Patent No. US20020150831A1
DEBURAL INFORMATION:
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: ACO, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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0.4%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Seed and Berry LLP STREET: 6100 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 14; DB 1;
100.0%; Pred. No. 6.7e+0
:ive 0; Mismatches
                                                                                           FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMABLETS, DAVID D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEFOMNINICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: (206) 632-6031
JINFORMATION FOR SEQ ID NO: 532:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 562:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3466 ATATATCTATATAT 3479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-263-959-532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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Batent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Kowen, Lere
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                   APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: ROSOP, Ben P.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98104-7092

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: IBM PC compatible
COMPUTE: IBM PC compatible
COMPUTE: OF SYTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: O5-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D.
NAME: MCMasters, David D.
REFERENCE/DOCKET NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Le . 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                       Sequence 530, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.4%; Sc
Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2826 ATATACATATAT 2839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-09-263-959-530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washing
                                                                                                                JS-09-263-959-530/c
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US-09-263-959-532
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GENERAL INFORMATION:
APPLICANT: Hood, Lercy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
APPLICANT: ROWEN, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
COMPUTER KEADABLE FORCE,
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SUBSTANTE: OS-MAR-1999
FILING DATE: OS-MAR-1999
CLASSIFICATION NUMBER: US/09/263,959
FILING DATE: OS-MAR-1999
CLASSIFICATION NUMBER: 33,963
REPERENCE/DOCKET NUMBER: 920010.426C2
RELEPHONE: (206) 682-6931
INPORMATION FOR SEQ ID NO: 658:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDTUM TYPE: F10Ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
NAME: MCMASTERE' 05-MAR-1999
CLASSIFICATION:
NAME: MCMASTERE' 05-MAR-1999
TELECOMMUNICATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010,426C2
TELECOMMUNICATION NUMBER: 920010,426C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-263-959-726/c; Sequence 726, Application US/09263959; Patent No. US20020150891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.4%; Scc
Best Local Similarity 100.0%; Pr
Matches 14; Conservative 0;
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 726
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2318 TGTGTGTGTGTGTG 2331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-263-959-726
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Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Lercy E.
APPLICANT: Rowen, Lee
APPLICANT: KOOP, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESSE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Rowen, Leercy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lip
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: Washington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ELBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/263,959

FILLNG DATE: 05-MAR-1999

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14; DB 1; Ld
Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 592:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                            Sequence 592, Application US/09263959
Patent No. US20020150891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

Best Local Similarity 100.0%; P.
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2826 ATATACATATAT 2839
                       3466 ATATATCTATATAT 3479
                                                                        1 ATATATCTATATAT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washingt
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98104-7092
                                                                                                                                                  RESULT 1500
US-09-263-959-592/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
US-09-263-959-592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1501
US-09-263-959-658
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Sequence 111, Application US/10292198
; Publication No. US2030157654A1
; GENERAL INFORMATION:
    APPLICANT: SHEN, BEN
; APPLICANT: SHEN, BEN
; TITLE OF INVENTION: BATHWAY
; FILE OF INVENTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.4%; Score 14; DB 1; Length 15;
100.0%; Pred. No. 7.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 14;
                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
ATTORNOV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.4%; Score 14; DB 1;
100.0%; Pred. No. 6.7e+0
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: McMatters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010,426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 822:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Streptomyces globisporus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pr
                                                                                                               OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2824 ATATATACATATAT 2837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3104 ATGGCGGAGAGTTT 3117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-09-263-959-822
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                                                                                   98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
CORRESPONDENCES: 1279
CORRESPONDENCE ADDRESS:
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OB 1; Le...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MARKET TO BOVID DAVID DAVID:
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 33,963
REPRENCE/DOCKET NUMBER: 34,963
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 752:
SEQUENCE CRARACTERISTICS:
LENGTH: 14 base pairs
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6300 Columbia Center, 701 Fifth Avenue
                    Query Match 0.4%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 6.7 Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 822, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        US-09-263-959-752
; Sequence 752, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
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APPLICANT: MCSWiggen, Jim
APPLICANT: StinchComb, Dan
APPLICANT: StinchComb, Dan
APPLICANT: StinchComb, Dan
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILS REFERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
NUMBER OF SEQ ID NOS: 2082-2
SOFTWARE: Patentin version 3.0
SEQ ID NO 6667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2748, Application US/10156306

Publication No. US20030119017A1

GENERAL INFORMATION:

APPLICANT: McSwiggen, James

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REPERENCE: MBHB01-664-A (400/050)

CURRENT APPLICANT: NOS: 0202-05-28

NUMBER OF SEQ ID NOS: 8013

SOFTWARE: Patentin version 3.0

SOFTWARE: Patentin version 3.0

SEQ ID NO 2748
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APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: MCSWiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relater
TITLE OF INVENTION: Levels of IKK-Gamma and PKR
PILE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8013
SOFTWARE: Patentin version 3.0
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100.0%; Pred. No. 8.2e+02;
Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 14; DB 1; Length 16;
50.0%; Pred. No. 7.7e+02;
tive 7; Mismatches 0; Indels
Ribozyme Pharmaceuticals, Inc.
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Publication No. US20030119017A1
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Best Local Similarity 100.'
Matches 14; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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CORGANISM: Homo sapiens
US-10-156-306-2748
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-6067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1509
US-10-156-306-2748/c
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LENGTH: 17
TYPE: RNA
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Publication No. US20040077565A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Bavco, Pam

APPLICANT: Brockleowb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT
                                                                                                                   APPLICANT: SHEN, BEN
APPLICANT: LIU, WEN
THISTERIANCE, SCOTT
TITLE OF INVENTION: ANTIBIOTIC C-1027
TITLE OF INVENTION: ANTIBIOTIC C-1027
TITLE OF INVENTION NUMBER: US/10/159,257A
CURRENT APPLICATION NUMBER: US/478, 188
PRIOR APPLICATION NUMBER: 09/478, 188
PRIOR PILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 60/115,434
PRIOR FILING DATE: 1999-01-06
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PATENTIN VOY: 2.1
SEQ ID NO 111
LENGTH: 15
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; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-159-257A-111
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Pred. No. 7.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.4%; Score 14; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 7.2e+02; Matches 14; Conservative 0; Mismatches 0; Indels
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Sequence 6067, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
                            Sequence 111, Application US/10159257A Publication No. US20040161828A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 50.0%;
Matches 7; Conservative '
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US-10-138-674-6067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1507
US-10-138-674-6067
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APPLICANT: ROSWIGGEN, Jim
APPLICANT: ROSWIGGEN, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re]
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MHHBOO-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT PILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: Patentin version 3.0
SEQ ID NO 8982
LENGTH: 17
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                                  Length 17;
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i Sequence 523, Application US/10676154

i Publication No. US20040081996A1

GENERAL INFORMATION:

APPLICANT: John Landers

APPLICANT: David Houseman

APPLICANT: David Houseman

APPLICANT: Alain Charest

ITLE OF INVENTION: Methods and Products Related to

TITLE OF INVENTION: Methods and Products Related

ITLE OF INVENTION: Methods and Products Related

PILE REFERENCE: MO656/7045(HCL/MAT)

CURRENT APPLICATION NUMBER: US/10/676,154

CURRENT FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: US/0/1077

PRIOR APPLICATION NUMBER: PCT/US99/22283

PRIOR PILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 691

SEQ ID NO 523

LENGTH: 17
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. 8.2e+02;
                              Query Match 0.4%; Score 14; DB 1; I Best Local Similarity 78.6%; Pred. No. 8.2e+02; Matches 11; Conservative 3; Mismatches 0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8982, Application US/10287949A Publication No. US20040102389A1 GENERAL INFORMATION:
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Local Similarity 100.0%; Pi
hes 14; Conservative 0;
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Best Local Similarity 78.6%;
Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-10-287-949A-8982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo Sapiens
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Matches
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ravco, Pam
...cruICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases
; CURRENT APLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8982
; TVDF
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                                                                 Score 14; DB 1; Length 1.,
Pred. No. 8.2e+02;
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100.0%; Pred. No. 8.2e+02;
tive 0; Mismatches 0; Indels
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; OTHER INFORMATION: CDKN2A Exon 2 fragment primer US-10-108-732-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Box, Neil F
APPLICANT: Duffy, David L
APPLICANT: Duffy, David L
APPLICANT: Hayward, Nicholas K
APPLICANT: Sturm, Richard A
APPLICANT: Sturm, Richard A
APPLICANT: Sturm, Richard A
APPLICANT: Van Der Velden, Pieter
APPLICANT: Prants, Neilek A
APPLICANT: Prants, Nima
APPLICANT: Nima
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                Query Match 0.4%; Sc
Best Local Similarity 100.0%; P
Matches 14; Conservative 0;
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                                                                                                                                                                                                                                   798 GGGCAATTCTATTG 811
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                                                                                                                                                                                                                                                                                                 17 GGGCAATTCTATTG 4
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Best Local Similarity 100.
Matches 14; Conservative
; ORGANISM: Homo sapiens US-10-156-306-3576
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US-10-138-674-8982
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LENGTH: 17
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APPLICANT: Syngente Participations AG
APPLICANT: Cornell Research Foundation, Inc.
APPLICANT: Turgeon, Barbara G.
APPLICANT: Turgeon, Barbara G.
APPLICANT: Turgeon, Barbara G.
APPLICANT: Lu, Shen-wen
TITLE OF INVENTION: Fungal Iron Reductase Gene
FILE OF INVENTION INVENTE: US 60/252,732
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 210
SOFTWARE: FastSEQ for Windows Version 4.0
ILENGTH: 18
                                                                Sequence 27, Application US/10432422 Publication No. US20040076981A1 GENERAL INFORMATION:
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100.0%; Pre
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 14; Conservative
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                                                US-10-432-422-27
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                                                                                                                                                                                                                                         APPLICANT: Chowritz, Bharat
APPLICANT: Chowritz, Bharat
APPLICANT: Chowritz, Bharat
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
FILE REFERENCE: MBHB00-882-C (400/019).
CURRENT APPLICATION NUMBER: US/10/712,672
CURRENT APPLICATION NUMBER: US/09/653,225
PRIOR FILING DATE: 2000-08-31
PRIOR PILING DATE: 2000-04-14
PRIOR PLILNG DATE: 2000-04-14
PRIOR PLILNG DATE: 2000-04-14
PRIOR PLILNG DATE: 2000-08-31
NUMBER: 06/150,713
NUMBER: PLING DATE: 1999-08-31
NUMBER: PLING DATE: 1999-08-31
NUMBER: PLING DATE: 1990-08-31
SOFTWARE: PLING DATE: 1990-08-31
NUMBER: PLING DATE: 2000-04-14
SEQ ID NO 2607
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Sequence 12, Application US/10416110

Sequence 12, Application US/10416110

Publication No. US20040072198A1

GENERAL INFORMATION:

APPLICANT: DIEK, Alexander

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with Cdk4

FILE REFERENCE: 5013.1018

CURRENT APPLICATION NUMBER: US/10/416,110

CURRENT FILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: DE 10054974.8

PRIOR APPLICATION NUMBER: DE 10054974.8

PRIOR FILING DATE: 2000-11-06

PRIOR FILING DATE: 2000-11-06

PRIOR FILING DATE: 2000-11-06

SEQ ID NO 12

LENGTH: 18
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100.0%; Pred. No. 8.7e+02;
tive 0; Mismatches 0; Indels
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red. No. 8.2e+02;
Mismatches 0; Indels
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                                                                                                                                            Sequence 2607, Application US/10712672
Publication No. US20040102413A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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4 CCAGAGUGACGUCU 17
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US-10-712-672-2607
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
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Publication No. US20030096241A1
GENERAL INFORMATION:
APPLICANT: ZERIA PHARACEUTICALS CO., LTD.
TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS
TITLE OF INVENTION: CELL CARCINOMA.
FILE REFERENCE: E6114-01
CURRENT PAPLICATION NUMBER: US/09/953,562
CURRENT APPLICATION NUMBER: US 2001-083352
FRIOR APPLICATION NUMBER: J 2 2001-08352
FRIOR FILING DATE: 2001-03-22
SEQ ID NOS: 27
SEQ ID NO 15
LENGTH: 19
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  Length 18;
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Score 14; DB 1; Le;
Pred. No. 8.7e+02;
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0.4%; Score 14; DB 1; Lv
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 0;
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                                                Mismatches
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; Sequence 86, Application US/09733294A
; Patent No. US20020045588A1
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Sequence 1. Application US/10362010

Publication No. US20040038247A1

GENERAL INFORMATION:
APPLICANT: Branner, Sidney
APPLICANT: Tan, Yin, Hwee
TITLE OF INVENTION: AND PHARMACEUTICAL COMPOSITIONS AND METHODS UTLLIZING SAME FOR TITLE OF INVENTION: AND PHARMACEUTICAL COMPOSITIONS AND METHODS UTLLIZING SAME FOR TITLE OF INVENTION: REGULATING T-CELL MEDIATED IMMUNE RESPONSE
FILE REFERENCE: 01/22004
CURRENT APPLICATION NUMBER: US/10/362,010
CURRENT FILING DATE: 2003-08-19
NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTIAN OF SEQ ID NOS: 27

SOFTWARE: PATENTIAN OF SEQ ID NOS: 27
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is Sequence 60, Application US/10126355;

is Sequence 60, Application No. US2030198965A1;

is CENERAL INFORMATION:

APPLICANT: SUBSOMER M. Freier;

ITILE OF INVENTION: ANTISENSE MODULATION OF HYDROXYSTEROID;

TITLE OF INVENTION: 11-BETA DEHYDROGENASE 1 EXPRESSION;

FILE REFERENCE: RTS-0428;

CURRENT APPLICATION NUMBER: US/10/126,355;

CURRENT FILING DATE: 2002-04-19;

NUMBER OF SEQ ID NOS: 122;

SOFTWARE: FastSEQ for Windows Version 4.0;

SEQ ID NO 60;

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                    Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Antisense Oligonucleotide US-10-181-846-66
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CURRENT APPLICATION NUMBER: US/10/181,846
CURRENT FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: PCT/US01/01416
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 176
LENGTH: 20
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Matches 14; Conservative
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LENGTH: 20
                                                                                                                                                                                                                          TYPE: DNA
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Sequence 5, Application US/09969037

Publication No. US20030022247A1

GENERAL INFORMATION:

APPLICANT: KYOWA HAKKO KOGYO CO., LTD.

TITLE OF INVENTION: For 1175-tyrosine phosphorylated KDR/Flk-1 and usages of the sam FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/969,037

CURRENT FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-124

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: a primer for replacing of human KDR/Flk-1 tyrosine residue at ; OTHER INFORMATION: position 801 to phenylalanine.
US-09-969-037-5
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                                                         APPLICANT: Susan Freier
APPLICANT: Edward V. Wancewicz
TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
FILE REPRENCE: ISPH-0527
CURRENT APPLICATION NUMBER: US/09/733,294A
CURRENT PILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/572,423
PRIOR FILING DATE: 2000-05-16
NUMBER OF SO ID NOS: 108
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TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
FILE REFERENCE: RTSP-0363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4%; Score 14; DB 1; Length 20; 100.0%; Pred. No. 9.7e+02; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 9.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-733-294A-86
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Publication No. US20030083297A1
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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     GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: William Gaarde
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Query Match

0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 70.6%; Pred. No. 9.7e+02;
Matches 12; Conservative 4; Mismatches 1; Indels
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
; FEATURE:
; NAMEYCKY: misc_feature
; LOCATION: (12) ... (12)
; OTHER INFORMATION: Any nucleotide
US-10-362-010-1
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0; Gaps

Search completed: October 28, 2004, 12:21:44 Job time : 110 secs

1669 AAGATCGCAGACTTCGG 1685 ||:||:||:||:|| 4 AARATHGCNGAYTTYGG 20

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compu	OM nucleic - nucleic search, using sw model	Run on: October 28, 2004, 12:01:21 ; Sear (witho		Title: US-10-630-401-10 Perfect score: 3799 Sequence: 1 angatuacacacactat	table: IDENTITY MIC		Searched: 3741 segs, 81979 residues	Total number of hits satisfying chosen parameters	sed length: 8	Maximum DB seq length: 50	Post-processing: Minimum Match 0%	Maximum Match 100% Listing first 2112 summaries	Database : rng10.seg:*	- A to the contract of the con	store greater than manage of testine predicted by	detreed by and		Result Query No. Score Match Length DB ID		2 36.4 1.0 49 1	35.6 0.9 50 35.6 0.9 50	5 35.6 0.9 50 1	7 35.6 0.9 50 I	35.2 0.9 48 1	10 34.6 0.9 46 1	34.4 0.9 44 1	34.2 0.9 42 1	14 34.2 0.9 47 15 34.2 0.9 47	34.2 0.9 47 1	18 34.2 0.9 47 1 18 34.2 0.9 47 1	19 33.8 0.9 37 1	20 33.8 0.9 38 I	33.8 0.9 38 1	23 33.8 0.9 38	33.8 0.9 39 1	26 33.8 0.9 39 1	33.8 0.9 39 1	29 33.8 0.9 40 1	31 33.8 0.9 40 1	C 32 33.8 0.9 40 1 AAT66051	33 33.8 0.9 40 I

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Human FGFR-3 antis	PGFR-3 anti PGFR-3 anti	FGRR-3 anti FGFR-3 anti	uman FGFR-3 uman GGFR-3 uman GGFR-3 uman GGFR-6 uman GGFR-7 uman GGFR-7	Human NOVX protein Human NOVX protein S'mRNA DNA preper PCR primer #6, use SSA primer 2 for a SNA profer 2 for a SNA profer course DFGF gene reverse DFGF gene reverse DFGF gene reverse DFGF gene forbe. Human VDeta gene r H. discus derived Protein 9.90 PCR p Human gene specifi SSA primer 1 for a PCR primer 1 for a PCR primer 1 for a
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Main Training Page	Simple sequence re	Synthetic oligonuc	1013	SSR motif #14. Un	Sheep prion protei	Mouse transforming	Human mPGES-1 chim	Human CRLR gene 5'	Extend primer 21 u	Sequence of a micr	Pur-specific RACE	Modified oligonucl	Modified oligonucl	c-KIT protooncogen	Human PUR-alpha ge	Nucleotide Sequenc	H. discus derived	Rat FGFR coding se	Human E2F transcri	Human hibeta4BP an	Human soluble LIGH	EST polymorphic un	PXA regulatory suc	Human oligonucleot	Human oligonucleot	Human PDE4A oligon	Alstroemeria gad3	AI095013-derived o	Human PDE4A-derive	Human transgiutamit arosesso-derived o	Human Vbeta gene r	Human Vbeta gene r	Rosa sp forward PC	Oligonucleotide as	Human mPGES-1 chim	Human mPGES-1 chim	Human mPGES-1 chim	Human Oligonucieou Himan ARCC5 DNA an	Human ABCC5 DNA an	Human acetyl choli	Cross-linking olig	Oligomer TNF21/ to	KHCV cDNA 3'-end r	Primer #1 for prep	HSV replication in	Peptide nucleic ac	Tyrosine kinase ge	Arteriosclerosis-d	Human B cell recep	Human secreted pro	Human Voeta gene 1	Human PBMC IL-12 p	Pectinatus frising	Human IL-2 cDNA PC	Interleukin-12 (15	VH back PCR primer	PCR prime	Left PCR primer us	H region a		
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Single nucleotide Human VBGRF.2 RT-P RTO PCR probe for Transgenic bovine Transgenic bovine Transgenic bovine Human Cmu and VH r Human heavy chain Human heavy chain Antibody related p RNA-protein fusion Microsatellite seq Microsatellite seq Microsatellite seq Purine-pyrimidine Purine-pyrimidine Purine-pyrimidine Purine-pyrimidine Purine-pyrimidine Purine-pyrimidine Furine-pyrimidine Furin
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Human secreted/tra Human secreted/tra Human secreted/tra Human PRO PCR prim	PCR primer #106 us Human secreted/tra	Human secreted/tra Human secreted/tra	Human secreted/tra Human secreted/tra	Human secreted/tra	Human secreted/tra Human secreted/tra	Human secreted/tra	Human secreted/tra Human secreted/tra	Human secreted/tra	Vector pEGFP(His)	Human secreted/tra	Human secreted/tra	Human secreted/tra	Human secreted/tra	Human secreted/tra	Human secreted/tra	Human PRO PCK prim Human LiPIN3 exon1	ACCase gene fragme	HIV gag homology r	Cyclin E fibozyme SNP specific lower	Cyclin E ribozyme	Human c-tos transc Human c-fos siNA l	Stearoyl-CoA desat	Stearoyl-CoA desat	Human VEGFR3 short	Human VEGFR3 short	Human VEGFKZ BIOLU Human Myb BiNA low	Human Myb transcri	Human BCLZ sinA up Human BCLZ sinA up	Protein tyrosine p	Protein tyrosine p	Human GAB2 short i	Human TERT transcr	Human TERT SINA LO	Human familial bip	B virus	m a	Hepatitis B virus	is B	Hepatitis B Virus Henatitis B virus	atitis B	ER1	Human HEK1 (EGFR) Human fibrocystin	Human purine P2Y11	1 primer 2 u						
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4 4 4 4 4 1 18 1 18 1 18 1 18 1 18 1 18	. 4 4		п.	18	18	18		4 18 18				- TT	4.4	י קי	₹1.	4 4	4	4	4 4	. 4	4.	4 4	4	4.	1 4	4	44	4	4 4	. 4.	4.	14	4.	4 4	4	4 4	. 4.	4	4.	. 4.	4	ব' ব	4	4.	4, <	i 4.	4.	4.4	4	
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WNV Hammerhead Rib Human MDZ3 scannin Human MDZ3 scannin Uman H-Das DND3	Human H-Rab DNAzym Human H-Rab DNAzym UDY hammarhaad rih	HBV indimension in HBV indix	Tumour suppression	Tumour suppression	Human NAC-1 gene-8	Human NOGO recepto	Human GRID mRNA su	Human GRID mRNA su	Hepatitis B virus	Hepatitis B virus	Mouse CD40 hairpin	Transforming growt	CUT1 gene promoter	Forward PCR primer	Rat mACHR-6 antise	Locus specific amp	Human PRO processic	HIV-1 related bind	Human secreted/tra	Novel human secret	Human secreted/tra	Human secreted/tra	Human secreted pro Human secreted / t	Human muscarinic a	Novel secreted and	Human secreted / t	Human secreted/tra	Human secreted/tra	Human PRO PCR prim	Human secreted/tra Human secreted/tra	Human PRO PCR prim	Human secreted/tra	Human secreted/tra	Human secreted/tra	Human PRO PCR prim	Human secreted/tra	Human secreted/tra	Human secreted/tra	Human secreted/tra	H G	Carboxypeptidase G									
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Chimeric phosphoro Chimeric phosphoro Chimeric phosphoro Human Jun W.termin P16DF PCR primer # Human mPGES-1 chim Human glucose tran Human DR1-associat Human DR1-associat Novel human CD25 a Human BAF53 antise Murine Angiopoieti Cow prion protein	HIA DRB345 gene PC Antitumoural phosp Yeast DOG2 stress Rice semi-dwarf (s Synthetic deoxyrib Poly h nucleotide Probe poly h for a Human single nucle Normalised library Probe APC 1-MUT. Polymorphism detec Human cDNA probe u Human oligonucleot AA497002-derived o Human nigonucleot AA497002-derived o Human Tryptase a o Human Oligonucleotide as	ohromosome 9; detection;
	AAC96591 AAC96591 AAT93819 AAT93819 AAT93819 AAT93819 AAT93819 AAT93819 AAT93819 AAT93819 AAT9406 AA	cDNA; 48 BP. entry) 536 polymorphic site, SEG citide polymorphism; SNP; ce therapy; 88. ation/Qualifiers lace(26,A) ag= a -US027293O0443199. P. MD;
	02093 02093 20094 20096 14.4 20097 14.4 02100 14.2 02100 021000 02100 02100 02100 02100 02100 02100 02100 02100 021000 02100 02100 02100 02100 02100 02100 02100 02100 021000 02100 02100 02100 02100 02100 02100 02100 02100 021000 02100 02100 02100 02100 02100 02100 02100 02100 021000 02100 02100 02100 02100 02100 02100 02100 02100 02100 02100 02100 02100 02100 02100 02100 02100 02100 02100	RESULT 1 AAA77334 ID AAA77334; XX AC AAA77334; XX DF 16-NOV-2000 (first XX DE Human clone cg440245 XX W Human; single nucleo XX XX XX S Homo sapiens. XX XX YX
Primer for the det Human MDC PCR prim Amino labelled oli Amino labelled oli Human gene signatu Probe for PZA-resi Prosphorothiate ol PCR primer used to Human ABO DNA PCR JNK- specific prob PCR primer used to PCR primer used to JNK antisense olig PCR primer for RT-PCR ONK antisense olig PCR primer for pea	Antisense IGFBP-5 Human protein kina Human protein kina Human CYPLAI RT-PC Cancer cells detec Human CYPLAI RT-PC Cancer cells detec Human APC primer # Xenobiotic respons Human antibody 146 Primer XyPy-415AT PCR primer used to Sphingosine-1-phos Human COREST antis Human COREST antis Human infertility Chicken ALASI gene Human noligonucleot Human oligonucleot Human oligonucleot	Human oligonucleot Human Tr-PCR rever A49144-derived oli Human myosin X-der A497002-derived A497002-derived A497002-derived A497002-derived A497002-derived A497002-derived A497002-derived Oligonucleotico Human glucocortico Chimeric phosphoro Chimeric phosphoro Chimeric phosphoro Chimeric phosphoro
		20 1 ABZ89355 20 1 ABZ88363 20 1 ABZ88355 20 1 ABZ88355 20 1 ABZ883135 20 1 ABZ883135 20 1 AABZ81313 20 1 AABZ2221 20 1 AABZ22364 20 1 AABZ229364 20 1 AABZ2593 20 1 AABZ2593 20 1 AABZ2593 20 1 AABZ2593 20 1 AABZ2964 20 1 AABZ2964 20 1 AABZ2964 20 1 AABZ2964 20 1 AABZ2964 20 1 AABZ2993 20 1 AABZ2993
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		0.00045 5 1 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

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Response element; Z-DNA; neoplasia; hexokinase II; glycolysis; cancer; gene therapy; diabetes; tumour; rat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New transcription regulating fragments of hexokinase II DNA contg. response element - and methods for diagnosis or treatment of neoplithat over-express hexokinase II and for regulating glycolysis.
                                                                                                                                                                                                                                                                                                                                                                  Hepatoma AS-30D Type II hexokinase promoter fragment from -3843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mathupala SP, Rempel A;
                                    Claim 1; Page 465; 543pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 11; 104pp; English.
                                                                                                                                                                                                                                                                                                                       ВР
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                                                                                                                                                                                                                                         1 Similarity 87.0%;
40; Conservative
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                                                                                                                                                                                                                                                                                                                       AAT80427 standard; DNA; 49
                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            Rattus rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                          06-FEB-1997
                                                                                                                                                                                                                                                                                                                                        AAT80427;
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                    Matches
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The present sequence represents a segment of the hepatoma AS-30D Type II

chackinase promoter region. Response elements (transcription factor
binding site) in this fragment may consist of all or part of the present
sequence. AS-30D is a new isolated hexokinase II. The present DNA
cc fragment is capable of regulating transcription of a downstream open
creading frame and contains at least one response element. The present DNA
cc reading frame and contains at least one response element. The present DNA
cc fragment may be coupled to a reporter gene and used to screen for
cpotential drugs that affect regulated transcription of tumour hexokinase
cc potential drugs that affect regulated transcription of tumour hexokinase
cc II. Alternatively it may be coupled to a toxic gene and used to treat
cc lis that over-express hexokinase II, such as those present in patients
with cancer. It may also be used in gene therapy to treat diabetes. The
complete that over-express plycolysis in cells and express homologous or
cherrologous protein. Probes of the DNA fragment are used in the method
for diagnosting a neoplasia that over-expresses hexokinase. The new
complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49 BP; 3 A; 5 C; 20 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%; Score 36.4; D
87.0%; Pred. No. 15;
tive 0; Mismatches
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Best Local Similarity 87.0°
Matches 40; Conservative
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17-JUN-1997
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$$9999999999998$$$
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                                                                                                                                                                                                                                                                                                                    which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112 (AAA76118-A7729) are consecutive pairs of nucleotides which contain allent SNPs. Sequences 1 to 1112 (AAA7430-A77509) are consecutive pairs of nucleotides which contain allent SNPs. Sequences 1113 to 1122 (AAA7430-A77509) are consecutive pairs of nucleotides containing SNPs which result in changes in the corresponding amino acid sequences (AAA74430-A77509) are consecutive amino acid sequences 1113 to 1128 (AAA77430-A77450) lead to conservative amino acid changes, while those in sequences 1129 to 1186 (AAA77450-A77503) result in changes, while those in sequences 1129 to 1186 (AAA77450-A77503) result in non-conservative changes. The SNPs in sequences 1187 to 1192 (AAA77504-A77509) generate frameshift mutations. The invention also relates to a method of detecting a polymorphic site in a nucleic acid and a method of detecting polymorphic sites, antibodies raised against such peptides und a method of detecting polymorphic correspondes using the antibodies. The nucleic acids are useful for proteins/peptides using the antibodies. The nucleic acids are useful for gene therapy of an individual having, suspected of having, or at risk of developing a pathological condition due to the presence of a sequence of polymorphism and antibodies related administration of the wild-companies.
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                                            Human nucleic acids containing single nucleotide polymorphisms, useful for treating a subject suffering, or at risk from a pathology due to the presence of a sequence polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type nucleic acid sequence. Antibodies raised against polymorphic peptides can also be used in the treatment of such individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.0%; Score 36.4; DB 1; Length 48; 37.0%; Pred. No. 15;
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Gaps

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6; Indels

DB 1; Length 49;

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                      Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                           Repeat sequence from polymorphic marker clone Mfd46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Col 9-10; 186pp; English
                                                                                                                                                                                       hybridisation; chromosome; ds.
          ВР
                                                                                                                                                                                                                                                                                                        94US-00222177.
                                                                                                                                                                                                                                                                                                                                    89US-00341562.
91US-00754351.
            AAT65746 standard; DNA; 50
                                                                      (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-042299/04.
                                                                                                                                                                                                                       Homo sapiens.
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05-SEP-1991;
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neoplasias

Gaps

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having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats. Primers based on these sequences can be used to detect these repeats. Primers based on these sequences can be used to detect these repeats such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome specific phage libraries with a synthetic poly (dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-76647. Those clones where the repeat sequence has been determined are shown in AAAT65704-797. This repeat sequence is from the marker clone Mdf15 which contains the repeat sequence is from
phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-777. This repeat sequence is from the marker clone MGf46 which contains the repeat sequence is from formula: (AC) 25. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the isolation of polymorphic repeat sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  formula: (AC)25. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35.6; DB 1; Length 50;
Pred. No. 20;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat sequence from polymorphic marker clone Mfd15.
                                                                                                                                                                                                                                                       Sequence 50 BP; 25 A; 25 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                  0.9%;
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91US-00754351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                          Local Similarity 82.0
les 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-1997
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                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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AAT65717/
AAT65717/
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DB 1, Length 50;

0.9%; Score 35.6;

Query Match

Sequence 50 BP; 25 A; 25 C; 0 G; 0 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AAZ99483-514 represent sequences from Haliotis discus, used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
                                                                                                                                                                                                                                                             DNA fragmentation; microsatellite DNA; DNA marker;
                  Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGT
                                                                        GTGCGTGTGTGTGTGTGTGCACATCCGCGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35.6; DB 1; Length 50;
Pred. No. 20;
                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50 BP; 25 A; 25 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
   Pred. No. 20;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 14; 35pp; Japanese.
                                                                                                                                                                                                                                 H. discus derived sequence #10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. discus derived sequence #30.
                                                                                                                                              AAZ98492 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                           99WO-JP003551
                                                                                                                                                                                                                                                                                                                                                                                                                        98JP-00232153
 82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.9%;
Best Local Similarity 82.0%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ98512 standard; DNA; 50
                                                                                                                                                                                                    19-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-2000 (first entry)
                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2316 TCTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fakahashi H, Sekino M;
                                                                                                                                                                                                                                                                            Haliotis discus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-224692/19.
                                                                                                                                                                                                                                                                sednence;
Best Local Similarity
Matches 41; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the invention
                                                                                                                                                                                                                                                                                                      Haliotis discus.
                                                                                                                                                                                                                                                                                                                                  WO200011156-A1.
                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                        18-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                02-MAR-2000
                                                                                                                                                                                                                                                             Satellite
                                                                                                                                                                         AAZ98492;
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AAZ98512/C
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AC AAZ985:
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XX
DT 19-JUN:
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DE H. disi
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AAZ98492/c
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The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AA298463-514 represent sequences from Haliotis discus, used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
                     Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide used to test inhibition of cylindrical formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGTG 2365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Terengial de la constant de la const
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capsid protein; HIV; protein cavity; capsid maturation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50 BP; 25 A; 25 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stemmler TL,
                                                                                                                                                                                                                                                                                                                                                                                                            MIN AGRIC FORESTRY & FISHERIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35.6; DE
Pred. No. 20;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 15; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang H, Hill CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2001; 2001US-0307998P.
26-NOV-2001; 2001US-0333553P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-2002; 2002WO-US023875
                                                                                                                                                                                                                                                                                         99WO-JP003551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sekino M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-224692/19.
                                                          Haliotis discus; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003013425-A2.
                                                                                                                  Haliotis discus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sundquist WI,
                                                                                                                                                                             WO200011156-A1
                                                                                                                                                                                                                                                                                                                                                                                                            (NORQ ) JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rakahashi H,
                                                                                                                                                                                                                                                                                                                                                          18-AUG-1998;
                                                                                                                                                                                                                                                                                                   01-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                     02-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2316
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Gaps

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Indels

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Length 50;

Alam S;

Davis DR,

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                                                                                                                              The specification describes a composition for assaying conformational change of a capsid protein. The composition comprises a Human farmunodeficiency virus (HIV) capsid protein which has a modification, and comprises a cavity of about 600 Angstrom cubed. The composition is useful for screening molecules that inhibit capsid carboxy terminal domain dimerisation. The composition is also useful in in vitro maturation assays, for inhibiting capsid maturation, in in vitro assembly assay, to assembly to inhibit to metate of the capsid protein, to alter the capsid protein assembly assay, to expresent an oligonucleotide used to test the inhibition of cylindrical formation of capsid and nucleocapsid proteins by compounds of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microsatellite; ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
                                   Composition for assaying conformational change of capsid proteins, comprises a modified HIV capsid protein comprising a 600 cubic angstrom
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of identifying or detecting
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                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                          9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human microsatellite D1S191 detection PCR primer #12.
                                                                                                                                                                                                                                                                                                                                          Sequence 50 BP; 0 A; 0 C; 25 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barnard R,
                                                                                                                                                                                                                                                                                                                                                                            Score 35.6; Di
Pred. No. 20;
0; Mismatches
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                                                                                                       Claim 106; Page 60; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assisted spacer addition assay.
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                                                                                                                                                                                                                                                                                                                                                                             0.9%;
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ABK24304 standard; DNA; 48
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                                                                                                                                                                                                                                                                                                                                                                                                               41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Timms P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DIAT-) DIATECH PTY LTD
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           WPI; 2003-268130/26
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
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                                                                                                                                                                                                                                                                                                                      invention
                                                                            cavity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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methods using gel electrophoresis and Southern transfer analysis. In particular, current diagnosis of Huntington's disease relies heavily upon the use of gel electrophoresis, a process that has proved difficult to automate or miniaturise. The LASA method allows total avoidance of this limiting step, making it a strong candidate for future use in clinical and laboratory procedures. ABK24276-ABK24313 represent primers used to
                                                                                                                                                                                                                                                                           polymorphisms or microsatellites as described in the method of the
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, single nucleotide polymorphism; SNP; chromosome 9; detection; identification; gene therapy; 88.
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                                                                                                                                                                                                                                                                                                                                                                 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGTG 2365
                                                                                                                                                                                                                                                                                                                          Score 35.2; DB 1; Length 48; Pred. No. 21; 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                          Human clone cg44024536 polymorphic site, SEQ ID NO:1018.
                                                                                                                                                                                                                                                                                                         Sequence 48 BP; 24 A; 24 C; 0 G; 0 T; 0 U; 0 Other;
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replace(26,G)
/*tag= a
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99US-00443199.
                                                                                                                                                                                                                                                                                                                          Query Match 0.9%;
Best Local Similarity 83.3%;
Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA77335 standard; cDNA; 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimkets RA, Leach MD;
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16-NOV-1999;
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                                                                                                                                                                                                                                                                                      invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA77335;
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which contain single nucleotide polymorphisms (SNPB). Sequences 1 to 1112 (AAA71318-A77429) are consecutive pairs of nucleotides which contain single nucleotide polymorphisms (SNPB). Sequences 1 to 1112 (AAA77430-A77509) are consecutive pairs of nucleotides containing SNPB which result in changes in the carresponding amino acid sequences (AAB1749-B11828). The SNPB in sequences 1113 to 1128 (AAA77430-A7746-B11828). The SNPB in conservative amino acid changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result con non-conservative changes. The SNPB in sequences 1187 to 1192 (AAA77504-A77509) generate frameshift mutations. The invention also relates to a method of detecting a polymorphic site in a nucleic acid and a method of detecting polymorphic site; antibodies raised cagainst such peptides containing polymorphic sites, antibodies raised against such peptides using the antibodies. The nucleic acids are useful for proteins/peptides using the antibodies. The nucleic acids are useful for gene therapy of an individual having, suspected of having, or at risk of developing a pathological condition due to the presence of a sequence of polymorphism. Such treatment would comprise administration of the wild-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                    Human nucleic acids containing single nucleotide polymorphisms, useful for treating a subject suffering, or at risk from a pathology due to the presence of a sequence polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; dis.
                                                                                                                                                                   Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymorphic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptides can also be used in the treatment of such individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34.8; DB 1; Length 48; Pred. No. 23; 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid sequence. Antibodies raised against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48 BP; 2 A; 2 C; 24 G; 20 T; 0 U; 0 Other;
                                                                                                                                 Claim 1; Page 466; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT65780 standard; DNA; 46 BP.
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91US-00754351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.9%;
Best Local Similarity 84.8%;
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-APR-1994;
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17-JUN-1997
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05-SEP-1991;
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human
                                                                                           The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone MdIIO9 which contains the repeat sequence is from the marker clone MdIIO9 which contains the repeat sequence leftom formula: GGGAAATAGG (CA)18. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
     Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                              DB 1, Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAT 2356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd69.
                                                                                                                                                                                                                                                                                                                                                          Sequence 46 BP; 22 A; 18 C; 5 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Score 34.6;
Pred. No. 23
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                                                                 Claim 1; Col 13-14; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT65763 standard; DNA; 44 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-00341562.
91US-00754351.
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                                                                                                                                                                                                                                                                                                                                                                                            0.9%;
Local Similarity 90.2%;
les 37; Conservative
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05-SEP-1991;
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46
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ID AAT6
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Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences which contain single nucleotide polymorphisms (SNRs). Sequences 1 to 1112 AAA76318-A77429) are consecutive pairs of nucleotides which contain silent SNPs. Sequences 1113 to 1192 (AAA7430-A77509) are consecutive pairs of nucleotides containing SNPs which result in changes in the sequences 1113 to 128 (AAA77449-B1828). The SNPs in the sequences 1113 to 1128 (AAA77445) lead to conservative amino acid sequences 1129 to 1186 (AAA77446-A77503) result in non-conservative changes. The SNPs in sequences 1187 to 1192 (AAA77504-A77509) generate frameshift mutations. The invention also relates to a method of determining the relatedness of two nucleic acid and a method of determining the relatedness of two nucleic acids It also
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genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf69 which contains the repeat sequence is from formula: (AC)18.5A(AC)3. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; single nucleotide polymorphism; SNP; chromosome 9; detection; identification; gene therapy; 88.
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                                                                                                                                                                                                            Score 34.4; DB 1; Length 44;
Pred. No. 23;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                 Human clone cg44024536 polymorphic site, SEQ ID NO:1019.
                                                                                                                                                                                                                                                                                                     Sequence 44 BP; 23 A; 21 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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99US-00443199.
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                                                                                                                                                                                                                   0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                           AAA77336 standard; cDNA; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                   Query Match 0.9
Best Local Similarity 86.4
Matches 38; Conservative
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16-NOV-1999;
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                                                                                                                                                                                                                                                                                                                         44
                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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encompasses peptides containing polymorphic sites, antibodies raised against such peptides, and a method of detecting polymorphic proteins/peptides using the antibodies. The nucleic actids are useful for gene therapy of an individual having, suspected of having, or at risk of developing a pathological condition due to the presence of a sequence bypymorphism. Such treatment would comprise administration of the wild-type nucleic acid sequence. Antibodies raised against polymorphic peptides can also be used in the treatment of such individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dY) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdf1 which contains the repeat sequence as from the marker clone Mdf1 which contains the repeat sequence having the formula: CATA(CA)19. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of polymorphic genetic markers of the form (dG-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                            DB 1; Length 44;
                                                                                                                                                                                                                                                                                                         GTGTGTGTGTGTGCACATCCG 2359
                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                Sequence 44 BP; 0 A; 2 C; 22 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat sequence from polymorphic marker clone Mfdl.
                                                                                                                                                                                                                        Score 34.4; DE Pred. No. 23; 0; Mismatches
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                                                                                                                                                                                                                                                                                                           2316 TCTGTGTGTGTGTGTGTGCGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT65797 standard; DNA; 42 BP
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91US-00754351.
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Best Local Similarity 86.4%;
Matches 38; Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-042299/04.
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05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                               AAT65797
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Seguence 42 BP; 21 A; 20 C; 0 G; 1 T; 0 U; 0 Other;

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
constant an (AF)15 and an (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
clones cross-hybridised. Assuming independent distribution of
constant and MboI sites, the frequency of (T6)n >9 microsatellites
constant and of the microsatellites is summarised in the
specification and indexed herein (see below). The sequence information
constream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
constantly individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
conomically important traits esp. in cattle, to allow selective
conomically see also AAQ33501-34437. (Updated on 25-WAR-2001 to correct PN
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                               Gaps
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                                                                                                                                                                                                                                                                                                                  PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
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 Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCATCCGCGTGT
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                                                                             41 GRGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAA
                                                              DB 1;
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                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA245.
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Score 34.2;
Pred. No. 23;
                               0; Mismatches
                                                                                                                                                                                                                                                                                                                               genetic mapping; traits; amplification; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Table 7; Page 263; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            92WO-US000340.
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Query Match 0.9%;
Best Local Similarity 92.3%;
Matches 36; Conservative
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Best Local Similarity 83.0%;
Matches 39; Conservative
                                                                                                                                                                     AAQ33834 standard; DNA; 47
                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENM-) GENMARK
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                                                                                                                                                                                                                                     25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                  Bos taurus.
                                                                                                                                                                                                        AAQ33834;
                                                                                                                                         RESULT 14
                                                                                                                                                             AAQ3383
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PCR; polymerase chain reaction; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                   Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 9-10; 186pp; English
                                                                                                                                                                                       89US-00341562.
91US-00754351.
                                                                                                                                                              94US-00222177.
                                                                                                                                                                                                                            (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                              WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                               14-APR-1994;
                                                                                                                                                                                         21-APR-1989;
05-SEP-1991;
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17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5582979-A
                                                                                      Homo sapiens
                                                                                                                                        10-DEC-1996.
                                                                                                              JS5582979-A
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                                                                                                                                                                                                                                                        Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT65755,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of concaining the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T6647. Those clone where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdfil which contains the repeat sequence is from the marker clone Mdfil which contains the repeat sequence having the formula: (AC)23A. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                     Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 34.2; DB 1; Length 47; 83.0%; Pred. No. 27; ive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat sequence from polymorphic marker clone Mfd14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47 BP; 24 A; 23 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                             Repeat sequence from polymorphic marker clone Mfdll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 9-10; 186pp; English.
                                                                                                                                                                                                                                                                                                                                            91US-00754351.
                                         AAT65713 standard; DNA; 47 BP
                                                                                                                                                                                                                                                                                                     94US-00222177
                                                                                                                                                                                                                                                                                                                              89US-00341562
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(first entry)
                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                    (MARS-) MARSHFIELD CLINIC.
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Matches 39; Conservative
                                                                                            (revised)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
17-JUN-1997
                                                                                                                                                                                                                             Ното варіеля
                                                                                                                                                                                                                                                                                                       04-APR-1994;
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05-SEP-1991;
                                                                                            25-MAR-2003
17-JUN-1997
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                                                                    AAT65713;
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ID AAT6

XX AAT6

XX AAT6

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DT 17-J

XX X
                 RESULT 15
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of Genetic disease, commercial animal or plant breeding or pedigree analysis of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf14 which contains the repeat sequence is from formula: (AC)23A. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat sequence from polymorphic marker clone Mfd59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 47 BP; 24 A; 23 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 34.2; E
83.0%; Pred. No: 27;
ive 0; Mismatches
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nes 39; Conservative
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94US-00309335. 95US-00531241.

Rowen L;

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The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers pecifically priming and allowing amplification of each Vbeta gene, vbetaRNA or CDNA. The kit is useful for diagnosing organ transplant respection and diagnosing and treating T-cell associated diseases including autoimmune disease, degenerative nervous system diseases, infectious diseases arophic gastritis. Degenerative nervous system diseases include multiple arrophic gastritis. Degenerative nervous system diseases include multiple arrophic gastritis begenerative nervous system diseases include multiple arrophic gastritis. Degenerative nervous system diseases include multiple in hypersensitivities such as those include and propersensitivities such as those of allergies. Type II hypersensitivities such as those present in allergies. Type II hypersensitivities such as those caused by the yeast genus Candida, parasitic infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by Mycobacterium. Neoplastic diseases include as those caused by Mycobacterium. Neoplastic diseases include as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                                                                                                                   Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCGCGTGT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 47 BP; 0 A; 0 C; 23 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microsatellite sequence from clone TGLA94.
                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 571; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ34178 standard; DNA; 37 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 39; Conservative
                                                                                                                                                                WPI; 2004-059052/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                     (HOOD/) HOOD L E. (ROWE/) ROWEN L.
               19-SEP-1994;
19-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus.
                                                                                                                                                                                                                                                               Pbeta gene
                                                                                                                             Hood LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ34178;
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AAQ34178
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                                                                                                                                                                                                                                                                                                                               The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of genetic disease, commercial sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 by primers APIG579-T66047. Those clones where the repeat sequence has been determined are shown in AAJ65704-797. This repeat begat sequence is from the marker clone Mdf59 which contains the repeat sequence is from the marker clone Mdf59 which contains the repeat sequence is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypersensitivity disease; infectious disease; neoplastic disease; hypersensitivity disease; infectious disease; neoplastic disease; hypersensitivity disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; parasitic infection; disease; viral infection; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                                                                                                                                                                                          Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          formula: (AC)23.5. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; T-cell associated disease; Vbeta; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 34.2; DB 1; Length 47; 13.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 47 BP; 24 A; 23 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Vbeta gene repeat sequence #167.
                                                                                                                                                                                                                                                                                                  Disclosure; Col 11-12; 186pp; English.
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                                  94US-00222177
                                                                       89US-00341562
91US-00754351
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                                                                                                                             (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 83.0
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           breast cancer;
                                  04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAR-1999;
                                                                       21-APR-1989;
05-SEP-1991;
10-DEC-1996
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                                                                                                                                                                  Weber JL;
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Gaps

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Score 34.2; DB 1; Length 47; Pred. No. 27;

0.9%; Sco. 83.0%; Pred. No. 2., 0; Mismatches

47

(first entry)

(revised)

91US-00642342. 92WO-US000340.

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AAT66048;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                   RESULT 21
                                                                                                                                                                                                                                                                                                                                                AAT66048/
                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                셤
                                                                                                                                  The sequence is a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50 clones cross-chybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for garentsge testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on
                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                             Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphism; repeat sequence; genetic marker; primer; amplification;
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                                                                                                                                                                                                                                                                                                                                                0.9%; Score 33.8; DB 1; Length 37;
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                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                  rable 7; Page 402; 517pp; English
                                                                                                                                                                                                                                                                                                      25-MAR-2003 to correct PN field.)
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Best Local Similarity 94.6%;
Matches 35; Conservative
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                                     маввеу ЛМ;
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                                                           WPI; 1992-284684/34.
              (GENM-) GENMARK
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05-SEP-1991;
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17-JUN-1997
                                      Georges M,
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                                                                                                                                                                                 The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of genetic disease, commercial repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Mdf50 which contains the repeat sequence is from the marker clone Md50 which contains the repeat sequence is from the marker clone Md50 which contains the repeat sequence is from the marker clone Md50 which contains the repeat sequence is from the marker clone Md50 which contains the repeat sequence is from the marker clone which contains the repeat sequence is from the marker clone which contains the contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 38;
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Pred. No. 23;
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using novel nucleic acid mols. as primers
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                                                                                                         Disclosure, Col 11-12; 186pp; English
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35; Conservative
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18-JUN-1997
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analysed, fall into 4 categories: 1) perfect repeats which are alternating tandem CA repeats with no interruptions and without adjacent repeats of another sequence; 2) imperfect repeats which are defined as 2 or more runs of uninterrupted CA repeats separated by no more than 3 consecutive non-repeat bases; 3) compound perfect repeats which are uninterrupted runs of CA separated by no more than 3 consecutive non-repeat bases from a run of at least 5 uninterrupted dinucleotide or longer repeats of a sequence other than (dC-dA)n. (dG-dT)n, or from at least 10 uninterrupted monomucleotides; and 4) imperfect compound repeats which are defined as for the perfect compound repeats except that the runs of CA are interrupted. The sequence presented here is an example of a perfect repeat sequence of structure: (AC)19. (Updated on 25-MAR-2003
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les 35, Conservative
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Selecting a domestic animal for having desired genotypic properties comprises testing the animal for the presence of a parentally imprinted quantitative trait locus which is related to muscle mass and/or fat
                                                                                                                                                                                                                                                                                                                                                                                         Porcine; pig; wild boar; quantitative trait locus; QTL; chromosome 2; mapping; 2p1.7; select breeding; genotype; phenotype; muscle mass; fat deposition; IGF2; insulin-like growth factor 2; microsatellite; ds.
                                                                                                                                                                                                                                                                                                             Porcine microsatellite PIGQTL3 oligonucleotide #31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spincemaille G;
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The present invention describes a method (MI) for selecting a domestic animal for having desired genotypic properties. The method comprises testing the animal for the presence of a parentally imprinted quantitative trait locus (QTL). The pig QTL is located at chromosome 2, mapping at around position 2pl.7. Also described are: (1) an isolated and/or recombinant nucleic acid (NI) comprising a parentally imprinted QTL or its functional fragment; (2) an isolated and/or recombinant nucleic acid (N2) constraing a synthetic parentally imprinted QTL or its functional fragment; (3) an isolated from at least one chromosome or its functional fragment; (3) an animal

Example 4; Fig 10; 107pp; English

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such as pig selected for having desired genotypic or potential phenotypic properties, (4) a transgenic animal comprising NI or N2; and (5) sperm or an embryo derived from the animal of (3) or (4). NI or its fragment is useful for selecting an animal destined for slaughter or a breeding
                                                                           animal having desired genotypic or potential phenotypic properties. The properties are related to muscle mass and/or fat deposition. The sperm or an embryo are useful in breeding animals destined for slaughter. The
                                                                                                                                        present sequence represents a microsatellite oligonucleotide, which is given in an example from the present invention for the identification of DNA sequence polymorphisms in the IGF2 (insulin-like growth factor 2) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microsatellite; ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
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                                                                                                                                                                                                                                          Sequence 38 BP; 19 A; 19 C; 0 G; 0 T; 0 U; 0 Other;
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Pred. No. 23;
0; Mismatches
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                                                                                                                                                                                                                                                                                                     ilarity 94.6%;
Conservative
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les 35; Conserv
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                                                                                                                                                                                                       flanking loci
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                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 23
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microorganisms, and for genotyping subjects including humans. The method cost is also useful for detecting certain cancers and other malignancies.

Moreover, the method can be used to provide markers for use in identification of human and non-human individuals, plants and comitor responses to therapies including the possibility of and to monitor responses to therapies including the possibility of concleic acid damage. The nucleotide polymorphisms may be used in forensic concleic acid damage. The nucleotide polymorphisms may be used in forensic crime, in gene mapping and population studies. LASA may also be used in the mannifecture of a fit for detecting and/or identifying nucleotide crime, in gene mapping and population studies. LASA may also be used in the LASA method avoids the time and cost required by prior art comme. The LASA method avoids the time and cost required by prior art commence using agel electrophoresis and Southern transfer analysis. In the use of gel electrophoresis a process that has proved difficult to the use of gel electrophoresis a process that has proved difficult to the use of gel electrophoresis and southers avoidance of this attong candidate for future use in clinical and laboratory procedures. ABK24276-ABK24313 represent primers used to interpret interior of the interior control of the interior of int
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38 BP; 19 A; 19 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsatellite sequence from clone MTGT4B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92WO-US000340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.9%;
Local Similarity 94.6%;
les 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ33648 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9213102-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ33648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
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The sequence is that of a bovine microsatellite sequence obtd. by

C creening a library of bovine MboI DNA fragments of between 250 and 500

C conse across-Mybridised. Assuming independent distribution of

C clones across-Mybridised. Assuming independent distribution of

C creation and MboI sites, the frequency of (T6)n >9 microsatellites

C for ca. 230 such bovine microsatellites is summarised in the

Specification and indexed herein (see below). The sequences upstream and

c specification and indexed herein (see below). The sequences upstream and

downstream of the microsatellite sequence were used to generate the

compact of identify individuals, for parentsege testing, and in the genetic

C used to identify individuals, for parentsege testing, and in the genetic

C mapping of economic trait loci, or genes involved the determinism of

c economically important traits esp. in cattle, to allow selective

D breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                           ö
for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective by receding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                     DB 1; Length 39;
                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                             Sequence 39 BP; 0 A; 0 C; 19 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                  2315 grererererererererererererere 2351
                                                                                                                                                                                                                                                                                                                                                                                        2 dicididicididididicidicididididididid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microsatellite sequence from clone TGLA227.
                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                       Score 33.8;
Pred. No. 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Table 7; Page 259; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ33825 standard; DNA; 39 BP
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                                                                                                                                                                                                                                                                           0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.6
Matches 35, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-1991;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ33825;
                                                                                                                                                                                                field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 25
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field.)

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol eites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information

Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

WPI; 1992-284684/34.

Table 7; Page 189; 517pp; English

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AAT65731/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 olds overlected by probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites on the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information for the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The constream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The sequence of the microsatellite sequence were used to generate the microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                 Gaps
                                                                                                                                                                                                                                                                          PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                 ö
                    Score 33.8; DB 1; Length 39; Pred. No. 24; 0; Mismatches 2; Indels
Sequence 39 BP; 0 A; 0 C; 19 G; 20 T; 0 U; 0 Other;
                                                                         Sequence 39 BP; 0 A; 0 C; 20 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                    Microsatellite sequence from clone TGLA213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Table 7; Page 252; 517pp; English.
                                                                                                                                                             AAQ33807 standard; DNA; 39 BP.
                                                                                                                                                                                                                                                                                                                                                                                          92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                                                  91US-00642342
                                   Local Similarity 94.6%; es 35; Conservative
                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Georges M, Massey JM;
                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                          WO9213102-A1.
                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                 06-AUG-1992.
                                                                                                                                                                                                              25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                  Bos taurus.
                                                                                                                                                                                      AAQ33807;
                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          field.)
                                                 Matches
                                                                                                                                      RESULT 26
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of Genetic disease, commercial expeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 by primers AAT65798-T66047. Those clones where the repeat sequence is from the marker clone Md£29 which contains the repeat sequence is from the marker clone Md£29 which contains the repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of polymorphic genetic markers of the form (dG-dA)n(dG-dT)n-using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                     PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                             amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ormula: (AC)19.5. (Updated on 25-MAR-2003 to correct PF field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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14.6%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                             primer;
                                                                                                                                                                                                 Repeat sequence from polymorphic marker clone Mfd29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 39 BP; 20 A; 19 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                             Polymorphism; repeat sequence; genetic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Col 9-10; 186pp; English.
  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-00341562.
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Matches 35; Conservative
AAT65731 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH70484 Btandard; DNA; 39
                                                                                                                 (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-1989;
05-SEP-1991;
                                                                                                              25-MAR-2003
17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5582979-A.
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                                                        AAT65731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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ADH70484
ID ADH70-
XX
AC ADH70-
XX
DT 25-MAI
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Gaps

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Score 33.8; DB 1; Length 39; Pred. No. 24; 0; Mismatches 2; Indels

94.68;

35; Conservative

Matches

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Query Match Best Local Similarity

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The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers associated diseases which comprises a panel of nucleic acid primers ("Vectarian parallification of each Vberta gene," Vbertan, The kit is useful for diagnosing organ transplant complete the complete of the complete o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a Vbeta gene.
                                                               degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; allergy; type II hypersensitivity; Goodpasture's syndrome; Hiv; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium, neoplastic disease; lymphoproliferalive disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphomas and cancers such as cancer of the brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 33.8; DB 1; Length 39;
94.6%; Pred. No. 24;
ive 0; Mismatches 2; Indels
                                              human; T-cell associated disease; Vbeta; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39 BP; 0 A; 0 C; 20 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 678; 164pp; English.
Human Vbeta gene repeat sequence #274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-00309335.
95US-00531241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00263959
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Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-059052/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rowen L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HOOD/) HOOD L E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROWE/) ROWEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002150891-A1.
                                                                                                                                                                                                                                                                                                                                                               breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .9-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-0CT-2002
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Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

91US-00642342. 92WO-US000340.

15-JAN-1992; .5-JAN-1991;

409213102-A1

Bos taurus.

36-AUG-1992.

Georges M, Massey JM; WPI; 1992-284684/34.

(GENM-) GENMARK.

PCR, selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

Sequence of a microsatellite from clone TGLA52.

(revised)
(first entry)

25-MAR-2003 02-FEB-1993

AAQ34091;

AAQ34091 standard; DNA; 40 BP.

4AQ34091

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The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine Mbol DNA fragments of between 250 and 500

CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50

CC ob with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50

CC ones cross-hybridised. Assuming independent distribution of 50

CC or an expectabilities and Mbol sites, the frequency of (TG)n >9 microsatellites

CC or a. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence supstream and specification and indexed herein (see below). The sequences upstream and commerce of the microsatellite sequence were used to generate the commerce of in vitro amplification of the corresp.

CC microsatellite (using the program OPTIRRIM). The microsatellites may be microsatellite supplied to identify individuals, for parentage testing, and in the genetic companion of economically important traits esp. in cattle, to allow selective fired in the correct of the corre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33.8; DB 1; Length 40;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40 BP; 0 A; 0 C; 20 G; 20 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Table 7; Page 368; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT66054 standard; DNA; 40 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%;
ilarity 94.6%;
Conservative
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tes 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
18-JUN-1997
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Gaps ;

2315 GICTGIGIGIGIGIGIGGGGGGGGGGGGGGGGGG 2351

δ 셤

ilarity 94.6%; Conservative

94US-00222177.

91US-00754351. 89US-00341562,

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
                                                                                                                                                                                                                                                                  Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                            Disclosure; Col 9-10; 186pp; English
                                                                                                                                                                                 (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                      WPI; 1997-042299/04.
                              Homo sapiens.
                                                                                                              04-APR-1994;
                                                                                                                                                        05-SEP-1991;
                                                                                                                                          21-APR-1989;
                                                       US5582979-A.
                                                                                   10-DEC-1996
                                                                                                                                                                                                               Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT66051,
                ઠે
                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial cannal or plant breeding or pedigree analysis. The repeats, when analysed, fall into 4 categories: 1) perfect repeats which are alternating tandem CA repeats with no interruptions and without adjacent or more runs of uninterrupted CA repeats separated by no more than 3 consecutive non-repeat bases; 3) compound perfect repeats which are defined as 2 consecutive non-repeat bases; 3) compound perfect repeats which are consecutive non-repeat bases; 5 uninterrupted dinuclectide or repeat bases from a run of at least 5 uninterrupted dinuclectide or longer repeats of a sequence other than (dC-dA)n.(dG-dA)n, or from at least 10 uninterrupted mononuclectides; and 4) imperfect compound repeats which are defined as for the perfect compound repeats except that the runs of CA are interrupted. The sequence presented here is an example of the perfect repeats sequence of structure: (CA)20. (Updated on 25-MAR-2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerse chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                            Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Score 33.8; DB 1; Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat sequence from polymorphic marker clone Mfd23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40 BP; 20 A; 20 C; 0 G; 0 T; 0 U; 0 Other;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Example 8; Col 57-58; 186pp; English.
                                                                                                                                                                                               89US-00341562.
91US-00754351.
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                                                                                                                                                                      94US-00222177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 94.6%;
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                         (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                   Homo sapiens
                                                                                                                                                                    04-APR-1994;
                                                                                                                                                                                                  21-APR-1989;
                                                                                                                                                                                                               05-SEP-1991;
                                                                                                              US5582979-A.
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17-JUN-1997
                                                                                                                                        10-DEC-1996
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                                                                                                                                                                                                                                                                     Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dA). (dg-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT55798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone MdE23 which contains the repeat sequence is from formula: (AC)20. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33.8; DB 1; Length 40; Pred. No. 24; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2315 GICTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40 BP; 20 A; 20 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (dC-dA)n.(dG-dT)n polymorphic repeat sequence #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00222177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.9%;
Best Local Similarity 94.6%;
Matches 35; Conservative
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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18-JUN-1997
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Forster JW, Jones ES;
                                WPI; 2001-512563/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK24300;
                                                                                               varieties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 34
ABK24300/c
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                                                                                                                                                        The invention relates to the isolation of polymorphic repeat sequences can having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human command or plant breeding or paternity or malysis. The repeats, commercial animal or plant breeding or pedigree analysis. The repeats, when can alysed, fall into 4 categories: 1) perfect repeats which are alacentaring tandem CA repeats with no interruptions and without adjacent crepeats of another sequence; 2) imperfect repeats which are defined as 2 cor more runs of uninterrupted CA repeats separated by no more than 3 consecutive non-repeat bases; 3) compound perfect repeats which are consecutive non-repeat bases; 2) imperfect repeat bases from a run of at least 5 uninterrupted dinucleotide or crepeat bases from a run of at least 5 uninterrupted dinucleotide or clonger repeats of a sequence other than (dC-dA)n. (dG-dT)n, or from at least 10 uninterrupted mononucleotides; and 4) imperfect compound repeats compound repeats control or from a consecutive or the perfect compound repeats except that the consecutive or the perfect compound repeats except that the consecutive or the perfect compound repeats an example of a perfect repeat sequence of structure; (AC)20. (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; profiling; grass profiling; seed batch purity testing.
                                                                                                Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0.9%; Score 33.8; DB 1; Length 40; 94.6%; Pred. No. 24; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2315 GICTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40 BP; 20 A; 20 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R. UNIV SOUTHERN CROSS. STATE VICTORIA DEPT NATURAL RES & ENVIRO. UNIV ADELAIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INT: MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                                                                         Example 8; Col 57-58; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simple sequence repeat, SSR, #44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JAN-2001; 2001NZ-00509193
       91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 94.6 ies 35; Conservative
                                (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                                                                                                                                                                                            to correct PF field.
                                                                              WPI; 1997-042299/04
       05-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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(UYSC-)
(VICT-)
(UYAD-)
(ITMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                        Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cereal
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The invention relates to a substantially purified or isolated nucleic acid (1) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements core corrected for amplifying an SSR, identifying (M1) an SSR by preparing a suitable for amplifying an SSR, identifying (M1) an SSR by preparing a corrected former in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs and and in the library containing SSRs, a library of ryegrass identifying clones in the library containing SSRs, a library of ryegrass or rereal breeding by identifying an SSR that is closely a speciated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a preferentially co-inherited, and selecting for the SSR in the breeding, and the differential species varieties by assessing method for DNA profiling grass or cereal species varieties or cereal breeding, for may be used in the selection of genes in grass or cereal breeding, for may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal seed batches, and for DNA profiling to establish the corrected string the purity of grass or cereal seed batches, and for DNA profiling to establish the selection of for DNA profiling to establish the selection of for DNA profiling to establish the sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microsatellite, ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40 BP; 20 A; 20 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.9%; Score 33.8; I Best Local Similarity 94.6%; Pred. No. 24; Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Timms P, Wolter L,
                                                                                                                                                                                                                                  Claim 13; Page 53; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK24300 standard; DNA; 40 BP
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10-MAY-2000; 2000US-0202559P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-2001; 2001WO-AU000526
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The invention relates to a method of identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length, comprising employing ligase-assisted spacer addition (LASA) assay. The method is useful in the identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length. In particular, the method is useful for identification of a nucleotide length polymorphism in animals or humans, which is associated with a neurodegenerative disease including fragile X syndrome, Huntington's disease, or muscular dystrophy. Purthermore, the method may be used for identifying and/or typing microorganisms; including yeasts and lower uni- and multi-cellular organisms. Purthermore, the method may be used to genotyping subjects including humans. The method is also useful for detecting certain cancers and other malignancies.

Moreover, the method can be used to provide markers for use in identification of human and non-human individuals, plants and identification of human and non-human individuals, plants and concernance of a identification of human and non-human individuals, plants and concernance of a crime, in gene mapping and population studies. LASA may also be used in the manufacture of a kit for detecting and/or identifying nucleotide crime, in gene mapping and population studies. LASA may also be used in the menthods using gel electrophoresis and Southern transfer analysis. In particular, current diagnosis of Huntington's disease relies heavily upon the use of gel electrophoresis, a process that has proved difficult to automate or miniaturies. The LASA method allows total avoidance of this mainiaturies and shorehor transfer analysis. In the use of gel electrophoresis, a process that has proved difficult to automate or miniaturies. The LASA method allows total avoidance of this and laboratory procedures. Aska method allows total avoidance of this and laboratory procedures. Aska detection seconds and laboratory procedures. Process that
                                                  Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligaseassisted spacer addition assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detect polymorphisms or microsatellites as described in the method of
                                                                                                                                                                                                                 Example 10; Page 55; 89pp; English.
WPI; 2002-121948/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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Seguence 40 BP; 20 A; 20 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö DB 1; Length 40; 2; Indels 2315 GTCTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTGT 2351 39 erererererererererererererererere 0; Mismatches Score 33.8; Pred. No. 24 ch 0.9%; 1 Similarity 94.6%; 35; Conservative Matches g

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AAT65710 standard; DNA; 41 BP AAT65710; RESULT 35
AAT65710/C
ID AAT65710/C
XX
AC AAT65
DT 25-MA
DT 17-JU
XX
DE Repea
XX
RW PCR;
KW PCR

(revised)
(first entry) 25-MAR-2003 17-JUN-1997

Repeat sequence from polymorphic marker clone Mfd8.

PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds. Polymorphism; repeat sequence; genetic marker; primer; amplification;

Homo sapiens

(MARS-) MARSHFIELD CLINIC.

Weber JL;

05-SEP-1991;

US5582979-A

10-DEC-1996

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The invention relates to the isolation of polymorphic repeat sequences markers. Primers based on these sequences can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of genetic disease, commercial repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AATGS798-166047. Those clones where the repeat sequence has been determined are shown in AATGS704-797. This repeat sequence has the marker clone Mdf8 which contains the repeat sequence is from the marker clone Mdf8 which contains the repeat sequence is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        formula: (AC)20A. (Updated on 25-MAR-2003 to correct PF field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33.8; DB 1; Length 41; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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91US-00754351.
                                               89US-00341562.
                                                                91US-00754351
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Best Local Similarity 94.6%;
Matches 35; Conservative
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                                                                                                (MARS-) MARSHFIELD CLINIC
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                                                                                                                                                                 WPI; 1997-042299/04.
                                                                05-SEP-1991;
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                                                 21-APR-1989;
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17-JUN-1997
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Gaps ö

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RESULT 38
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                                                                              The invention relates to the isolation of polymorphic repeat sequences having the sequence (dG-dA)n.(dG-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dG-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf45 which contains the repeat sequence is from the marker clone Mdf45 which contains the repeat sequence having the formula: (CA)20.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                       Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                2315 GTCTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                         Sequence 41 BP; 20 A; 21 C; 0 G; 0 T; 0 U; 0 Other;
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                                                               Disclosure; Col 9-10; 186pp; English.
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91US-00754351.
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                                                                                                                                                                                                                                                                                                Local Similarity 94.6%;
nes 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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     WPI; 1997-042299/04.
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05-SEP-1991;
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17-JUN-1997
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Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
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repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dA). (dg-dr) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdf63 which contains the repeat sequence is from the marker clone Mdf63 which contains the repeat sequence having the formula: (CA)20.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; T-cell associated disease; Vbeta; autoimmune disease; degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity; disease; type I hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; defectious disease; viral infection; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoporoliferative disease; leukaemia; lymphoma; cancer; brain cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33.8;
Pred. No. 25
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95US-00531241.
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Best Local Similarity 94.6%;
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 breast cancer; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002150891-A1.
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CC rejection and diagnosing and treating T-cell associated diseases
including autoimmune diseases, degenerative nervous system diseases,
including autoimmune diseases, degenerative nervous system diseases,
craft versus host disease, hypersensitivity diseases, infectious diseases,
and neoplastic diseases. Autoimmune diseases include Addison's disease,
atrophic gastritis. Degenerative nervous system diseases include multiple
catrophic gastritis. Degenerative nervous system diseases include multiple
catrophic gastrities us as contact with allergens that lead to
allergies, Type II hypersensitivities such as those present in
Caodpasture's syndrome and Type IV hypersensitivities such as those
caused by viruses such as HIV, fungal infections such as those caused by
the yeast genus Candida, parasitic infections such as those caused by
schistosomes, filaria and bacterial infections such as those caused by
Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
such as leukaemias, lymphomas and cancers such as cancer of the brain,
breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bow with an (AC)15 and a (TC)15 oligonucleocide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                               Sequence 41 BP; 0 A; 0 C; 21 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 cicicicicicididicionale 37
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA175.
                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.8;
                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rable 7; Page 238; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ33770 standard; DNA; 42 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92WO-US000340
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                                                                                                                                                                                                                                                                                                                                                                                                        0.98;
                                                                                                                                                                                                                                                                                                                                                                                                                        94.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
02-FEB-1993
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AAQ33770
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required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective bisecoing. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
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                                                                                                                                                                                                                  DB 1; Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat sequence from polymorphic marker clone Mfd62.
                                                                                                                                                                                                                                                                                                       2315 GrcrGrGrGrGrGrGrGrGrGrGrGrGrGrGrGrG 2351
                                                                                                                                                                        Sequence 42 BP; 0 A; 0 C; 21 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 42 BP; 21 A; 21 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                Query Match 0.9%; Score 33.8; E
Best Local Similarity 94.6%; Pred. No. 26;
Matches 35; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT65757 standard; DNA; 42 BP.
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91US-00754351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-1994;
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                                                                                                                                  field.)
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ID AAT6571
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Pred. No.

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The invention relates to a substantially purified or isolated mucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements or from ryegrass or more tandemly repeated nucleotide core elements or suitable for amplifying an SSR, identifying (M1) an SSR by preparing a suitable for amplifying an SSR, identifying (M1) an SSR by preparing a cantishe for amplifying an SSR, identifying SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs and core elements or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely conferentially co-inherited, and selecting for the SSR in the breeding, a preferentially co-inherited, and selecting for the SSR in the breeding, and core conference of preferentially co-inherites and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs can be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal seed batches, and for DNA profiling to establish the calenty of distinct identity, uniformity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                       tandem repeat;
                                   Gaps
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                                                                                                                                                                                                                                                                                                                                     Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tar
cereal profiling; grass profiling; seed batch purity testing
Length 42;
                                   2; Indels
                                                                    2315 Grengrenergrenergrecergrenergrenerg 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
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DB 1;
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                                   Mismatches
                    26;
Score 33.8;
Pred. No. 26
                                                                                                                                                                                                                                                                                                        Simple sequence repeat, SSR, #32
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04-MAY-2000; 2000AU-00007310
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 Query Match
Best Local Similarity 94.6%;
Matches 35; Conservative
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AAS13735 standard; DNA; 42
                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                      08-MAY-2002
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(UYAD-)
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                                                                                                                                                                 RESULT 41
AAS13735/c
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0.9%; Score 33.8; DB 1; Length 42;

BP; 21 A; 21 C; 0 G; 0 T; 0 U; 0 Other;

Sequence 42

Query Match

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The invention relates to a method of identifying or detecting a mucleotide repeat region in a nucleic acid molecule characterised by a mucleotide repeat region in a nucleic acid molecule characterised by a comprising employing ligase-assisted spacer addition classes. The method is useful in the identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a nucleotide length. In particular, the method is useful for identification of a nucleotide length polymorphism in animals or humans, which is associated with a neurodegenerative disease including fragile X syndrome, a useciated with a neurodegenerative disease including fragile X syndrome, be used for identifying and/or typing microorganisms including yeasts and lower uni- and multi-cellular organisms, as well as prokaryotic microorganisms; and for genocyping subjects including humans. The method can be used to provide markers for use in Moreover, the method can be used to provide markers for use in identification of human and non-human individuals, plants and identification of human and non-human individuals, plants and microorganisms, to ascertain parentage of human or non-human individual, crime, in gene mapping and population studies including the possibility of science to identify a particular victim or an alleged perpetrator of a crime, in gene mapping and population studies. LASA may also be used in the manufacture of a kit for detecting and/or identifying nucleotide crime and complement and southern transfer analysis. In methods using gelelectrophoresis and Southern transfer analysis. In methods using gelelectrophoresis and southern transfer analysis. In particular, current diagnosis of Huntington's disease relies heavily upon the use of gel electrophoresis, a process that has proved difficult to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligase-
                                                                                                                                                                                                                                                                                                                                                                                         Microsatellite, ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
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                  2; Indels
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                                                            GTGTGTGTGTGTG 2351
                                                                                                        41 grarararararararararararararararara 5
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                0; Mismatches
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                                                                   2315 Grererererererererecei
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10-MAY-2000; 2000US-0202559P.
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                                                                                                                                                                                                                        ABK24301 standard; DNA; 42
                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 94.6
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brockhurst V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                 09-APR-2002
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automate or miniaturise. The LASA method allows total avoidance of this limiting step, making it a strong candidate for future use in clinical and laboratory procedures. ABK24276-ABK24313 represent primers used to detect polymorphisms or microsatellites as described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n-using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR; polymerase chain reaction, paternity; maternity; humān; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphism; repeat sequence; genetic marker; primer; amplification;
                                                                                                                                                                                             Gaps
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                                                                                                                                                       DB 1; Length 42;
                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat sequence from polymorphic marker clone Mfd123.
                                                                                                                 Sequence 42 BP; 21 A; 21 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                   Score 33.8; DE
Pred. No. 26;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                         0.9%;
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                                                                                                                                               Query Match
Best Local Similarity 94.6
Matches 35, Conservative
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                                                                                                                                                                                                                                                                                                                               RESULT 43
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DB 1; Length 43;

Score 33.8; 1 Pred. No. 27;

0.9%;

Best Local Similarity

Query Match

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In section and individuals, for parentage testing, and in the genetic mapping of conomic trait loci, or genes involved the determinism of breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of a bovine microsatellite sequence obtd. by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                     PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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2315 GTCTGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44 BP; 0 A; 0 C; 22 G; 22 T; 0 U; 0 Other;
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                            42 grerererererererererererererererere
                                                                                                                                                                                                         Microsatellite sequence from clone MTGT11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Table 7; Page 184; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                            92WO-US000340
                                                                                                                                                                                                                                                                                                                                                                                                         91US-00642342
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ilarity 94.6%;
Conservative
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                                                                                                     AAQ33636 standard; DNA; 44
                                                                                                                                                                               (first entry)
                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-284684/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                             .5-JAN-1992;
                                                                                                                                                                                                                                                                                                                  WO9213102-A1
                                                                                                                                                               25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                             06-AUG-1992.
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                                                                                                                                                                                                                                                                                      Bos taurus.
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                                                                                                                                   AAQ33636;
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Best Local
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                                                                         RESULT 44
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Bos taurus.

AAQ33983;

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The sequence is that of a bovine microsatellite sequence obtd. by
conservating a library of bovine MboI DNA fragments of between 250 and 500
conservation and (TC)15 oligonucleotide probe. One out of 50
conservation and TC)15 oligonucleotide probe. One out of 50
conservation and TC)15 oligonucleotide probe. One out of 50
conservation of TC)15 oligonucleotide probe. One out of 50
conservation of TC)15 oligonucleotide probe of 50
conservation of TC)15 oligonucleotide of TC)
conservation of TC)
conservation of Experiment of TC)
conservation of the microsatellite sequence where used to generate the conservation of the microsatellite sequence were used to generate the microsatellite fusing the program OPTIPRIM). The microsatellites may be microsatellite fusing the program OPTIPRIM). The microsatellites may be microsatellity individuals, for parentage testing, and in the genetic conservation of trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.9%; Score 33.8; DB 1; Length 44; 94.6%; Pred. No. 27; 27; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat sequence from polymorphic marker clone Mfd66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44 BP; 0 A; 0 C; 22 G; 22 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                       Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                               WPI; 1992-284684/34.
                                                                                                                                                                                                                                           (GENM-) GENMARK
                                                                                                                                                                                                15-JAN-1991;
                                                               WO9213102-A1
                                                                                                                                                      L5-JAN-1992;
                                                                                                            06-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mool DNA fragments of between 250 and 500
creening a library of bovine Mool DNA fragments of between 250 and 500
compared by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mool sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
cfor ca. 210 such bovine microsatellites is summarised in the
specification and indexed horein (see below). The sequences upstream and
downstream of the microsatellite sequence were used to generate the
crequired PCR primers for in vitro amplification of the corresp.
microsatellite (using the program opripring). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
cmapping of economic trait los; or genes involved the determinism of
economically important traite esp. in cattle, to allow selective
ceconomically important traite sp. in cattle, to allow selective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                             PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 33.8; DB 1; Length 44;
94.6%; Pred. No. 27;
ive 0; Mismatches 2; Indels
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                                                                                                                                        Microsatellite sequence from clone TGLA381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Table 7; Page 323; 517pp; English
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35; Conservative
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(first entry)
                                                                                                  (first entry)
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                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-284684/34.
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Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENM-) GENMARK.
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02-FEB-1993
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                                                                           25-MAR-2003
02-FEB-1993
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AAQ34113;

XXXEX BX BX AXX

AAQ34113

Query Match

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Gaps ;. 0

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repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly (GC-dA). (GG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-766047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf49 which contains the repeat sequence is from the marker clone Mdf49 which contains the repeat sequence is from formula: (CA)22. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length, comprising employing ligase-assisted spacer addition (LASA) assay. The method is useful in the identifying or detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsatellite; ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                     The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these
                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giffard PM;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human microsatellite D1S191 detection PCR primer #10.
                                                                                                                                                                                                                                                                                                                                           Sequence 44 BP; 22 A; 22 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2315 GTCTGTGTGTGTGTGTGCGTGTGTGTGTGTGTG 2351
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                                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 33.8; E
14.6%; Pred. No. 27;
.ve 0; Mismatches
                                                    Disclosure; Col 11-12; 186pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assisted spacer addition assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-2001; 2001WO-AU000526.
                                                                                                                                                                                                                                                                                                                                                                                               ilarity 94.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK24302 standard; DNA; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Matches 35; Conserv
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                                                                                                                                                                                                                                                                 The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-707. This repeat sequence is from the marker clone Mdf66 which contains the repeat sequence is from the marker clone Mdf66 which contains the repeat sequence is from formula: (AC)22. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                               Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n-using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.8; DB 1; Length 44;
Pred. No. 27;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44 BP; 22 A; 22 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                     Disclosure; Col 11-12; 186pp; English
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                  89US-00341562.
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                                                                      (MARS-) MARSHFIELD CLINIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Conservative
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                                                                                                                                           WPI; 1997-042299/04
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                    21-APR-1989;
05-SEP-1991;
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05-SEP-1991;
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                                                                                                          Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT65749;
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cc nucleotide repeat region in a nucleic acid molecule characterised by a particular length. In particular, the method is useful for identification of a nucleotide length polymorphism in animals or humans, which is cassociated with a neurodegenerative disease including fragile X syndrome, thurtington's disease, or muscular dystrophy. Furthermore, the method may be used for identifying and/or typing microorganisms including yeasts and construction of the method can be used to recorganisms including yeasts and microorganisms; as well as prokaryotic microorganisms; and for genotyping subjects including humans. The method can be used to provide markers for use in microorganisms, to ascertain cancers and other malignancies. Moreover, the method can be used to provide markers for use in microorganisms, to ascertain parentage of human or non-human individual, and to monitor responses to therapies including the possibility of crime, in gene mapping and population studies. Lash may be used in forensic conclence to identify a particular victim or an alleged perpetrator of a crime, in gene mapping and population studies. Lash may also be used in the manufacture of a kit for detecting and/or identifying nucleotide repeat regions such as a nucleotide length polymorphism in a eukaryotic repeat regions uch as a nucleotide length polymorphism in a eukaryotic repeat regions uch as a nucleotide length polymorphism in a cukaryotic genome. The Lash method avoids the time and cost required by prior art methods using gel electrophoresis and southern transfer analysis. In particular, current diagnosis of Huntington's disease relies heavily upon the use of gel electrophoresis, a process that has proved difficult to the use of gel electrophoresis mand shallows total avoidance of this automate or miniaturise. The Lash method allows total avoidance of this caucomate or miniaturise. The Lash method allows total avoidance of this caucomate or miniaturise. The Lash method allows the particular propression of the particular procession of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detect polymorphisms or microsatellites as described in the method of the invention
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Best Local Similarity 94.6%;
Matches 35; Conservative (
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02-FEB-1993
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Table 7; Page 295; 517pp; English. mapping, and selective breeding.

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The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine Mbo! DNA fragments of between 250 and 500

CC clones cross-hybridised. Assuming independent distribution of

CC clones cross-hybridised. Assuming independent distribution of

CC microsatellites and Mbo! sites, the frequency of (T6)n >9 microsatellites

CC in the bovine genome is estimated at >100,000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the

CC specification and indexed herein (see below). The sequences upstream and

CC downstream of the microsatellite sequence ware used to generate the

CC microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite (using the program OPTIPRIM). The microsatellites may be

CC used to identify individuals, for parentage teating, and in the genetic

CC mapping of economic trait loc; or genes involved the determinism of

CC contract DAQ33501-34437. (Updated on 25-MAR-2003 to correct PN

CC breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                        DB 1; Length 45;
                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 45 BP; 0 A; 0 C; 22 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                            Score 33.8; 1
Pred. No. 28;
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Best Local Similarity 94.6'
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02-FEB-1993
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                                                                                                                                                                                                                                                                                 field.)
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AAQ33939 standard, DNA; 46

RESULT 53

AAQ33939

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Length 46; Indels

DB 1;

Score 33.8; DE Pred. No. 29; 0; Mismatches

0.9%; larity 94.6%; Conservative

Local Similarity nes 35; Conserv

Matches

Query Match

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC1)5 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information consistent of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The equired PCR primers for in vitro amplification of the corresp.

The country individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                  DB 1; Length 45;
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                                                                                                                                              Sequence 45 BP; 0 A; 0 C; 23 G; 22 T; 0 U; 0 Other;
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Pred. No. 28;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     AAQ33840 standard; DNA; 46 BP.
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Best Local Similarity 94.6%;
Matches 35; Conservative
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02-FEB-1993
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                                                                                                            field.)
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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

WO9213102-A1

06-AUG-1992

Microsatellite sequence from clone TGLA340.

(revised)
(first entry)

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AAQ33939;

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35; Conservative
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used in genetic identification, gene

91US-00642342. 92WO-US000340.

15-JAN-1991; 15-JAN-1992;

Georges M, Massey JM;

GENM-) GENMARK

Table 7; Page 305; 517pp; English Polymorphic bovine DNA markers - mapping, and selective breeding.

54 RESULT

Sequence 46 BP; 0 A; 0 C; 23 G; 23 T; 0 U; 0 Other;

Eield.)

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Polymorphism; repeat sequence; genetic marker; primer; amplification;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used to detect these narkers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the animal or plant breeding or pedigree analysis. Clones containing the phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. Those clones where the repeat sequence has by primers AAT65794-76647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the repeat sequence is from the marker clone Mdf17 which contains the marker clone which marker clone wh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                      Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 33.8; DB 1; Length 46;
14.6%; Pred. No. 29;
ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat sequence from polymorphic marker clone Mfd61.
                                                                                                                                        Repeat sequence from polymorphic marker clone Mfd17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2315 Grendrengrengreneracentererererere 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46 BP; 23 A; 23 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Col 9-10; 186pp; English
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                            ВР.
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(first entry)
                            AAT65719 standard; DNA; 46
                                                                                           (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-042299/04.
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                04-APR-1994;
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17-JUN-1997
                                                                                         25-MAR-2003
17-JUN-1997
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                                                             AAT65719;
          Matches
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the animal or plant breeding or pedigree analysis. Clones containing the phage libraries were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AMF65798-f6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf61 which contains the repeat sequence is from the marker clone Mdf61 which contains the repeat sequence having the formula: (CA)23. (Updated on 25-MAR-2003 to correct PF field.)
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PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of polymorphic genetic markers of the form (dC_\tau dA)\,n\,(dG_\tau dT)\,n using novel nucleic acid mols. as primers.
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0.9%; Score 33.8; DB 1; Length 46;
Best Local Similarity 94.6%; Pred. No. 29;
Matches 35; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46 BP; 23 A; 23 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 11-12; 186pp; English
                                                                                     hybridisation; chromosome; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-00754351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89US-00341562.
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AAT65709 standard; DNA; 46
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05-SEP-1991;
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17-JUN-1997
                                                                                                                                                                               Homo sapiens
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Glones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from
                                                                                                                                                                                                                                                     Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the marker clone Mdf7 which contains the repeat sequence having the formula: (CA)20TA(CA)2. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46 BP; 23 A; 22 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                       Claim 1; Col 9-10; 186pp; English.
                      94US-00222177
                                                              89US-00341562
                                                                                    91US-00754351
                                                                                                                          (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                               WPI; 1997-042299/04.
                      04-APR-1994;
                                                              21-APR-1989;
                                                                                    05-SEP-1991;
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Gaps
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 Score 33.8; DB 1; Length 46; Pred. No. 29; 0; Mismatches 2; Indels
                                                             2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                            Query Match 0.94;
Best Local Similarity 94.68;
Matches 35; Conservative
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Human microsatellite D1S191 detection PCR primer #11.
       ABK24303 standard; DNA; 46 BP
                        (first entry)
                                                                    WO200185987-A1
                                                            Homo sapiens.
                        09-APR-2002
                ABK24303;
RESULT 57
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Microsatellite; ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.

L5-NOV-2001

09-MAY-2001; 2001WO-AU000526

09-MAY-2000; 2000US-0202771P.

(DIAT-) DIATECH PTY LTD.

Barnard R, Giffard PM; Wolter L, Brockhurst V, Timms P, WPI; 2002-121948/16.

Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligaseassisted spacer addition assay.

Example 10; Page 55; 89pp; English.

The invention relates to a method of identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length, comprising employing ligase-assisted spacer addition (LASA) assay. The method is useful in the identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a particular length. In particular, the method is useful for identification of a mucleotide length polymorphism in animals or humans, which is associated with a neurodegenerative disease including fragile X syndrome, Huntington's disease, or muscular dystrophy. Furthermore, the method may consist and for genotyping subjects including humans. The method lower uni- and multi-cellular organisms, as well as prokaryotic microorganisms; and for genotyping subjects including humans. The method can be used to provide markers for useful for detecting certain cancers and other malignancies. Moreover, the method can be used to provide markers for use in cleantification of human and non-human individuals, plants and microorganisms, to ascertain parentage of human or non-human individual, and to concert responses to therapies including the possibility of conclor responses to therapies including the possibility of crime, in gene mapping and population studies. LASA may also be used in the manufacture of a kit for detecting or an alleged perpetrator of a crime, in gene mapping and population studies. LASA method avoide the time and cost required by the creating crepts and cost required by an electrical and cost required by an electrical and cost required by the an autocotical and cost required by an electrical particular, current diagnosis of Huntington's disease relies heavily upon the use of gel electrophoresis, a process that has proved difficult to attomate or miniaturise. The LASA method allows total avoidance of this limiting step, making it a strong candidate for future use in clinical and laboratory procedures. ABX4376-ABX4313 represent primers used to detect polymorphisms or microsatellites as described in the method of the methods using gel electrophoresis and Southern transfer analysis. In nvention

Seguence 46 BP; 23 A; 23 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö 0.9%; Score 33.8; DB 1; Length 46; 94.6%; Pred. No. 29; ve 0; Mismatches 2; Indels ilarity 94.6%; Conservative Local Similarity les 35; Conserv Query Match Best Loca Matches

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ВP ADH70581 standard; DNA; 48 (first entry) 25-MAR-2004 ADH70581; ADH70581/c RESULT 58

Human Vbeta gene repeat sequence #371.

human; T-cell associated disease; Wheta; autoimmune disease; degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infections disease; neoplastic disease; Addison's disease; atrophic gastritis; Addison's disease; atrophic gastritis; Alzelemer's disease; hypersensitivity disease; type I hypersensitivity doodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; doodpasture's syndrome; type IV hypersensitivity; dections disease; viral infection; filaria; bacterial infection, Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;

breast cancer; ds.

Homo sapiens

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The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each 'Ubera gene, 'DetaRNA or cDNA. The kit is useful for diagnosing organ transplant completed and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, and neoplastic diseases, hyperenativity diseases, infectious disease, and neoplastic diseases, Autoimmune diseases include Addison's disease, arrophic gastritis. Degenerative nervous system diseases include multiple strophic gastritis and Alzheimer's disease. Hypersensitivity diseases include Type in hypersensitivities such as chose present in C doodpasture's syndrome and Type IV hypersensitivities such as those caused by viruses such as Those caused by viruses such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and pacterial infections such as those caused by contacterium Neoplastic diseases include any paper.
                                                                                                                                                                                                                                                                                                                                                                                         Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat sequence from polymorphic marker clone Mfd115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48 BP; 23 A; 23 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 775; 164pp; English.
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95US-00531241.
                                                                                                                                             99US-00263959
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Best Local Similarity 84.4
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-059052/06
                                                                                                                                                                                                                                                                                                                  Hood LE, Rowen L;
                                                                                                                                                                                                                                                    (HOOD/) HOOD L E.
                                                                                                                                                                                                                                                                            (ROWE/) ROWEN L.
                                                           US2002150891-A1.
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17-JUN-1997
                      Homo sapiens.
                                                                                                                                             05-MAR-1999;
                                                                                                                                                                                        19-SEP-1994;
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                                                                                                      .7-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vbeta gene
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Gaps

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-da)n. (dg-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Gnes containing the animal or plant breeding or pedigree analysis. Octaming the phage libraries were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dA). (dg-dT) probe. Over 100 repeat blocks were isolated The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdflis which contains the repeat sequence is from the marker clone Mdflis which contains the repeat sequence having the formula: ATAGGAGAG(AC)17.5. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analyais; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat sequence from polymorphic marker clone Mfd9.
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                                                                                                                                                                                                                                                                                                                                                 Claim 1, Col 13-14; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2318 TGTGTGTGTGTGTGTGCGTGT
                                                                                                                                                                91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 90.0%;
36; Conservative
                                                                                                             94US-00222177.
                                                                                                                                              89US-00341562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT65711 standard; DNA; 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                              (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                 WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5582979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
17-JUN-1997
                                                                                                                04-APR-1994;
                                                                                                                                              21-APR-1989;
                                                                                                                                                                  05-SEP-1991;
                                               US5582979-A.
                                                                               10-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT65711;
                                                                                                                                                                                                                                   Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 60
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having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e-g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66647. Those clones where the repeat sequence has been determined are shown in AAT65704-737. This repeat sequence has the marker clone Mdf9 which contains the repeat sequence is from the marker clone Mdf9 which contains the repeat sequence having the formula: (CA)17G. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n-using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                    The invention relates to the isolation of polymorphic repeat sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35 BP; 17 A; 17 C; 1 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                     Claim 1; Col 9-10; 186pp; English.
89US-00341562
91US-00754351
                                                                  (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                   WPI; 1997-042299/04.
21-APR-1989;
05-SEP-1991;
                                                                                                                       Weber JL;
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ö Score 33.4; DB 1; Length 35; Pred. No. 23; 0; Mismatches 1; Indels 2317 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 35 crererererererererererererererere Query Match
Best Local Similarity 97.1%;
Matches 34; Conservative δ 셤

AAQ34006 standard; DNA; 43 25-MAR-2003 02-FEB-1993 AAQ34006; RESULT 61 AAQ34006

BP

(first entry) (revised)

Microsatellite sequence from clone TGLA414.

PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

Bos taurus

WO9213102-A1

06-AUG-1992

92WO-US000340 15-JAN-1992; 91US-00642342

(GENM-) GENMARK.

15-JAN-1991;

Georges M, Massey JM;

WPI; 1992-284684/34.

Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

Table 7; Page 333; 517pp; English

The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
compared by with an (AC)15 and a (TC)15 and and a (TC)15 and a

ö 0.9%; Score 33.4; DB 1; Length 43; 86.0%; Pred. No. 30; tive 0; Mismatches 6; Indels Seguence 43 BP; 2 A; 0 C; 19 G; 22 T; 0 U; 0 Other; Local Similarity 86.0 Query Match Matches

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Gaps

ઠ 셤 RESULT 62 AAX28288/c

뮵 AAX28288 standard; DNA; 41 AAX28288;

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Gaps

17-JUN-1999 (first entry)

Human CYP3A4 gene polymorphism #2.

CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism; CYP3A4 substrate; drug-drug interaction identification; toxin exposure; genetic linkage detection; phenotypic variation; ss.

Homo sapiens

WO9913106-A1

18-MAR-1999.

98WO-US018158. 02-SEP-1998; 97US-0058612P. 10-SEP-1997;

(AXYS-) AXYS PHARM INC.

Guida M; Lichter JB,

WPI; 1999-215070/18.

New isolated CYP3A4 polymorphic sequences.

Claim 2; Page 35; 40pp; English

This sequence represents a CYP3A4 sequence polymorphism of the invention, which is part of a non-naturally occurring chromosome. Nucleic acids comprising the CYP3A4 polymorphic sequences can be used to screen patients for altered metabolism for CYP3A4 substrates, potential drug-drug interactions, and adverse/side effects as well as diseases that result from environmental or occupational exposure to toxins. They can also be used to establish animal, cell culture and in vitro cell-free models for drug metabolism. Polymorphic CYP3A4 gene sequences can be used for expression studies to determine the effect of promoter and/or intron sequence variations on mRNA expression and stability. The polymorphisms

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
downstream of the microsatellite sequence water used to generate the
required PCR primers for in vitro amplification of the corresp.
incrosatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
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are also used as single nucleotide polymorphisms to detect genetic linkage to phenotypic variation in activity and expression of CYP3A4. The nucleic acids can also be used to generate genetically modified non-human animals or site specific gene modifications in cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR; 'selection, primers, OPTIPRIM, breeding, cattle, parentage, genetic mapping, traits, amplification, ss.
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                                                                                                                                                                                                                                                 Score 33; DB 1; Length 41;
Pred. No. 31;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                        41 rererererererererererererererererananaece 1
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                                                                                                                                                                              Sequence 41 BP; 17 A; 16 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsatellite sequence from clone TGLA377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rable 7; Page 319; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ33974 standard; DNA; 36 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-00642342
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                                                                                                                                                                                                                                                     ch 0.9%;
(1 Similarity 87.8%;
36; Conservative
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(first entry)
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                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 63
AAQ33974
AAQ33974
AAQ33974
AAC33974
AA
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleocide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (TG)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information specification and indexed herein (see below). The sequence information specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32.8; DB 1; Length 36; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2316 rengingrenergierererererererere 2351
2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
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                           1 Grerererererererererererererererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                          Microsatellite sequence from clone TGLA35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Table 7; Page 311; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - mapping, and selective breeding.
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                                                                                                               ВЪ
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                                                                                                                                                                                                                                                                                                                                                                                                         92WO-US000340.
                                                                                                               AAQ33953 standard; DNA; 36
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.9
Best Local Similarity 94.4
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Georges M, Massey JM;
                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                            LS-JAN-1992;
                                                                                                                                                                                                                                                                                                                                             WO9213102-A1
                                                                                                                                                                                25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1992.
                                                                                                                                                                                                                                                                                                                Bos taurus.
                                                                                                                                                 AAQ33953;
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ID AAQ3
XX
                                                                                  RESULT 64
                                                                                                   AAQ33953
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AAQ34068 standard; DNA; 36

Gaps

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Query Match 0.9%; Score 32.8; DB 1; Length 36; Best Local Similarity 94.4%; Pred. No. 28; Matches 34; Conservative 0; Mismatches 2; Indels

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information specification and indexed herain (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primars for in vitro amplification of the corresp. microsatellite (using the program OPTIPRM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trail loci, or genes involved the determinism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.9%; Score 32.8; DB 1; Length 36; Best Local Similarity 94.4%; Pred. No. 28; Matches 34; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2316 rererererererererererererererere 2351
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                                                                                                                                                                                                                                                                                                                                                                                                      Table 7; Page 261; 517pp; English
                                                                                                                                                                                                                                                                                                                                                          mapping, and selective breeding.
                                                                                                                          92WO-US000340.
                                                                                                                                                                    91US-00642342.
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(first entry)
                                                                                                                                                                                                                                                     Seorges M, Massey JM;
                                                                                                                                                                                                                                                                                               WPI; 1992-284684/34.
                                                                                                                                                                                                           (GENM-) GENMARK
                                         WO9213102-A1.
                                                                                                                                                                  15-JAN-1991;
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02-FEB-1993
                                                                                 06-AUG-1992
  Bos taurus.
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ID AAQ3
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screening a library of bovine Mbol DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
con the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comparisem of the microsatellite sequence ware used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
first.

Contract PN
Freeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                            PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 grererererererererererererererererer 36
                                                                                                    Microsatellite sequence from clone TGLA445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microsatellite sequence from clone TGLA23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 0.9%; Score 32.8;
1. Similarity 94.4%; Pred. No. 28
34; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Table 7; Page 358; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ33828 standard; DNA; 36 BP
                                                                                                                                                                                                                                                                                                                                      92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                91US-00642342
                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
02-FEB-1993
                                       25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                     WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                                                15-JAN-1991;
                                                                                                                                                                                                                                                                                            06-AUG-1992
                                                                                                                                                                                                              Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ33828;
AAQ34068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Gaps ö

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information of opecification and indexed herein (see below). The sequence information specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                       Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Grererererererererererererererer 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ch 0.9%; Score 32.8; I Similarity 94.4%; Pred. No. 28; 34; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microsatellite sequence from clone TGLA222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic mapping; traits; amplification; ss
                                                                                                                                             Table 7; Page 292; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92WO-US000340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georges M, Massey JM;
                                маввеу ЛМ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-284684/34.
                                                              WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENM-) GENMARK.
(GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9213102-A1
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
                                Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ33819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 68
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Table 7; Page 257; 517pp; English

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Gaps

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The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine Mbol DNA fragments of between 250 and 500

compared by with an (AF)15 and a (TF)15 oligonucleotide probe. One out of 50

clones cross-hybridised. Assuming independent distribution of

microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites

compared bovine genome is estimated at >100, 000. The sequence information

for ca. 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

downstream of the microsatellite sequence were used to generate the

required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite (using the program OPTIPRIM). The microsatellites may be

concomically important trait loci, or genes involved the determinism of

connomically important traits espi in cattle, to allow selective

breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herain (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                          Score 32.8; DB 1; Length 36; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                   Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite sequence from clone TGLA303.
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Table 7; Page 282; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ33882 standard; DNA; 36 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                            0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-00642342.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 34, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9213102-A1
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02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
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X355555555555555555
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Gaps

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5, DB 1;

0.9%; Score 32.8; Ilarity 94.4%; Pred. No. 28; Conservative 0; Mismatches

Best Local Similarity Matches 34; Conserv

Query Match

2350

36 ererérérérererererererererererer

2315 GTCTGTGTGTGTGT

ВР

AAT65720 standard; DNA; 36

RESULT 71 AAT65720,

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Length 36; Indels

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required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                        Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols, as primers.
                                                                                                                                                           Gaps
                                                                                                                                                           ö
                                                                                                                                DB 1; Length 36;
                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                  Repeat sequence from polymorphic marker clone Mfd113.
                                                                                                       Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                  2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                           renererererererererererererererereres
                                                                                                                             Score 32.8; DE
Pred. No. 28;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Col 13-14; 186pp; English.
                                                                                                                                                                                                                                                                         AAT65784 standard; DNA; 36 BP
                                                                                                                               Query Match
Best Local Similarity 94.4%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00222177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89US-00341562
91US-00754351
                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MARS-) MARSHFIELD CLINIC,
                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-1991;
                                                                                                                                                                                                                                                                                                                           25-MAR-2003
17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5582979-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weber JL;
                                                                                                                                                                                                                                                                                                   AAT65784;
                                                                             field.)
                                                                                                                                                                                                                                                 RESULT 70
                                                                                                                                                                                                                                                           888888888888
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Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.

Homo sapiens.

US5582979-A 10-DEC-1996 94US-00222177.

04-APR-1994;

91US-00754351

05-SEP-1991; 21-APR-1989;

(MARS-) MARSHFIELD CLINIC

Repeat sequence from polymorphic marker clone Mfd18.

(revised)
(first entry)

25-MAR-2003 17-JUN-1997

AAT65720;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf18 which contains the repeat sequence is from formula: (AC)18. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 32.8; DB 1; Length 36; 4.4%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36 BP; 18 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 9-10; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 94.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                     Weber JL;
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RESULT

Sequence 36 BP; 18 A; 18 C; 0 G; 0 T; 0 U; 0 Other;

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdfill which contains the repeat sequence is from the marker clone Mdfill which contains the repeat sequence laving the formula: (AC)18. (Updated on 25-MAR-2003 to correct PF field.)

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36 digitaricitaricitaricitationalisticitation 1

Microsatellite; ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.

Human microsatellite D18191 detection PCR primer #6.

(first entry)

09-APR-2002

ABK24298;

ABK24298 standard; DNA; 36 BP

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New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                      Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32.8; DB 1; Length 36; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36 BP; 0 A; 0 C; 18 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                            UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
UNIV ADELAIDE.
                                                                                                                                                                                                                                   STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                                                                                                                                                                                                         INT MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence is a ryegrass or fescue SSR
                                                                     Simple sequence repeat, SSR, #10.
                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 51; 72pp; English.
                                                                                                                                                                                                     24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
                                                                                                                                                                                  03-JAN-2001; 2001NZ-00509193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.48;
          AAS13713 standard; DNA; 36
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 94.4
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                Forster JW, Jones ES;
                                                                                                                                                                                                                                                                                                                  WPI; 2001-512563/56.
                                                   08-MAY-2002
                                                                                                                                                                25-MAY-2001
                                                                                                                                            NZ509193-A.
                                                                                                                                                                                                                                                                                                                                                                      varieties
                              AAS13713;
                                                                                                                                                                                                                                    (SAUS-)
                                                                                                                                                                                                                                               (UYSC-)
(VICT-)
                                                                                                                                                                                                                                                                              ITMA-)
                                                                                                                                                                                                                                                                   (UXAD-)
                                                                                                                         Poeae.
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Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligase-

Example 10; Page 55; 89pp; English assisted spacer addition assay

Barnard R, Giffard PM;

Brockhurst V, Timms P, Wolter L,

WPI; 2002-121948/16.

(DIAT-) DIATECH PTY LTD.

09-MAY-2001; 2001WO-AU000526 09-MAY-2000; 2000US-0202771P. 10-MAY-2000; 2000US-0202559P.

WO200185987-A1. Homo sapiens.

15-NOV-2001.

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The invention relates to a method of identifying or detecting a cucleotide repeat region in a nucleic acid molecule characterised by a cucleotide repeat region in a nucleic acid molecule characterised by a cucleotide repeat region in a nucleic acid molecule characterised by a cucleotide repeat region in a nucleic acid molecule characterised by a nucleotide repeat region in a nucleic acid molecule characterised by a particular in particular, the method is useful for identification of a mucleotide length polymorphism in animals or humans, which is a neucleotide length polymorphism in animals or humans, which is consociated with a neurodegenerative disease including fragile x syndrome, be used for identifying and/or typing microorganisms including yeasts and conservant. And multi-cellular organisms, as well as prokaryotic microorganisms, and for genotyping subjects including humans. The method con peused for genotyping subjects including humans. The method con be used for provide markers for use in identification of human and non-human individuals, plants and identification of human and non-human individuals, plants and contour responses to therapies including the possibility of microorganisms, to ascertain parentage of human or non-human individuals, and to monitor responses to therapies including the possibility of crime, in gene mapping and population studies. LASA may also be used in forensic repeat regions such as a nucleotide length polymorphism in a eukaryotic repeat regions such as a nucleotide length polymorphism in a eukaryotic methods using gel electrophoresis and Southern transfer analysis. In particular, current diagnosis of Huntington's disease relies heavily upon the use of gel electrophoresis, a process that has proved difficult to authored and laboratory procedures. AbK2476-ABK24313 represent primers used to detect polymorphisms or microsatellites as described in the method of the
The invention relates to a substantially purified or isolated nucleic acid (1) from ryegrass or fescue species including a simple sequence cepeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer 2-6 nucleotides in length. Also included are a nucleic acid primer cuitable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a second for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal seed batches, and for DNA profiling to establish the distinct identity, uniformity and/or stability of a cultivar. The present
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Score 32.8; DB 1; Length 36; Pred. No. 28;
Sequence 36 BP; 18 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
                                    0.9%;
                                                   Best Local Similarity
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2316 rerererererererecerererererere 2351

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RESULT 73 ABK24298/c

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ADO80224/c
ID ADO80224 standard; DNA; 36 BP.
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                                                                                                                                                                                                                                                                                                                                           Triticum.
                                                                                                                    ADO80224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a method of typing (MI) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DMA region of (I) that includes PML, using as template a DMA sample containing at least one segment of (I); and determining the length of the resulting amplicon(s). Also described are: a method of determining (M2) microsatellite markers (MM) for predisposition to a disease, associated with a gene that includes one or more PML; and predisposis (M3) of diseases associated with gene that include PML. The method is used to identify microsatellite markers, in a disease related gene, that are associated with a predisposition to diseases and for prediagnosis of such Myperthermia syndrome in pigs and metabolic diseases; also to type genes that encode milk proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hormones or transcription factors. The method is simpler, quicker and particularly less expensive than known methods based on sequencing. This sequence represents a prion protein polymorphic microsatellite marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.
                                                                                                                                                                                                                                                                                                                                                                  Prion protein polymorphic microsatellite marker consensus sequence #12.
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                       disease predisposition, microsatellite marker, prion disease, cystic fibrosis, malignant hyperthermia syndrome, metabolic disease, milk protein, hormone, transcription factor, pT7-blue-vector, sheep,
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2; Indels
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                                             2316 rererererererererererererererere 2351
                                                                                                                                                                                                                                                                                                                                                                                                                  gene typing, polymorphic microsatellite loci; PML;
                                                                         Score 32.8; DE Pred. No. 28; 0; Mismatches
Mismatches
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                                                                                                                                                                                                                    ADO81134 standard; DNA; 36 BP
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1 Similarity 94.4%;
34; Conservative
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34; Conservative
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ADO81134/C
ADO81134/C
ADO8111,
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ADO811,
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ADO811,
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ADO811
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The invention relates to a novel method for selecting highly-dormant wheat using a genetic marker associated with a gene that provides high dormancy to the seeds. In the method of the invention, the genetic marker exists specifically in the genetic region within 44 cM from the gene associated with high dormancy in chromosome 4a. The method is useful for selecting highly-dormant wheat. This polynucleotide sequence represents a
                                                                                     highly-dormant wheat; genetic marker; high dormancy; seed; chromosome 4A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Selecting highly-dormant wheat using genetic marker associated with gene
that provides high dormancy to seeds.
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                                        Wheat SSR containing amplification genetic marker, Xgwm637
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Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wheat genetic marker of the invention.
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Best Local Similarity 94.4%;
Matches 34; Conservative
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(first entry)
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mapping, and selective breeding.
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The microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of the condition in increase the condition is a second or considered the determinism of the condition in the sequence with the sequence of the condition is a second or condition of the condition of the condition or conditions and the determinism of the condition of the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                      rable 7; Page 347; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ33900 standard; DNA; 37 BP
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Local Similarity 94.4%;
les 34; Conservative
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                                                                                          Маввеу
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                                                          (GENM-) GENMARK
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                             15-JAN-1991;
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                                                                                          Georges M,
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AAQ33900
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The sequence is that of a bovine microsatellite sequence obtd. by

creening a library of bovine MboI DNA fragments of between 250 and 500

creening a library of bovine MboI DNA fragments of between 250 and 500

creening a library of bovine MboI DNA fragments of between 250 and 500

creening cross-hybridised. Assuming independent distribution of

microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

creening genome is estimated at >100, 000. The sequence information

for ca. 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

creduired PCR primers for in vitro amplification of the corresp.

creduired PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite (using the program OPTIPRIM). The microsatellites may be

creduited trait loci, or genes involved the determinism of

conomically important traits esp. in cattle, to allow selective

breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37 BP; 0 A; 0 C; 18 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 36
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rable 7; Page 289; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hybridisation; chromosome; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-00222177.
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91US-00754351.
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Best Local Similarity 94.4%;
Matches 34; Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-042299/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-APR-1994;
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05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT65732/
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
conservation of a cross-hybridised. Assuming independent distribution of forces cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information of for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the capuired PCR primers for in vitro amplification of the corresp.

Incrosatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of connecting See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                  ö
repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AnfeS798-76647. Those clones where the repeat sequence has been determined are shown in AATG5704-797. This repeat sequence is from the marker clone Mdf30 which contains the repeat sequence is from the marker clone Mdf30 which contains the repeat sequence having the formula: (AC)18.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                          DB 1; Length 37;
                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                     Sequence 37 BP; 19 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                       2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                            37 rererererererererererererererere
                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microsatellite sequence from clone TGLA153.
                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                        Score 32.8;
Pred. No. 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Page 225; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ33737 standard; DNA; 39 BP.
                                                                                                                                                                                                                                                        0.98;
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                                                                                                                                                                                                                                                                                                Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ33737;
                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 75
AAQ33737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112 AAAA6519-A77429) are consecutive pairs of nucleotides which contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive pairs of nucleotides containing SNPs which result in changes in the corresponding amino acid sequences (AAB1749-B1828). The SNPs in sequences 1131 to 1128 (AAA77445) lead to conservative amino acid changes, while those in sequences 1129 to 1186 (AAA77446-A7503) result in non- conservative changes. The SNPs in sequences 1187 to 1192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human nucleic acids containing single nucleotide polymorphisms, useful for treating a subject suffering, or at risk from a pathology due to the presence of a sequence polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Human; single nucleotide polymorphism; SNP; chromosome 9; detection; identification; gene therapy; ss.
                                                                                         .;
0
                                              Query Match 0.9%; Score 32.8; DB 1; Length 39; Best Local Similarity 94.4%; Pred. No. 31; Matches 34; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                     Human clone cg44024536 polymorphic site, SEQ ID NO:1020.
                 Sequence 39 BP; 2 A; 0 C; 17 G; 20 T; 0 U; 0 Other;
                                                                                                                          2316 TCTGTGTGTGTGTGTGCGTGTGTGTGTGTGTG 2351
                                                                                                                                                   Location/Qualifiers
replace(26,G)
/*tag= a
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                                                                                                                                                                                                                                                          AAA77337 standard; cDNA; 44 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US027293.
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99US-00443199.
                                                                                                                                                                                                                                                                                                                                    16-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variation
                                                                                                                                                                                                                                                                                               AAA77337;
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vivlemore401-10.rng

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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                      Microsatellite sequence from clone TGLA126.
                                 AAQ33692 standard; DNA; 34 BP.
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                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                    (GENM-) GENMARK.
                                                                                                                                                                                                                                                                    15-JAN-1992;
                                                                                                                                                                                                                                                                                           15-JAN-1991;
                                                                                                                                                                                                                 WO9213102-A1
                                                                                      25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                          36-AUG-1992.
                                                                                                                                                                                        Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                            AAQ33692;
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          RESULT 82
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                        AAQ3369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n.(dg-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dA).(dg-dT) probe. Over 100 by primers AuT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf52 which contains the repeat sequence is from the marker clone Mdf52 which contains the repeat sequence is from the marker clone Mdf52 which contains the repeat sequence having the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       formula: (AC)18TTG(CA)3. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                   Gaps
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0
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                         DB 1; Length 44;
                                                                          2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACATCCG 2359
                                                   7; Indels
                                                                                          Repeat sequence from polymorphic marker clone Mfd52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45 BP; 21 A; 21 C; 1 G; 2 T; 0 U; 0 Other;
Sequence 44 BP; 1 A; 2 C; 21 G; 20 T; 0 U; 0 Other;
                         0.9%; Score 32.8; D
84.1%; Pred. No. 36;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 11-12; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            94US-00222177.
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91US-00754351.
                                                                                                                                                                     AAT65751 standard; DNA; 45
                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MARS-) MARSHFIELD CLINIC.
                                        Best Local Similarity 84.1
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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17-JUN-1997
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                            Query Match
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Matches
                                                                                                                                                           RESULT 81
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92WO-US000340.

(first entry)

(revised)

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The sequence is that of a bovine microsatellite sequence obtd. by

C screening a library of bovine MboI DNA fragments of between 250 and 500

C screening a library of bovine MboI DNA fragments of between 250 and 500

CC opposition and (TC)15 oligonuclocided probe. One out of 50

CC clones cross-hybridised. Assuming independent distribution of

CM in the bovine genome is estimated at >100, 000. The sequence information

CC in the bovine genome microsatellites is summarised in the

Specification and indexed herein (see below). The sequences upstream and

CM downstream of the microsatellite sequence where used to generate the

CC downstream of the microsatellite sequence where used to generate the

CC microsatellite (using the program OPTIPRIM). The microsatellites may be

CC microsatellity individuals, for parentage testing, and in the genetic

CC mapping of economic trait loci, or genes involved the determinism of

CC conformically important traits esp. in cattle, to allow selective

CC find (CC) in the CC) in cattle, to allow selective

CC find (CC) in the CC) in cattle, to allow correct PN

CC find (CC) in the CC) in cattle, to allow correct PN

CC find (CC) in the CC)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                      rable 7; Page 207; 517pp; English.
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ilarity 97.1%;
Conservative (
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(first entry)
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Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                                                                       Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32.4; DB 1; Length 34;
Pred. No. 29;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat sequence from polymorphic marker clone Mfd44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34 BP; 0 A; 0 C; 17 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2318 TGTGTGTGTGTGTGCGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                               Table 7; Page 279; 517pp; English.
                                                                                          91US-00642342.
                                 92WO-US000340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 0.9%;
1 Similarity 97.1%;
33; Conservative (
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                                                                                       15-JAN-1991;
                                 15-JAN-1992;
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mool DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50 clones cross-hybridised Assuming independent distribution of microsatellites and Mool sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellites sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage teeting, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene
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                                                         PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Microsatellite sequence from clone TGLA179.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Table 7; Page 240; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mapping, and selective breeding.
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                                                                                                                                                                                having the sequence (dd-dd)n. dd-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dd-dd). (dd-df) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdf44 which contains the repeat sequence is from the marker clone Mdf44 which contains the repeat sequence is from the marker clone Mdf44 which contains the repeat sequence is from formula: (CA)17. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microsatellite; ligase-assisted spacer addition assay; LASA; cancer; nucleotide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
                                                                                                                                                                      The invention relates to the isolation of polymorphic repeat sequences
                                                                        Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
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                                                                                                                                   Disclosure; Col 9-10; 186pp; English.
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ABK24297 standard; DNA; 34 BP.
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10-MAY-2000; 2000US-0202559P.
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       Weber JL;
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The invention relates to a method of identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a carticular length, comprising employing ligase-assisted spacer addition (LASA) assay. The method is useful in the identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a nucleotide repeat region in a nucleic acid molecule characterised by a condition of particular length. In particular, the method is useful for identification of a nucleotide length polymorphism in animals or humans, which is associated with a neurodegenerative disease including fragile X syndrome, thuntington's disease, or muscular dystrophy. Furthermore, the method may condition and multi-cellular organisms, Purthermore, the method may condition of human and non-human including humans. The method is also useful for detecting oertain cancers and other malignancies.

Condition of human and non-human individuals, plants and identification of human and non-human individuals, plants and identification of human and non-human individuals, plants and identification of human and non-human individuals, plants and complete responses to therapies including the possibility of mucleic acid damage. The nucleotide polymorphisms may be used in forensic condition mapping and population studies lash may also be used in the manufacture of a kit for detecting and/or identifying nucleotide repeat regions such as a nucleotide length polymorphism in a eukaryotic crame, in gene mapping and population studies lash may also be used in crepaat regions such as a nucleotide length polymorphism in a eukaryotic crame. The Lash method avoids the time and cost required by prior art crepaat regions con an alleged perpendent and lasmosis of Huntington's disease relies heaving content diagnosis of Huntington's disease relies heaving content allegenes and laboratory procedures. Askantendent and allows the prior art content diagnosis of maniature say proceded in the energy of miniaturise. The Lash method all
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AAQ68850;
                                                                                                                      field.)
                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ношо
                                                                                                                                                                                                                                                                          RESULT 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleoride probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
                                                                                                                markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dA). (dc-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has the marker clone Mdf47 which contains the repeat sequence is from the marker clone Mdf47 which contains the repeat sequence is from formula: (AC)17.5. (Updated on 25-MAR-2003 to correct PF field.)
                                 Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n - using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                            The invention relates to the isolation of polymorphic repeat seques having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                     Score 32.4; DB 1; Length 35; Pred. No. 30; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                Sequence 35 BP; 18 A; 17 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                      2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                            rererererererererererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microsatellite sequence from clone TGLA112.
                                                                    Disclosure; Col 9-10; 186pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33669 standard; DNA; 37 BP
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 97.1%;
Marches 33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
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         WPI; 1997-042299/04.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                            35
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ33669;
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 88
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in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traites esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     using in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast Artificial Chromosome; YAC; polymerase chain reaction; PCR; sequence tagged site; genetic disorder; diagnosis; abnormality; Prader-Willi; Angelman; Beckwith-Wiedermann; syndrome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                           Sequence 37 BP; 1 A; 1 C; 18 G; 17 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 32.4; 1
Pred. No. 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 8; Page 64; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human chromosomal repeat element
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                                                                                                                                                                                                                                                                                                                                                                                                              ch 0.9%;
1 Similarity 97.1%;
33; Conservative
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5...6
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2318 TGTGTGTGTGTGTGTGTG
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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28-OCT-1994
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RESULT 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n - using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                    Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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                                               Gaps
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                       Length 38;
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                                               Indels
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Seguence 38 BP; 19 A; 19 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                             Repeat sequence from polymorphic marker clone Mfd6.
                        DB 1;
                                                                        38 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5
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0; Mismatches
                                               0; Mismatches
                       Score 32.4; |
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Col 9-10; 186pp; English
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                     0.9%;
Local Similarity 97.1%;
les 33; Conservative
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                                                                                                                                                  708/c
AAT65708 standard; DNA; 38
                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                             (revised)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                             US5582979-A.
                                                                                                                                                                                                                                                                                                                                                                                     10-DEC-1996.
                                                                                                                                                                                                             25-MAR-2003
                                                                                                                                                                                                                        17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weber JL;
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                        Query Match
                                                Matches
                                                                                                                                    Matches
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Glones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf12 which contains the repeat sequence is from the marker clone Mdf12 which contains the repeat sequence is from formula: (AC)11AT(AC)8A. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                          PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                             Polymorphism; repeat sequence; genetic marker; primer; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                               Repeat sequence from polymorphic marker clone Mfd12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39 BP; 20 A; 18 C; 0 G; 1 T; 0 U; 0 Other;
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AAT65714 standard; DNA; 39 BP.
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Best Local Similarity 91.9%;
Matches 34; Conservative (
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(first entry)
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(first entry)
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05-SEP-1991;
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17-JUN-1997
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17-JUN-1997
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                                                             AAT65714;
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ID AAT657:
XX
AC AAT657:
XX
DT 25-MAR:
DT 17-JUN
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2315 Grergrergrergrererecergrergrergrerg 2351

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ઠ 셤 vivlemore401-10.rng

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of polymorphic genetic markers of the form (dC-dA) \, n \, (dG-dT) \, n using novel nucleic acid mols. as primers.
                                                                         Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymorase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
Repeat sequence from polymorphic marker clone Mfd34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat sequence from polymorphic marker clone Mfd42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 40 BP; 20 A; 19 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 erererererererererererererererere
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 9-10; 186pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-00341562.
91US-00754351.
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Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                        US5582979-A.
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weber JL;
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AAT65743 RESULT

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the phage libraries were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-737. This repeat sequence is from the marker clone Mdf42 which contains the repeat sequence is from the marker clone Mdf42 which contains the repeat sequence is from formula: (CA)16T(AC)3.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                  Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
Haliotis discus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32.2; DB 1; Length 40; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 40 BP; 20 A; 19 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                  Disclosure; Col 9-10; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. discus derived sequence #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                           94US-00222177.
                                                                                                          91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 91.9%; es 34; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-JP003551.
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                                                                                            89US-00341562
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                                                                                                                                          (MARS-) MARSHFIELD CLINIC.
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                                                                                                                                                                                                      WPI; 1997-042299/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200011156-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1999;
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                                                            04-APR-1994;
                                                                                             21-APR-1989;
                                                                                                            05-SEP-1991;
 US5582979-A.
                               10-DEC-1996.
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                                                                                                                                                                         Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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ZXCX#X##X#X#X#X#X#X#X#X
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Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.

Example 5; Page 14; 35pp; Japanese.

sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AAZ98483-514 represent sequences from Haliotis discus, used in the method The invention provides a novel method for isolation of satellite of the invention

Sequence 40 BP; 19 A; 19 C; 0 G; 2 T; 0 U; 0 Other;

ö Length 40; 3; Indels DB 1; Score 32.2; I Pred. No. 38; 0; Mismatches 0.8%; 34; Conservative Local Similarity Query Match Best Local S g

776/c AAT65776 standard; DNA; 42 BP. RESULT 95 AAT65776/c

AAT65776;

(first entry) (revised) 25-MAR-2003 17-JUN-1997

Repeat sequence from polymorphic marker clone Mfd105.

Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds

Homo sapiens

US5582979-A.

10-DEC-1996.

94US-00222177. 04-APR-1994;

89US-00341562 91US-00754351 21-APR-1989; 05-SEP-1991;

(MARS-) MARSHFIELD CLINIC.

Weber JL;

WPI; 1997-042299/04.

Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.

Claim 1; Col 13-14; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific

phage libraries with a synthetic poly(dc-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf105 which contains the repeat sequence having the formula: TCAAACACAA(AC)16. (Updated on 25-MAR-2003 to correct PF field.) 888888888

Sequence 42 BP; 22 A; 19 C; 0 G; 1 T; 0 U; 0 Other;

Gaps ö 42; 3; Indels DB 1; Length O.8%; Score 32.2; I ilarity 91.9%; Pred. No. 40; Conservative 0; Mismatches Local Similarity les 34; Conserv Query Match Best Loc Matches

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2315 GICTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351 42 grererererererererererererererererere 원 ઠે

ADH70603/c RESULT 96

BP ADH70603 standard; DNA; 44

ADH70603;

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Gaps

(first entry) 25-MAR-2004 Human Vbeta gene repeat sequence #393.

human; T-cell associated disease; Wheta; autoimmune disease;

Addison's disease; infectious disease; neoplastic disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity; deodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; parasitic infections disease; viral infection; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection, Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;

breast cancer; ds.

Homo sapiens,

US2002150891-A1.

17-OCT-2002.

99US-00263959. 05-MAR-1999;

95US-00531241. 94US-00309335 19-SEP-1994; 19-SEP-1995;

HOOD/) HOOD L E.

(ROWE/) ROWEN L.

Rowen L; Hood LE,

WPI; 2004-059052/06.

Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a *V*beta gene

Disclosure; SEQ ID NO 797; 164pp; English.

The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Vbeta gene, VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, graft versus host disease, hypersensitivity diseases, infectious diseases

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                             atrophic gastritis. Degenerative nervous system diseases include multiple sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type I hypersensitivities such as contact with allergens that lead to allergies, Type II hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infectious diseases include viral infections caused by viruses such as HIV, fungal infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by schicosomes, filaria and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
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   neoplastic diseases. Autoimmune diseases include Addison's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32.2; DB 1; Length 44;
Pred. No. 42;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat sequence from polymorphic marker clone Mfd36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 44 BP; 22 A; 21 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT65737 standard; DNA; 45 BP
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91US-00754351,
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il Similarity 91.9%;
34; Conservative
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(first entry)
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05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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AAT65737/O
AAT6573/O
AAT657
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
corrections and (TC)15 and and mboI sites, the frequency of (T6)n >9 microsatellites
and the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
downstream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
conomically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf36 which contains the repeat sequence having the formula: (AC)15AT(AC)6A. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                           Gaps
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                                                                                                          DB 1; Length 45;
                                                                                                                                                                              Sequence 33 BP; 0 A; 0 C; 16 G; 17 T; 0 U; 0 Other;
                                                                       Sequence 45 BP; 23 A; 21 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                               40 ererereraterererererererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of a microsatellite from clone TGLA54
                                                                                                                        43;
                                                                                                                                             0; Mismatches
                                                                                                        Score 32.2;
Pred. No. 43,
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                                                                                                      0.8%;
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Best Local Similarity 97.0%;
Marches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                        Best Local Similarity 91.9
Matches 34; Conservative
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02-FEB-1993
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                                                                                                          Query Match
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AAQ34097
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(revised)
(first entry)

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Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                              Repeat sequence from polymorphic marker clone Mfd58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 11-12; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                       (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPI; 1997-042299/04.
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05-SEP-1991;
                                                                                                                                                                                                            Homo sapiens.
            25-MAR-2003
17-JUN-1997
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CC cores a library of bovine MboI DNA fragments of between 250 and 500

CC copes across-Mybridised. Assuming independent distribution of

CC clones across-Mybridised. Assuming independent distribution of

CC clones across-Mybridised. Assuming independent distribution of

CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

CC for ca. 210 such bovine microsatellites is summarised in the

CC for ca. 210 such bovine microsatellite sequence were used to generate the

CC downstream of the microsatellite sequence were used to generate the

CC downstream of the microsatellite sequence was used to generate the

Microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite (using the program OPTIPRIM). The microsatellites may be

CC used to identify individuals, for parentage testing, and in the genetic

CC mapping of economic trait loci, or genes involved the determinism of

CC connomically important traits esp. in cattle, to allow selective

CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                  PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33 BP; 0 A; 0 C; 16 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                Microsatellite sequence from clone TGLA415.
        2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rable 7; Page 334; 517pp; English.
                                                                                                                                                AAQ34009 standard; DNA; 33 BP
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Best Local Similarity 97.0
Matches 32; Conservative
                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Georges M, Massey JM;
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02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus.
                                                                                                                                                                                          AAQ34009;
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89US-00341562. 91US-00754351. 94US-00222177.

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dd-dA)n. (dd-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dd-dA). (dg-dT) probe. Over 100 repeat blocks were isolated. Those clones where amplified by primers AAT65794-76647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf58 which contains the repeat sequence having the formula: (CA)16.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analyais; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1, Indels
                                                                                                                                                                                                                                                                                                                                                                Sequence 33 BP; 16 A; 17 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat sequence from polymorphic marker clone Mfd3.
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                                                                                                                                                                                                                                                                                                                                                                                                              0.8%; Scott No. 3., 97.0%; Pred. No. 3., ...
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Best Local Similarity 97.09
Matches 32, Conservative
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17-JUN-1997
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2318 rerererererererererererererer 2350 rererererererererererererererer

AAT65754 standard; DNA; 33 BP.

RESULT 100 AAT65754/

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AAT65754;

Weber JL;

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New transgenic mice having a genetically modified fibroblast growth factor receptor gene, useful as a model for human chondrodysplasia, e.g. achondroplasia characterized by shortening of the limbs, midface hypoplasia or large skull.
                                                                                                                                                                                                                                                                                                           The invention relates to an animal model for chondrodysplasia, more particularly, to a transgenic mouse model for achondroplasia. This transgenic mouse contains a fibroblast growth factor receptor 3 (FGFR3) gene including a G to A point mutation changing Gly to Arg in codon 380 in its genome. The transgenic mouse is useful as a model for FGFR-associated chondrodysplasia, particularly FGFR3 achondroplasia, e.g. shortening of the limbs, midface hypoplasia and large skull. This model may be exploited to gain better understanding of the disease and as an experimental model with which experimental therapy to chondrodysplasias can be exercised. The transgenic mouse is particularly useful as a tool for screening, developing and evaluating drugs with a potential of relieving or abolishing chondrodysplasia syndromes and/or symptoms. The present sequence is a PCR primer used to detect mouse FGFR3 allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic bovine DNA markers - used in genetic identification, gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33 BP; 8 A; 11 C; 11 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          818 CTCATCACTCTGCGTGGTGGTGCTGCCAG 850
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                                                                                                                                                                                                                                                                        Example, Col 14, 49pp; English,
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(PROC-) PROCHON BIOTECH LTD
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(first entry)
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                                                                                                              WPI; 2001-463946/50
                                                                   Segev O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ33921;
                                                                      Yayon A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdf3 which contains the repeat sequence is from formula: (CA)16C. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic
                                                                                                                                                                                                                                                                                                                                                                                                         Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
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91US-00754351.
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Local Similarity 97.0%;
nes 32; Conservative (
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                            Homo sapiens.
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Query Match

Best Loca Matches

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RESULT 102

Mus sp.

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Gaps

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The sequence is that of a bovine microsatellite sequence obtd. by

Screening a library of bovine Mool DNA fragments of between 250 and 500

Screening a library of bovine Mool DNA fragments of between 250 and 500

CC clones cross-hybridised. Assuming independent distribution of

CC clones cross-hybridised. Assuming independent distribution of

CC clones across-hybridised. Assuming independent distribution of

CC clones genome is estimated at >100, 000. The sequence information

CC cr ca. 230 such bovine microsatellites is summarised in the

Specification and indexed herein (see below). The sequences upstream and

CC composite of the microsatellite sequence waset to generate the

CC downstream of the microsatellite sequence waset to generate the

CC microsatellite (using the program OPTIPRIM). The microsatellites may be

MICROSATELITY individuals, for parentage testing, and in the genetic

CC mapping of economic trait loci, or genes involved the determinism of

CC conformation trait sep. in cattle, to allow selective

CC preding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct. PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               field.)
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Gaps ö ch 0.8%; Score 31.4; DB 1; Length 34; 1 Similarity 97.0%; Pred. No. 38; 32; Conservative 0; Mismatches 1; Indels Sequence 34 BP; 0 A; 0 C; 17 G; 17 T; 0 U; 0 Other; 2319 GIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIG 2351 Local Similarity Query Match Matches

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Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; Repeat sequence from polymorphic marker clone Mfd20. ВР AAT65722 standard; DNA; 34 (revised)
(first entry) 25-MAR-2003 17-JUN-1997 AAT65722; RESULT 104 AAT65722, 용

hybridisation; chromosome; ds 94US-00222177. Homo sapiens 04-APR-1994; US5582979-A. 10-DEC-1996.

89US-00341562. 91US-00754351. (MARS-) MARSHFIELD CLINIC. 21-APR-1989; 05-SEP-1991;

Weber JL;

WPI; 1997-042299/04.

Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.

Disclosure; Col 9-10; 186pp; English

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the

Sequence 34 BP; 17 A; 17 C; 0 G; 0 T; 0 U; 0 Other;

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of genetic disease, commercial regeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. Those close where the repeat sequence has by primers AAT65798-76647. Those close where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker close Mdf48 which contains the repeat sequence is from formula: (AC)17. (Updated on 25-MAR-2003 to correct PF field.)
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repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAF5798-R66047. Those clones where the repeat sequence has been determined are shown in AAF65704-797. This repeat sequence is from the marker clone Mdf20 which contains the repeat sequence is from formula: (AC)17. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                         Score 31.4; DB 1; Length 34;
Pred. No. 38;
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat sequence from polymorphic marker clone Mfd48.
                                                                                                                                             Sequence 34 BP; 17 A; 17 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       GTGTGTGTGTGTGCGTGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 11-12; 186pp; English.
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                                                                                                                                                                                  0.8%;
Local Similarity 97.0%;
hes 32; Conservative
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AAT65748 standard; DNA; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-1989;
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17-JUN-1997
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                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                  RESULT 105
                                                                                                                                                                                                                             Matches
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Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.

Homo sapiens

US5582979-A.

10-DEC-1996

94US-00222177. 89US-00341562. 91US-00754351.

04-APR-1994; 21-APR-1989; 05-SEP-1991; (MARS-) MARSHFIELD CLINIC.

WPI; 1997-042299/04.

Weber JL;

Repeat sequence from polymorphic marker clone Mfd101.

(first entry)

(revised)

25-MAR-2003 17-JUN-1997

AAT65772;

BP.

AAT65772 standard; DNA; 34

vivlemore401-10.rng

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AAT65772/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf14 which contains the repeat sequence is from formula: (AC)17. (Updated on 25-MAR-2003 to correct PP field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphism; repeat sequence; genetic marker; primer; amplification;
                                                    Gaps
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     Length 34;
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                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat sequence from polymorphic marker clone Mfd41.
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  DB 1;
                                                                                                 rGTGTGTGTGTG 2351
                                                                                                                                                 34 Grererererererererererererere
1) Score 31.4; Diarity 97.0%; Pred. No. 38; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hybridisation; chromosome; ds.
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                                                                                                 2319 GTGTGTGTGTGTGTGCGTG
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                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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17-JUN-1997
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                                                  32;
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     Query Match
                           Best Loca
Matches
                                                                                                                                                                                                                    RESULT 106
                                                                                                                                                                                                                                           AAT65742/AAT65742/AAT65742/AAT65742/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/AAT65/
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Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.

Claim 1; Col 13-14; 186pp; English

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                                                                                  repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly (dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdf101 which contains the repeat sequence is from the marker clone Mdf101 which contains the repeat sequence having the formula: (AC)17. (Updated on 25-MAR-2003 to correct PF field.)
The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31.4; DB 1; Length 34;
Pred. No. 38;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34 BP; 17 A; 17 C; 0 G; 0 T; 0 U; 0 Other;
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nes 32; Conservative
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(first entry)
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Gaps

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1; Indels

0; Mismatches

32; Conservative

Best Local Similarity

Matches

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Query Match

2319 GTGTGTGTGTGTGCGTGTGTGTGTGTGTG 2351

34 GTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2

RESULT 107

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                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly (dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. Those close where the amplified by primers AAT65798-T6647. Those close where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf117 which contains the repeat sequence is from the marker clone Adf117 which contains the repeat sequence having the formula: GCAGCAACAT(AC)16.5. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps .
                                                                                                                                                                                                                                                                                                                                                           Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.8%; Score 31.4; DB 1; Length 43; Best Local Similarity 97.0%; Pred. No. 51; Matches 32; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of a microsatellite from clone TGLA6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Col 13-14; 186pp; English.
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                                                          hybridisation; chromosome; ds
                                                                                                                                                                                      94US-00222177.
                                                                                                                                                                                                                     89US-00341562.
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(first entry)
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02-FEB-1993
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05-SEP-1991;
                                                                                            Homo sapiens
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The sequence is that of a bovine microsatellite sequence obtd. by
conservating a library of bovine MboI DNA fragments of between 250 and 500
conservation of TCD15 oligonucleotide probe. One out of 50
conservation are acrosa-Pybridised. Assuming independent distribution of
conservation are setimated at >100, 000. The sequence information
in the bovine genome is estimated at >100, 000. The sequence information
constraint of the microsatellite sequence where used to generate the
conservation and indexed herein (see below). The sequences upstream and
specification and indexed herein (see below). The sequences upstream and
constream of the microsatellite sequence where used to generate the
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellity individuals. for parentage testing, and in the generic
cused to identify individuals. for parentage testing, and in the generic
cused to identify individuals. for parentage testing, and in the generic
cusping of economic trait loci, or genes involved the determinism of
connected program of AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
prediator.
                                                                                                                                               - used in genetic identification, gene
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/standard name= "single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2330 TGTGCGTGTGTGTGTGTGCACATCCGCGTGTGCCTGTGTG 2373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31.2; 1
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                      Table 7; Page 372; 517pp; English.
                                                                                                                                                     Polymorphic bovine DNA markers - mapping, and selective breeding.
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22-MAY-2000; 2000US-0206129P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%;
ilarity 81.8%;
Conservative
92WO-US000340.
                          91US-00642342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                            Massey JM;
                                                                                                                         WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity
36; Conserv
                                                              (GENM-) GENMARK.
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15-JAN-1992;
                               15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Variation
                                                                                              Georges M,
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Matches
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ID AAI3
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Lander

Ireland JS,

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Human, resequence, genotype, disease, forensic, paternity testing, single nucleotide polymorphism, SNP, ss.
                                                                                                                                                                                                                                                                                                                Human single nucleotide polymorphism (SNP) FGFR3 2.
                                                                                                                                                                   Sequence 31 BP; 9 A; 10 C; 6 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                 1928 ACTGCACACACCACCTGTACATGATCATGCG 1958
                                                                                                                                                                                                                         ACTGCACACACGACCTGTACATGATCATGCG 31
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                                                                         Claim 1; Page 87; 145pp; English.
                                                                                                                                                                                                                                                                     AAI30470 standard; DNA; 31 BP
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22-MAY-2000; 2000US-0206129P
                                                                                                                                                                                                 31; Conservative
                                                           particular genotype.
                                                                                                                                                                                          Best Local Similarity
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                     WPI; 2001-522952/57
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Variation
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                                                                                                                                                                                   Query Match
      Cargill
                                                                                                                                                     testing
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(first entry)

Location/Qualifiers

replace (16,G)

DB 1; Length 31; 38;

Indels

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0.8%; Scor. 100.0%; Pred. No. J., ... 0; Mismatches

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The invention relates to the identification of nucleic acid molecules (AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or discorder (e.g. diabetes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity
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                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/standard name= "single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                      DB 1; Length 31;
38;
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                                                                                                                                                                                                                                                                         Sequence 31 BP; 3 A; 13 C; 12 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Accedecearcerecaeceeecreceec 31
                                                                                                                                                                                                                                                                                                                    Query Match 0.8%; Score 31; DB Best Local Similarity 100.0%; Pred. No. 38; Matches 31; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 87; 145pp; English.
Claim 1; Page 87; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP,
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22-MAY-2000; 2000US-0206129P
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Variation
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single
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                                                                                                                                                                                                                                                                                              (AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype.
                                                                                                                                    sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a
                                                                                                            molecules from the human genome which include polymorphic
                                                                                                                                                                                                                                                                           invention relates to the identification of nucleic acid molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Addison's disease, atrophic gastrifits, degenerative nervous system disease; multiple sclerosis, degenerative nervous system disease; multiple sclerosis hypersensitivity doodpasture's syndrome; type II hypersensitivity, Goodpasture's syndrome; type II hypersensitivity, infections disease, viral infection; HIV; fungal infection, Candida; parasitic infection; schistosome; filaria, bacterial infection, Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     human; T-cell associated disease; Vbeta; autoimmune disease;
degenerative nervous system disease; graft versus host disease;
hypersensitivity disease; infectious disease; neoplastic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allergies, Type II hypersensitivities such as those present in
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                                                                         0.8%; Score 31; DB 1; Length 31;
100.0%; Pred. No. 38;
iive 0; Mismatches 0; Indels
                                       Sequence 31 BP; 3 A; 11 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                       1407 CTGCACGCAGGCGGCCCCTGTACGTGCTG 1437
                                                                                                                                                                               Disclosure; SEQ ID NO 711; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       Human Vbeta gene repeat sequence #307.
                                                                                                                                                                                                                                                                                            BP.
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                                                                                                   Local Similarity 100.
nes 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HOOD/) HOOD L E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROWEN L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            breast cancer;
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19-SEP-1995;
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                                                                                     Query Match
           testing
                                                                                                                                                                                                                                                          RESULT 113
                                                                                                                         Matches
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The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine MboI DNA fragments of between 250 and 500

conserved and (TC)15 oligomucleotide probe. One out of 50

conserved arcosa-hybridised. Assuming independent distribution of

microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

in the bovine genome is estimated at >100, 000. The sequence information

for ca. 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

specification and indexed herein (see below). The sequences upstream and

compensate of the microsatellite sequence ware used to generate the

downstream of the microsatellite sequence ware used to generate the

required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite trait loci, for parentage testing, and in the genetic

cused to identify individuals, for parentage testing, and in the genetic

connomically important traits esp.; in cattle, to allow selective

connomically important traits esp.; in cattle, to allow selective
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Goodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infectious diseases include viral infections caused by viruses such as HIV, fungal infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%; Score 30.8; DB 1; Length 34;
14.1%; Pred. No. 45;
ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                         Sequence 34 BP; 0 A; 1 C; 17 G; 16 T; 0 U; 0 Other;
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(first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Sequence 35 BP; 1 A; 0 C; 17 G; 17 T; 0 U; 0 Other;

Matches

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
c in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
c specification and indexed herein (see below). The sequences upstream and
c comparteem of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
c microsatellite (using the program OPITPRIM). The microsatellites may be
c microsatellite (using the program OPITPRIM). The microsatellites may be
compared to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
c economically important traits esp. in cattle, to allow selective
preeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                            PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30.4; DB 1; Length 32;
Pred. No. 47;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32 BP; 0 A; 0 C; 16 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence of a microsatellite from clone TGLA67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grendrengrenererererererer 32
                                                                                                                                                                        Microsatellite sequence from clone TGLA111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Table 7; Page 196; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВР.
                    AAQ33666 standard; DNA; 32 BP
                                                                                                                                                                                                                                                                                                                                                                                                                  92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 0.8%;
il Similarity 96.9%;
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ34119 standard; DNA; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENM-) GENMARK,
                                                                                                                                                                                                                                                                                                                              WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-1992;
                                                                                                        25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                         06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-1993
                                                                                                                                                                                                                                                                                     Bos taurus.
                                                               AAQ33666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ34119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ34119
                                           8X4X24X8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdf108 which contains the repeat sequence laring the formula: GTGGTAAAT(AC)16. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 42;
Length 35;
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2319 GTGTGTGTGTGTGCGTGTGTGTGTGTGTGTGCACATCCGC 2360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grererererererererererererererererarraseceae 1
                                                                                                                                                                                                                                                                                                                                                                                         Repeat sequence from polymorphic marker clone Mfd108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42 BP; 19 A; 17 C; 3 G; 3 T; 0 U; 0 Other;
                                        2,
DB 1;
                                                                                                        2 IGTGTGTGTGTGTGTGTGTGTATGTGTGTGTG
Score 30.8; D
Pred. No. 47;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 58;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Col 13-14; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-00222177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89US-00341562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-00754351
Match 0.8%;
Local Similarity 94.1%;
es 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.3%;
                                                                                                                                                                                                                        3779/c
AAT65779 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-1989;
05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                            25-MAR-2003
17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5582979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weber JL;
                                                                                                                                                                                                                                                                                   AAT65779;
Query Match
Best Local $
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Gape

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8

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Table 7; Page 378; 517pp; English.
                                                                                                                                                                                                       AAT65790 standard; DNA; 32
                                                         Georges M, Massey JM;
                                                                 WPI; 1992-284684/34.
                                                                                                                                                               Query Match
Best Local Similarity
                                                  (GENM-) GENMARK
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                  US5582979-A.
                                                                                                                                                                                                                      25-MAR-2003
17-JUN-1997
                                           15-JAN-1991;
                                   15-JAN-1992;
                     WO9213102-A1
                             36-AUG-1992
             Bos taurus.
                                                                                                                                                                                                               AAT65790;
                                                                                                                                                                                                 RESULT 118
                                                                                                                                                                       Matches
                                                                                                                                                                                                    AAT65790/
                                                                                                                                                                                                            셤
                                                                                                                                                                               ð
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n. (dd-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the arguences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly (dc-dA). (dg-dT) probe. Over 100 phage libraries with a synthetic poly (dc-dA). (dg-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf119 which contains the repeat sequence is from the marker clone Mdf119 which contains the repeat sequence is from formula: (AC)16. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                            Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30.4; DB 1; Length 32; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat sequence from polymorphic marker clone Mfd55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32 BP; 16 A; 16 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2319 GIGIGIGIGIGIGIGIGIGIGIGIGIGIGI 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Col 13-14; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT65752 standard; DNA; 32 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hybridisation; chromosome; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89US-00341562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00222177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%;
nilarity 96.9%;
Conservative 0
                                         94US-00222177.
                                                                               89US-00341562.
91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                               (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                   WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                           04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5582979-A
                                                                                    21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-1997
                                                                                                             05-SEP-1991;
10-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT65752;
                                                                                                                                                                                             Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine Mbol DNA fragments of between 250 and 500

co by with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50

co clones cross-Pybridised. Assuming independent distribution of

co clones cross-Pybridised.

co clones cross-Pybridised.

co microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites

co consumer of the microsatellites is summarised in the

coperation and indexed herein (see below). The sequences upstream and

specification and indexed herein (see below). The sequences upstream and

coperation of the microsatellite sequence where used to generate the

comparing PCR primers for in vitro amplification of the corresp.

concert to identify individuals, for parentage testing, and in the genetic

cused to identify individuals, for parentage testing, and in the genetic

concomically important traits esp. in cattle, to allow selective

concomically important traits esp. in cattle, to allow selective

concomically important traits esp. in cattle, to allow selective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                             PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 0.8%; Score 30.4; DB 1; Length 32; al Similarity 96.9%; Pred. No. 47; 31; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat sequence from polymorphic marker clone Mfd119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32 BP; 0 A; 1 C; 16 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                   92WO-US000340.
                                                                                                                                                                                                                                                                               91US-00642342
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(first entry)
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(MARS-) MARSHFIELD CLINIC.

Weber JL;

05-SEP-1991;

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Gaps

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Human alpha-7 neuronal nicotinic acetylcholine receptor and related
                                                       Disclosure; Col 11-12; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                Angelman's syndrome; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 63; 104pp; English
                                                                                                                                                                                                                                                                                                                                   AAX56155 standard; DNA; 32 BP
                                                                                                                                                                                                                                               31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leonard S, Freedman
         WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-288306/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FREE/) FREEDMAN R.
                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LEON/) LEONARD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymucleotides.
                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9920757-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-APR-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                    32
                                                                                                                                                                                                                                                                                                                                                      AAX56155;
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                               RESULT 12
AAX56155/
AAX56155/
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AAX5
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AAX5
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AAX5
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AAX5
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Human
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encoding at least a portion of the human alpha-7 neuronal nicotinic acetylcholine receptor (alpha-hnAchR). Also described are: (1) a peptide encoded by (1); (2) a vector comprising (1); (3) a host cell transformed with a vector of (2); (4) a polynucleotide comprising at least 15 nucleotides which hybridises under stringent conditions to at least a coption of (1); (5) a method for detection of a polynucleotide encoding alpha 7-hnAchR in a biological sample; and (6) a method for amplification of uncleic acid from a sample suspected of containing nucleic acid nucleic acid from a sample suspected of containing nucleic acid invention can be used on brain tissue and blood samples of humans cuspected of suffering from schizophrenia, small cell lung carcinoma, breast cancer and nicotine-dependent illness. This is particularly useful cordined/diagnosed are epilepsy (e.g. juvenile myoclonic epilepsy) and prader-Willi and Angelman's syndromes The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AAZ98483-514 represent sequences from Haliotis discus, used in the method Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation. sequence; DNA fragmentation; microsatellite DNA; DNA marker; DB 1; Length 32; Indels Sequence 32 BP; 16 A; 16 C; 0 G; 0 T; 0 U; 0 Other; 1; Score 30.4; DB Pred. No. 47; 0; Mismatches (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES 32 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT Example 5; Page 14; 35pp; Japanese. H. discus derived sequence #5. ВР 99WO-JP003551 0.8%; 98JP-00232153 AAZ98487 standard; DNA; 32 (first entry) Matches 31; Conservative rakahashi H, Sekino M; WPI; 2000-224692/19. Haliotis discus; ss Query Match Best Local Similarity Haliotis discus WO200011156-A1 01-JUL-1999; L8-AUG-1998; 19-JUN-2000 02-MAR-2000. Satellite AAZ98487; RESULT 121 AAZ98487, 8\$8888888888888888 음 ઠ ö having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AARS798-T6647. Those clones where the repeat sequence has been determined are shown in AAAS5704-797. This repeat sequence has been determined are shown in AAAS5704-797. This repeat sequence is from the marker clone Mdf55 which contains the repeat sequence is from the marker clone Mdf55 which contains the repeat sequence having the formula: (AC)16. (Updated on 25-MAR-2003 to correct PF field.) Detection of polymorphic genetic markers of the form $(dC-dA)\,n(dG-dT)\,n$ using novel nucleic acid mols. as primers. sednences Human; alpha-7 nicotinic receptor; neuronal; hybridisation; probe; alpha-7 neuronal nicotinic acetylcholine receptor; schizophrenia; small cell lung carcinoma; breast cancer; nicotine-dependent illness; epilepsy; juvenile myoclonic epilepsy; Prader-Willi syndrome; Gaps ö repeat 0.8%; Score 30.4; DB 1; Length 32; 96.9%; Pred. No. 47; The invention relates to the isolation of polymorphic reper having the sequence (dC-dA)n.(dG-dT)n which can be used as Indels Human alpha-7 nicotinic receptor probe SEQ ID NO:10. Sequence 32 BP; 16 A; 16 C; 0 G; 0 T; 0 U; 0 Other; 2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350 0; Mismatches Grerererererererererererererer 98WO-US021762 97US-00956518 (first entry)

Sequence 32 BP; 16 A; 16 C; 0 G; 0 T; 0 U; 0 Other;

The present invention describes an isolated nucleotide sequence (I)

the invention

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Gaps

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The invention relates to a method of identifying or detecting a nucleotide repeat region in a nucleic acid molecule characterised by a nucleotide repeat region in a nucleic acid molecule characterised by a comprising employing ligase-assisted spacer addition particular length, comprising employing ligase-assisted spacer addition completed and a nucleic acid molecule characterised by a nucleotide repeat region in a nucleic acid molecule characterised by a conclectide length. In particular, the method is useful for identification of associated with a neurodegenerative disease including fragile X syndrome, associated with a neurodegenerative disease including fragile X syndrome, concept and and/or typing microcrganisms including yeasts and lower uni- and multi-cellular organisms, as well as prokaryotic concept in a slow useful for detecting certain cancers and other malignancies. Moreover, the method can be used to provide markers for use in moreover, the method can be used to provide markers for use in dentification of human and non-human individuals, plants and including the possibility of and to monitor responses to therapies including the possibility of and to monitor responses to therapies including the possibility of and to monitor responses to therapies including the possibility of and crime, in gene mapping and population studies. LASA may also be used in crime, in gene mapping and population studies. LASA may also be used in crime, in gene mapping and population studies. LASA may also be used in crepeat regions such as a nucleotide length polymorphism in a eukaryotic geneat regions such as a nucleotide length polymorphism in a eukaryotic geneat regions such as a nucleotide length polymorphism in a eukaryotic geneat regions such as a nucleotide length polymorphism in a eukaryotic methods using gel electrophoresis and southern transfer analysis. In
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a nucleotide repeat region in a nucleic acid having a particular length, useful for identifying nucleotide length polymorphism associated with a neurodegenerative disease, comprises using a ligaseassisted spacer addition assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microsatellite, ligase-assisted spacer addition assay; LASA; cancer; nuclocide length polymorphism detection; neurodegenerative disease; fragile X syndrome; Huntington's disease; muscular dystrophy; forensic; gene mapping; population study; human; primer; ss.
                                                                 Gaps
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Length 32;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human microsatellite D1S191 detection PCR primer #4.
   DB 1;
                                                                                                                                           2318 TGTGTGTGTGTGTGTGTGTGTGTGTG 2349
                                                                                                                                                                                                                 32 rerererererererererererererer
                                  Pred. No. 47;
       Score 30.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 10; Page 55; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wolter L,
                                                                                                                                                                                                                                                                                                                                                                                                              BP.
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10-MAY-2000; 2000US-0202559P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2001; 2001WO-AU000526.
0.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                             31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brockhurst V, Timms P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-121948/16.
       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK24296;
                                                                                                                                                                                                                                                                                                                                                    RESULT 122
                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                               ABK24296/
XXX ABK2
XXX ABK2
XXX ABK2
XXX ABK2
XXX ABK2
XXX ABK2
XXX ABK3
XXX ABX3
XX
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dd-dA)n. (dd-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Glones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dd-dA). (dg-dT) probe. Over 100 phage libraries with a synthetic poly(dd-dA). (dg-dT) probe. Over 100 repeat blocks were isolated The inserts from the clones were amplified by primers AnfeSy94-r6647. Those clones where the repeat sequence has been determined are shown in AAA65704-797. This repeat sequence is from the marker clone Mdf107 which contains the repeat sequence is from formula: TGCCCGGCCT(AC)16. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                         ö
                    the use of gel electrophoresis, a process that has proved difficult to automate or miniaturise. The LASA method allows total avoidance of this limiting step, making it a strong candidate for future use in clinical and laboratory procedures. ABK24276-ABK24313 represent primers used to detect polymorphisms or microsatellites as described in the method of the
current diagnosis of Huntington's disease relies heavily upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mole. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                     Score 30.4; DB 1; Length 32; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd107.
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                                                                                                                                                                                                                                                               Sequence 32 BP; 16 A; 16 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 rererererererererererere 1
                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hybridisation; chromosome; ds.
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91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT65778 standard; DNA; 42 BP.
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                                                                                                                                                                                                                                                                                                                                      Match 0.8%;
Local Similarity 96.9%;
es 31; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2318
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                                                                                                                                                                                                                         invention
                                                                                                                                                                                                                                                                                                                                                    Query Match
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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

92WO-US000340. 91US-00642342.

WO9213102-A1.

30s taurus.

06-AUG-1992.

Georges M, Massey JM; WPI; 1992-284684/34.

GENM-) GENMARK

15-JAN-1991; 15-JAN-1992;

Microsatellite sequence from clone TGLA122.

(first entry) (revised)

25-MAR-2003 02-FEB-1993

AAQ33681;

BP.

AAQ33681 standard; DNA; 41

AAQ33681 ID AAQ3

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AF)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites and mboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is unmmarised in the specification and indexed herein (see below). The sequences upstream and commitream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The sequired PCR primers for in vitro amplification of the corresp.

The increase of the microsatellite sequence were used to generate the microsatellite (using the program OPTTPRIM). The microsatellites may be microsatellite in vitro ampling of economic trait loci, or genes involved the determinism of economically important trait loci, or genes involved the determinism of preeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
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0
           Length 42;
                                             Indels
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                                             1;
           DB 1;
                                                                                2350
                                                                                                                42 érérérérérérérérérérérérérérérer 11
         ; Score 30.4; DE
; Pred. No. 65;
0; Mismatches
                                                                                                                                                                                                                                                                                                                              Microsatellite sequence from clone TGLA309.
                                                                                                                                                                                                                                                                                                                                                                                   genetic mapping; traits; amplification; ss
                                                                             2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rable 7; Page 287; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mapping, and selective breeding.
                                                                                                                                                                                                      AAQ33894 standard; DNA; 38 BP.
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Query Match
Best Local Similarity 96.9%;
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                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georges M, Маввеу JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus
                                                                                                                                                                                                                                         AAQ33894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Field.)
                                                                                                                                                                     RESULT 124
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- used in genetic identification, gene

rable 7; Page 202; 517pp; English. Polymorphic bovine DNA markers - mapping, and selective breeding.

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 between 250 and 500 with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and mbol sites, the frequency of (T6)n >9 microsatellites is estimated at >100,000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and chowing the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 0.8%; Score 29.6; Di
Best Local Similarity 88.9%; Pred. No. 79;
Matches 32; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsatellite sequence from clone TGLA436.
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Pred. No. 79;
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(first entry)
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02-FEB-1993
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0; Gaps

2; Indels

2319 GTGTGTGTGTGTGCGTGTGTGTGTGTGTG 2351

RESULT 125

0.8%; Score 29.8; DB 1; Length 38; 93.9%; Pred. No. 68;

Pred. No. 68; 0; Mismatches

31; Conservative

Matches

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Local Similarity

Query Match

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15-JAN-1991;
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02-FEB-1993
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 128
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screening a library of bovine MDOI DNA fragments of between 250 and 500
screening a library of bovine MDOI DNA fragments of between 250 and 500
clones cross-hybridised. Assuming independent distribution of
microsatellites and MDOI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
downstream of the microsatellite sequence water used to generate the
committed PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits egp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Best Local Similarity 96.8<sup>3</sup>
Matches 30; Conservative
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                                                                                                                                                                           Georges M, Massey JM;
                                                                                                                                                                                                WPI; 1992-284684/34.
                                                                                                                                                    (GENM-) GENMARK.
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02-FEB-1993
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                                         Bos taurus
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
corpus cross-hybridised. Assuming independent distribution of
conse cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
for ca. 330 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
specification and indexed herein (see below). The sequences upstream and
committee PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
concomically important traits esp. for parentage testing, and in the genetic
economically important traits esp. in cattle, to allow selective
first. Preeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                         rable 7; Page 276; 517pp; English
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91US-00642342.
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                                                                                                                                   Georges M, Massey JM;
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hes 30; Conservative
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Screening a library of bovine Mbol DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comnstream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
considered to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breading. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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Pred. No. 59;
0; Mismatches 1; Indels
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                                                                                            Table 7; Page 343; 517pp; English.
and selective breeding.
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(first entry)
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02-FEB-1993
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    mapping,
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for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective by receding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.8%; Score 29.4; DB 1; Length 31; 96.8%; Pred. No. 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31 BP; 0 A; 0 C; 15 G; 16 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 31
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AAT65759 standard; DNA; 31
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05-SEP-1991;
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                                                                                                                                                                                                           Homo sapiens
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17-JUN-1997
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                                                        AAT65759;
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          RESULT 132
                       AAT65759/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                       Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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                        DB 1; Length 31;
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                                                                                                                                                                                                                                                Repeat sequence from polymorphic marker clone Mfd79.
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Sequence 31 BP; 0 A; 0 C; 15 G; 16 T; 0 U; 0 Other;
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91US-00754351
                          0.8%;
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                                                                                                                                                                                                                             (first entry)
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Best Local Similarity 96.8
Matches 30; Conservative
                                      Local Similarity 96.8
les 30, Conservative
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05-SEP-1991;
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17-JUN-1997
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                                                    Matches
                                                                                                                                        RESULT 131
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                                                                                                                                                                                                                                                                                                                                          Polymorphism, repeat sequence; genetic marker; primer, amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
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0.8%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 59;
Matches 30; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                Repeat sequence from polymorphic marker clone Mfd64.
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1D AAT65753 standard; DNA; 31 BP.

XX AC AAT65753;

XX DT 25-MAR-2003 (revised)

DT 17-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hybridisation; chromosome; ds.
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91US-00754351.
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                                                                                                                                                         (revised)
(first entry)
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(AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity
                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the identification of nucleic acid molecules
/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat sequence from polymorphic marker clone Mfd111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31 BP; 7 A; 6 C; 15 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        642 GCACGTGGAGGTGAATGGCAGCAAGGTGGGC 672
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06.8%; Pred. No. 59;
                                                                                                                                                                                                             (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                      Lander ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 87; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89US-00341562.
91US-00754351.
                                                                                                                07-MAR-2001; 2001WO-US007268
                                                                                                                                                    07-MAR-2000; 2000US-0187510P
22-MAY-2000; 2000US-0206129P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 96.8
les 30; Conservative
                                                                                                                                                                                                                                                    Cargill M, Ireland JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                         WPI; 2001-522952/57.
                                    WO200166800-A2
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05-SEP-1991;
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                                                                         13-SEP-2001.
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence is from the marker clone Mdf57 which contains the repeat sequence is from the marker clone Mdf57 which contains the repeat sequence is from
                                                    Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; resequence, genotype, disease, forensic; paternity testing; single nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          formula: (CA)15.5. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 29.4; DB 1; Length 31;
16.8%; Pred. No. 59;
ve 0; Mismatches 1; Indels
                Repeat sequence from polymorphic marker clone Mfd57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31 BP; 15 A; 16 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Col 11-12; 186pp; English
                                                                                                                                                                                                                                                                                                             89US-00341562.
91US-00754351.
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                                                                                                                                                                                                                                                                                                                                                                      (MARS-) MARSHFIELD CLINIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-042299/04.
                                                                                                                                                      Homo sapiens
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Variation
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Matches

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Gaps

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DB 1; Length 31; Indels

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Detection of polymorphic genetic markers of the form (dC-dA) \, n \, (dG-dT) \, n using novel nucleic acid mols. as primers.
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                                                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd112.
                                                                                                                                                                                                                                                                                 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                  41 rererererererererererererer 11
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91US-00754351.
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                                                                                                                                                                                                                                           Query Match
Best Local Similarity 96.8'
Matches 30; Conservative
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                         WPI; 1997-042299/04
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17-JUN-1997
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         Weber JL;
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                                                                                                                                                                                                                                                                                                                               RESULT 136
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0; Mismatches

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repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dc-dA). (dg-dT) probe. Over 100 repeat blocks were isolated The inserts from the clones were amplified ben primare Anfe7579-f6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf112 which contains the repeat sequence is from the marker clone Mdf112 which contains the repeat sequence having the
                   The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n.(dg-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41 BP; 18 A; 18 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             field.)
X88888888888888888888888
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                                                                                                                                                                                                                                                                                                                                                             The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Parlmers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-76647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf111 which contains the repeat sequence is from the marker clone Mdf111 which contains the repeat sequence laying the formula: TGAGACCCTG(AC)15.5. (Updated on 25-MAR-2001 to correct PF
                                                                                                                                                                                Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 41;
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Pred. No. 83
                                                                                                                                                                                                                                                                                                      Claim 1; Col 13-14; 186pp; English.
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Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.
                                                                                                                                                                                                                                                Human; drug metabolising enzyme; gene; drug metabolism; chromosome 17; polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                                                                                                /standard_name= "Single nucleotide polymorphism (SNP)"
                           Gaps
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 DB 1; Length 41;
                                                                                                                                                                                                                         Human N-methyltransferase PEMT gene polymorphic site, #117.
                         1; Indels
                                                     2318 TGTGTGTGTGTGTGTGTGTGTGTGTGT 2348
Score 29.4; DB
Pred. No. 83;
0; Mismatches
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                                                                                                                                              ABZ43333 standard; DNA; 41 BP.
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02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
                                                                                                                                                                                                                                                                                                                                                         replace (21,G)
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/ Match 0.8%;
Local Similarity 96.8%;
nes 30; Conservative
                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-583571/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RIKE ) RIKEN KK.
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                                                                                                                                                                                                                                                                                                                                                          variation
                                                                                                                                                                         ABZ43333;
    Query Match
                                                                                                                     RESULT 137
                 Best Loc
Matches
                                                                                                                                   ABZ43333
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                                                                                                                                                  Gaps
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                                                                                                                                                1; Indels
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Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes

Claim 23; Page 65; 2785pp; English.

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to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The come polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from AB24317-AB250887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations the above respects as they are stable in populations, occur in the above respects as they are stable in populations, occur in the above respects as they are stable in populations, occur in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genesic profile of individual patient.

This would not only take the guessork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also greates. For example, individuals could be selected for clinical trials only if their genetic profiles individuals and compositions of the invention may therefore lead to an increase in the range of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug fleeting the inventions, failed drug trials, the time time the or a drug to be approved to take before finding an effectione a driffer
encoding enzymes associated with drug metabolism. The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; drug metabolising enzyme; gene; drug metabolism; chromosome 17; polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
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/standard_name= "Single nucleotide polymorphism (SNP)"
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0; Mismatches
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ABZ48673
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Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The cone polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ4217-ABZS0887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of arrays and pCR-based methods. The invention also encompasses methods of arrays and pCR-based methods. The invention also encompasses methods of avaiety of detection assays, including hybridisation assays, nucleic acid arrays and pCR-based methods. The invention also encompasses methods of polymorphism data. particularly that relating to single nucleotide polymorphism data. particularly that relating to single nucleotide polymorphism sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genes with the grue encoding drug metabolising enzymes allows the customisation of drug therapeutic effect for a particular patient. Dut would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of the invention may therefore lead to an increase in the range of possible drug candidates could be revived if they were matched with more appropriate patient populations. The methods of adverse reactions of adverse reactions of the invention may therefore lead to an increase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                          Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 29.2; DB 1; Length 41; 91.2%; Pred. No. 88; 1; Indels 1; o Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41 BP; 4 A; 2 C; 18 G; 17 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA132.
                                                                                                                    Saito S;
                                                                                                                                                                                                                                                                                                                                     Claim 23; Page 171; 2785pp; English.
                                                                                                                 Iida A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ33710 standard; DNA; 37 BP.
02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Conservative
                                                                                                                 Nakamura Y, Sekine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                 WPI; 2002-583571/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 31; Conserv
                                                                    (RIKE ) RIKEN KK
                                                                                                                                                                                                                                                                                          nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 139
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27-DEC-2000; 2000JP-00399443.
02-MAY-2001; 2001JP-00135256.
27-AUG-2001; 2001JP-00256862.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replace (21, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-DEC-2001; 2001WO-JP011592
                           89US-00341562.
91US-00754351.
94US-00222177
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                                                                            (MARS-) MARSHFIELD CLINIC.
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                                                                                                                                            WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 32; Conserv
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 04-APR-1994;
                                21-APR-1989;
                                                 05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-2003
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variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ49485;
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                                                                                                                 Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 141
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                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine Mool DNA fragments of between 250 and 500

considerable and (TC)15 oligonucleotide probe. One out of 50

clones cross-bybridised. Assuming independent distribution of

clones cross-bybridised. Assuming independent distribution of

microsatellites and Mool sites, the frequency of (T6)n >9 microsatellites

in the bovine genome is estimated at >100, 000. The sequence information

for ca. 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

downstream of the microsatellite sequence were used to generate the

cquired PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite (using the program OPTIPRIM). The microsatellites may be

used to identify individuals, for parentage testing, and in the genetic

capping of economic trait loci, or genes involved the determinism of

connecting See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                              markers - used in genetic identification, gene
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0
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Pred. No. 82;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat sequence from polymorphic marker clone Mfd104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2320 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACAT 2356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37 BP; 4 A; 0 C; 14 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                 Table 7; Page 214; 517pp; English.
                                                                                                                                                                                                                                                                                                                  mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.8%;
Best Local Similarity 86.5%;
Matches 32; Conservative
                                                                                                                                       92WO-US000340
                                                                                                                                                                       91US-00642342
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                                                                                                                                                                                                                                                                                                     Polymorphic bovine DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                        Georges M, Massey JM;
                                                                                                                                                                                                                                                                    WPI; 1992-284684/34.
                                                                                                                                                                                                         (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                         15-JAN-1991;
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17-JUN-1997
                                                                                                                                         15-JAN-1992;
                                                                          WO9213102-A1
                                                                                                          06-AUG-1992.
                                            Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT65775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              field.)
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XX BX SX KK KK XX BX B B B B X Y X X X B X X B X X B X X B X X B X X B X X B X

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SNP; da
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name= "Single nucleotide polymorphism (SNP)"
Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human glutathione-S-transferase GSTPi gene polymorphic site, #6268.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 0.8%; Score 29; DB 1; Length 39; 1 Similarity 86.5%; Pred. No. 87; 32; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2320 TGTGTGTGTGTGCGTGTGTGTGTGTGTGTGCACAT 2356
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39 BP; 19 A; 14 C; 0 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTGTGTGTGTGTGTGTGTGTGTGTATATAT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                   Claim 1; Col 13-14; 186pp; English
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(RIKE) RIKEN KK.

Nakamura Y, Sekine A, Iida A, Saito S;

WPI; 2002-583571/62

Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme

Claim 23; Page 190; 2785pp; English.

To mecroas and compositions to reneutrying individuals who have at least one polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ARZ4311-ARZ50887 using a carays and percetion assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of arrays and PCR-based methods. The invention also encompasses methods of carays and PCR-based methods. The invention also encompasses methods of carays and PCR-based methods. The invention also encompasses methods of polymorphism data, particularly that relating to single uncleotide polymorphism data, particularly that relating to single nucleotide polymorphism (SNPs), may be used in studying the relationship between the respectate as they are stable in populations, and the respectas as they are stable in populations, occur cause or exacerbate certain diseases. SNPs are particularly useful cause or exacerbate certain diseases. SNPs are particularly useful cauch as repeating sequences. The detection and analysis of polymorphisms of such as repeating sequences. The detection and analysis of polymorphisms could not only take the guesswork out of selecting the drug with the carry therefore the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and capproval processes. Por example, individuals could be selected for capable of responding to a particular drug or drug class, and previously called drug candidates could be revived if they were matched with more capable of responding to a particular drug or drug class, and previously called drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to a an increase in the range of the invention may therefore lead to a an increase in the range of capacities and decreases in the mush of a drug capacities of drug candidates and decreases. reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least

Sequence 41 BP; 0 A; 5 C; 21 G; 15 T; 0 U; 0 Other;

Gaps ö 0.8%; Score 29; DB 1; Length 41; 86.5%; Pred. No. 92; 5; Indels 0; Mismatches 32, Conservative Local Similarity Query Match Matches

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1 Grenerececerecererecererereres 37

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RESULT 142 ABZ43946 **££££**£££££££££

ABZ43946 standard; DNA; 41 BP

ABZ43946;

(first entry) 26-JUN-2003

Human glutathione-S-transferase GSTPi gene polymorphic site, #730

Human; drug metabolising enzyme; gene; drug metabolism; chromosome 11; polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

/*tag= a /standard_name= "Single nucleotide polymorphism (SNP)" Location/Qualifiers replace (21, A) Homo sapiens. variation

WO200252044-A2.

04-JUL-2002.

27-DEC-2001; 2001WO-JP011592

27-DEC-2000; 2000JP-00399443. 02-MAY-2001; 2001JP-00135256. 27-AUG-2001; 2001JP-00256862.

(RIKE) RIKEN KK.

Nakamura Y, Sekine A, Iida A, Saito S;

WPI; 2002-583571/62.

Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid

Claim 23; Page 76; 2785pp; English.

Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates concethed and compositions for identifying individuals who have at least con emethods and compositions for identifying individuals who have at least con emethods and composition and mucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, mucleic acid availety of detection assays, including hybridisation assays, mucleic acid avaiety of detection assays, be used in studying the relations methods of arrays and pCR-based methods. The invention also encompasses methods of arrays and pCR-based methods. The invention also encompasses methods of colymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases. SNRs are particularly useful colymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases. SNRs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations cut in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations in genese encoding drug metabolising enzymes allows the customasation of drug therapies based upon the genetic profile of individual patients.

This would not only take the guesswork out of selection the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby individual patient for a particular drug or drug class, and previously the invention may therefore lead to a particular drug or drug class, and previously compable of responding to a particular drug or drug class, and previously reactions, failed drug tradets and decreases in the number of adverse reactions, the emphase and composition are also me

Sequence 41 BP; 0 A; 5 C; 21 G; 15 T; 0 U; 0 Other;

ö DB 1; Length 41; 5; Indels 0.8%; Score 29; DB 86.5%; Pred. No. 92; tive 0; Mismatches Local Similarity 86.5 es 32, Conservative Louery Match

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2315 GTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2351 ВЪ.

AAQ33965 standard; DNA; 30

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AA033965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E CA are interrupted. This sequence is an example of an imperfect sequence of structure: (CA)11CT(CA)4. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection of polymorphic genetic markers of the form (dG-dA) \, n \, (dG-dT) \, n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 28.8; DB 1; Length 32; 33.8%; Pred. No. 72; 2; Indels ve 0; Mismatches 2; Indels
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             GTGTGTGCGCGTGCGTGTGTGTGTGCGTGTGTG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (dC-dA)n.(dG-dT)n polymorphic repeat sequence #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Col 57-58; 186pp; English
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Best Local Similarity 93.8%;
Matches 30; Conservative
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91US-00754351
                                                                                                                                                                                                                                  AAT66057 standard; DNA; 32
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                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-042299/04.
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                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
18-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-1996.
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                                                                                                                                                                                                                                                                                                                            AAT66057;
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                                                                                                                                                RESULT 143
AAT66057/C
LD AAT6605
XX
AC AAT660
XX
DT 25-MAR
DT 18-UNN
XX
XX
XX
XX
XX
HOMO E
XX
PCR; E
XX
PC
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The sequence is that of a bovine microsatellite sequence obtd. by coreening a library of bovine Mbol DNA fragments of between 250 and 500 core screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of 50 clones cross-hybridised. Assuming independent distribution of 60 clones are littles and Mbol sites, the frequency of (TG)n >9 microsatellites of in the bovine genome is estimated at >100, 000. The sequence information for car 230 such bovine microsatellites is summarised in the microsatellite sequence were used to generate the correct of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The microsatellite (using the program OPTIPRIM). The microsatellites may be consomic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                              PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.7%; Score 28.4; DB 1; Length 30; 96.7%; Pred. No. 74; 1; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat sequence from polymorphic marker clone Mfd118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 BP; 0 A; 0 C; 15 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 rerererererererererere
                                                                                                   Microsatellite sequence from clone TGLA357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Table 7; Page 316; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                91US-00642342.
                                                                                                                                                                                                                                                                                92WO-US000340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                         (revised)
(first entry)
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Best Local Similarity 96.7
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                    L5-JAN-1992;
                                                                                                                                                                                                                                                                                                                15-JAN-1991;
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17-JUN-1997
                                                       25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                    W09213102-A1
                                                                                                                                                                                                                                                    06-AUG-1992.
                                                                                                                                                                                         Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT65789
                            AAQ33965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 145
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ID AAT65
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XC AAT65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T6647. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdfill Which contains the repeat sequence is from the marker clone Mdfill which contains the repeat sequence aving the formula: (AC)15. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromsome; ds.
                                                                                                                                                                                                                                                                                                                                                                                markers of the form (dC-dA)n(dG-dT)n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.7%; Score 28.4; DB 1; Length 30; 36.7%; Pred. No. 74; Ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30 BP; 15 A; 15 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2319 GTGTGTGTGTGTGTGTGTGTGTGTGT 2348
                                                                                                                                                                                                                                                                                                                                                                              Detection of polymorphic genetic markers of using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 crerererererererererererer 1
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Col 13-14; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simple sequence repeat, SSR, #59.
                                                                                                                                                                                                                        89US-00341562.
91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS13788 standard; DNA; 30 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 96.7%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                          (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                                                                                                                                              WPI; 1997-042299/04
                                                                                                                                                                                        04-APR-1994;
                                                                                                                                                                                                                                          05-SEP-1991;
                                                                                     Homo sapiens
                                                                                                                                                                                                                         21-APR-1989;
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                                                                                                                    US5582979-A.
                                                                                                                                                      10-DEC-1996,
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                                                                                                                                                                                                                                                                                                            Weber JL;
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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence core decide (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primar cutable for amplifying an SSR, identifying (MI) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the MI, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely a ssociated with the gene such that the SSR and the gene are contained for DNA profiling grass or cereal species varieties by assessing contained for DNA profiling grass or cereal species varieties by assessing variation within seed batch of an SSR. The SSRs can be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the printy of grass or cereal species varieties, for testing the printy of grass or cereal species varieties, for testing the printy of grass or cereal species varieties, for testing the printy of grass or cereal species varieties, for testing the printy of grass or cereal species varieties, for testing the printy of grass or cereal species varieties, for testing the printy of sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                   New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simple sequence repeat, plant, ds, SSR; ryegrass, fescue; tandem repeat, cereal profiling, grass profiling; seed batch purity testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.7%; Score 28.4; DB 1; Length 30; 96.7%; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30 BP; 15 A; 15 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                        UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
UNIV ADELAIDE.
                                                                  STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318 rerererererererererere 2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                               (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simple sequence repeat, SSR, #58.
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Page 53; 72pp; English.
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24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
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Matches 29; Conservative
                                                                                                                                                                                                                                                         WPI; 2001-512563/56.
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                                                                                                                                                                                                               Forster JW,
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                                                                                                                                                                                                                                                                                                                                                                              rarieties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS13787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                          (UYSC-)
(VICT-)
                                                                    (SAUS-)
                                                                                                                                           UYAD-)
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Gaps

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BB

sequence derived from

vivlemore401-10.rng

(ITMA-)

SAUS-) (VICT-) UYAD-)

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information for ca. 210 such bovine microsatellite see low). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.
                                                                                                              new microsatellite DNA derived from a Pyrus plant and discrimination of
                                                                                                                                                                                                                                                                           Pyrus plants. The invention also comprises a method for discriminating Pyrus plants - utilising the novel Pyrus microsatellite DNA. The novel microsatellite DNA sequence can be used in discriminating Pyrus plants.
                                                                                                                                                                                                                                                                                                                                                                     The present DNA sequence represents a probe specific for a novel Pyrus pyrifolia (sand pear) microsatellite DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.7%; Score 28.4; DB 1; Length 30; 96.7%; Pred. No. 74; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30 BP; 0 A; 0 C; 15 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                          The invention comprises a novel microsatellite DNA
(DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2319 GIGIGIGIGIGIGIGIGIGIGIGIGIGIGI 2348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite sequence from clone TGLA342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 crererererererererererererer 30
                                                                                                                                                                                                    Example 1; Page 22; 22pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Table 7; Page 307; 517pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                              Pyrus plants by using it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 96.7
nes 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-284684/34.
                                                           WPI; 2002-298819/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-1991;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ33944;
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Matches
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  &XXXTTXXXX000000XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer suitable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and clentifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing.

Containing prass or cereal species and testing the purity of grass or cereal seed batches by assessing varieties and testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, and for DNA profiling to establish the grass or cereal species varieties, and cereal present the present present processed to the processed to the present present processed to the pre
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                                                                                                                                                                                                                                                                                                                                          New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species varieties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sand pear; ss; probe; novel microsatellite DNA sequence; Pyrus plant discrimination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30 BP; 0 A; 0 C; 15 G; 15 T; 0 U; 0 Other;
                                                        STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                   UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2319 GTGTGTGTGTGTGCGTGTGTGTGTGTGT 2348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 74;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel sand pear microsatellite DNA probe 3.
                                                                                                                                                                      INT MAIZE & WHEAT IMPROVEMENT CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 grererererererererererererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28.4;
Pred. No. 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 53; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAL42354 standard; DNA; 30 BP.
  04-MAY-2000; 2000AU-00007310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-2000; 2000JP-00220339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-2000; 2000JP-00220339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 96.7
Matches 29, Conservative
                                                                                                                                           UNIV ADELAIDE
                                                                                                                                                                                                                                  Forster JW, Jones ES
                                                                                                                                                                                                                                                                                          WPI; 2001-512563/56.
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AAL42354;

RESULT 148 AAL42354

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Gaps

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Indela

Length 33;

DB 1;

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information for ca. 230 such bovine microsatellite sequence were used to generate the sequired PCR primers for in vitro amplification of the corresp.

The proposed PCR primers for in vitro amplification of the corresp.

The country of economic trait loci, or genes involved the determinism of economic trait loci, or genes involved the determinism of economic trait seps. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
used to identify individuals, for parentage testing, and in the genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  selection; primers; OPTIPRIM; breeding; cattle; parentage;
                                                                                                     Sequence 33 BP; 1 A; 1 C; 15 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 37 BP; 2 A; 1 C; 15 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                       2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                          TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 33
                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Microsatellite sequence from clone TGLA128.
                                                                                                                                   Score 28.2; I
Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic mapping; traits; amplification; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Table 7; Page 209; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                     0.7%;
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                                                                                                                                                                                                                                                                                                                          AAQ33698 standard; DNA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                   Local Similarity 90.5 nes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9213102-A1
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02-FEB-1993
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              mapping of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Georges M,
                                                                                                                                                                                                                                                                                                                                                              AAQ33698;
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             field.)
                                                                   field.)
                                                                                                                                                                                                                                                                                              RESULT 150
                                                                                                                                                                        Matches
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ID AAQ3
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by with an (AC)15 and a (TC)15 oligonuclectide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of clones cross-hybridised. Assuming independent distribution of microsatellites and Mboi sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information specification and indexed herein (see below). The sequence information downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

Used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of a bovine microsatellite sequence obtd. by
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                                                                                                                                                                                                                                                                      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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0
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35 BP; 3 A; 1 C; 15 G; 16 T; 0 U; 0 Other;
3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 27.6; DB 1;
Pred. No. 1.1e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2316 rengrerererererecerererererere 2349
                         GCGTGTGTGTGTGT 2350
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                                                          1 rererererererarerererererererer 33
0; Mismatches
                                                                                                                                                                                                                                           Microsatellite sequence from clone TGLA127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Table 7; Page 208; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US000340.
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                                                                                                                                   AAQ33695 standard; DNA; 35
                                                                                                                                                                                               (revised)
(first entry)
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Best Local Similarity 88.2
Matches 30; Conservative
 Conservative
                              2318 TGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-1991;
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02-FBB-1993
                                                                                                                                                                                                                                                                                                                                                                                06-AUG-1992.
30;
                                                                                                                                                                                                                                                                                                                       Bos taurus.
                                                                                                                                                                  AAQ33695;
                                                                                                      RESULT 151
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 Matches
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ID AAQ3
                                                                                                                      AAQ3369!
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Score 28.2; DB 1; Length 37; Pred. No. 1e+02;

0.7%;

Best Local Similarity

Query Match

Bos taurus.

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The sequence is that of a bovine microsatellite sequence obtd, by screening a library of bovine Mbol DNA fragments of between 250 and 500 screening a library of bovine Mbol DNA fragments of between 250 and 500 close cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information in the bovine microsatellites is summarised in the genefication and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

In increasellite (Using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of the content trait sep. in cattle, to allow selective contents of the content trait sep. in cattle, to allow selective contents and the contents of the content trait sep. in cattle, to allow selective contents and contents of the conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                 PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.7%; Score 27.6; DB 1; Length 38; 88.2%; Pred. No. 1.2e+02; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38 BP; 4 A; 0 C; 19 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2318 rererererererecerererererere 2351
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                                                                                                                                        Microsatellite sequence from clone TGLA172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Table 7; Page 236; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               92WO-US000340.
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(first entry)
                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.2
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-284684/34.
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02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-1992;
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                                                                   25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                         Bos taurus
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                         AAQ33767;
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The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MboI DNA fragments of between 250 and 500

CC clones cross-hybridised. Assuming independent distribution of

CC clones cross-hybridised. Assuming independent distribution of

CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

microsatellites and mboI sites, the frequency of (T6)n >9 microsatellites

CC for ca. 230 such bovine microsatellites is summarised in the

CS specification and indexed herein (see below). The sequences upstream and

CC downstream of the microsatellite sequence where used to generate the

Microsatellite (usin vitro amplification of the corresp.

CC macrosatellite (usin vitro amplification of the corresp.

CC used to identify individuals, for parentage teating, and in the genetic

CC used to identify individuals, for parentage teating, and in the genetic

CC mapping of economic trait loci or genes involved the determinism of

CC conomically important traits esp. in cattle, to allow selective
                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 29 BP; 0 A; 0 C; 14 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27.4; DE Pred. No. 93; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                              Table 7; Page 204; 517pp; English.
                                                                                                                92WO-US000340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity 96.6%;
Conservative
                                                                                                                                                                                                                         Georges M, Massey JM;
                                                                                                                                                                                                                                                         PI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 28; Conserv
                                                                                                                                                                                      (GENM-) GENMARK.
                                                                                                                                                     .5-JAN-1991;
                                                                                                                      15-JAN-1992;
                                                 W09213102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

92WO-US000340. 91US-00642342

15-JAN-1992; 15-JAN-1991;

06-AUG-1992

WO9213102-A1

Bos taurus.

Microsatellite sequence from clone TGLA257.

(first entry) (revised)

25-MAR-2003 02-FEB-1993

AAQ33846;

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Gaps

.. 0

AAQ33846 standard; DNA; 29 BP.

AAQ33846

Table 7; Page 312; 517pp; English.

маввеу ЛМ;

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mool DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mool sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellites sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective
                                                                                                                                                                                                                                                                                                                                                                                                             breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR; selection; primers, OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29 BP; 0 A; 0 C; 14 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microsatellite sequence from clone TGLA351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGTGTGTGTGTGTGTGTGTGTGTGT 29
                                                                                                                                                        Table 7; Page 268; 517pp; English.
                                                                                                                         mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ33956 standard; DNA; 29 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 96.6
Matches 28; Conservative
                                                                        WPI; 1992-284684/34
              (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-1991;
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02-FEB-1993
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                                            Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ33956;
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Gaps

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DB 1; Length 29; 1; Indels

Score 27.4; DE Pred. No. 93; 0; Mismatches

0.7%;

Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

Georges M, Massey JM;

WPI; 1992-284684/34.

92WO-US000340 91US-00642342

(first entry)

(revised)

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The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine MboI DNA fragments of between 250 and 500

co by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50

colones cross-hybridised. Assuming independent distribution of

clones cross-hybridised. Assuming independent distribution of

colones cross-hybridised. Assuming independent distribution of

construction and indexed herein (see below). The sequences information

colones cross-hybridises for in vitro amplification of the corresp.

colonically individuals, for parentage testing, and in the genetic

mapping of economic trait loci, or genes involved the determinism of

conomically important traits esp. in cattle, to allow selective

preeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is setimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specification and indexed herein (see below). The sequences upstream and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                 0.7%; Score 27.4; DB 1; Length 29; 16.6%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                 Sequence 29 BP; 0 A; 0 C; 14 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                          <del>ا</del>:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2318 TGTGTGTGTGTGTGCGTGTGTGTGTGT 2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microsatellite sequence from clone TGLA378.
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Table 7; Page 320; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-00642342
                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 96.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ33977 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ33977;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthesis of branched polymers and novel branched polymeric structures - used as molecular probes esp. for detecting poly-nucleotide(s).
                                                                                                                                                                                                                                                                                                                                                                                                ಹ
downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                              monomer containing
p = phosphodiester
                                                                                                                                                                                                                                                                                                                                                       ppp = a linkage or monomer containing
functionality, and p = phosphodiester
                                                                                                                                                                                                                                                                                                                                                                                               ppp = a linkage or monomer containing
functionality, and p = phosphodiester
                                                                                                        Gaps
                                                                                                                                                                                                                                                       HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
                                                                                                                                                                                                                                       Oligonucleotide clamp q, for producing comb-type brached polymer.
                                                                                                        ö
                                                                                        Length 29;
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= d
/note= "Modified with -NH-C(=O)CH2Br"
                                                                                                                                                                                                                                                                                                                pnp = a linkage or
functionality, and
                                                                        Sequence 29 BP; 0 A; 0 C; 14 G; 15 T; 0 U; 0 Other;
                                                                                          DB 1;
                                                                                                                          2318 TGTGTGTGTGTGTGTGTGTGTGTGTGT 2346
                                                                                          Score 27.4; I
Pred. No. 93;
                                                                                                          Mismatches
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               /note= "A(pnp)C,
bromoacetylamino
                                                                                                                                                                                                                                                                                                                 /note= "A(pnp)C,
bromoacetylamino
                                                                                                                                                                                                                                                                                                                                                        /note = "A(pnp)C,
bromoacetylamino
                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-00087386.
                                                                                          0.7%;
                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                          /*tag= c
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                  linkage"
                                                                                                                                                                                                                                                                                                                                                                         linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                 linkage"
                                                                                                                                                                                   AAQ83953 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                  /*tag=
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                                                                                                 Similarity
                                                                                                                                                                                                                                                                                           Key
modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gryaznov SM;
                                                                                                                                                                                                                 25-MAR-2003
04-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JAN-1995
                                                                                                           28;
                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                 AAQ83953;
                                                                                           Query Match
                                                                                                    Local
                                                            field.)
                                                                                                                                                                   Matches
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Example 9; Page 34; 52pp; English

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The sequences given in AAQ83339, AAQ83953 and AAQ839940 are used in the construction of an oligonuclectide clamp. The clamp is a comb-type construction of an oligonuclectide clamp. The clamp is a comb-type branched polymer which has 5' termini and was used to bind a target correct comprising a segment of the HIV pol and nef genes in single cranded or double stranded forms. An oligonuclectide clamp is a compound complex after specificially binding to the target polynuclectide complex after specific binding to the target polynuclectide complex after specific binding to the target molecule and one or more pairs of binding moieties covalently linked to the oligonuclectide control of the oligonuclectide and one or moieties. Upon annealing of the oligonuclectides moieties to the target olynuclectide, the binding moieties of a pair are bought into inxaposition so that they form a stable covalent or non-covalent linkage or complex. The interaction of the binding moieties effectively clamps the specifically annealed oligonuclectide moieties to the target copynuclectide. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the isolation of polymorphic repeat sequences having the sequence (dc-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat sequence from polymorphic marker clone Mfd65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29 BP; 14 A; 15 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.7%; Score 27.4;
46.6%; Pred. No. 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-00341562.
91US-00754351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-042299/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-APR-1994;
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT65760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Gaps

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Indels

ï DB 1;

0.7%; Score 27.4; ilarity 96.6%; Pred. No. 93; Conservative 0; Mismatches

Query Match Best Local Similarity

28;

Matches

2346

29 rererererererererererererer

2318 TGTGTGTGTGTGTGTG

8

Length 29;

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-979. This repeat sequence is from the marker clone Mdf10 which contains the repeat sequence is from formula: (AC)14A. (Updated on 25-MAR-2003 to correct PF field.)
repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(GC-dA). (GG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence has the marker clone Mdf65 which contains the repeat sequence 1s from formula: (CA)14.5. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29 BP; 15 A; 14 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1989;
05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5582979-A
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                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                                                         AAT65712;
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                                                                                                                                                                                                                                                                                                                        RESULT 159
                                                                                                                                                                                                                                                                                                                                        AAT65712,
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                                                                                                                                                                                                                                                            Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of polymorphic genetic markers of the form (dC-dA) n(dG-dT) n using novel nucleic acid mols. as primers.
                                                                Gaps
                                                                ÷
                                           DB 1; Length 29;
                                                                1; Indels
                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd10.
                      Sequence 29 BP; 14 A; 15 C; 0 G; 0 T; 0 U; 0 Other;
                                         Score 27.4; DE Pred. No. 93; 0; Mismatches
                                                                                      PGTGTGTG 2347
                                                                                                           Grererererererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Col 9-10; 186pp; English.
                                                                                      2319 Grererererereceren
                                                                                                                                                                                                                                                                                                                                                                                    94US-00222177
                                                                                                                                                                                                                                                                                                                                                                                                         89US-00341562
91US-00754351
                                           Query Match
Best Local Similarity 96.6%;
Matches 28; Conservative
                                                                                                                                                               AAT65712 standard; DNA; 29
                                                                                                                                                                                                          (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthesizing branched nucleic acids useful as diagnostic and molecular probes, involves combining first units having haloalkylamino groups and second units having thiol or phosphorothioate groups.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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16.6%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29 BP; 14 A; 15 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 9; Col 19-20; 20pp; English
                                                ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                        97US-00787321.
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ33731 standard; DNA; 33
                                             AAF60474 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                  Oligonucleotide clamp #23.
                                                                                                                                                                                                                                   Oligonucleotide clamp; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-201911/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                            US6180777-B1
                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                      03-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001.
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02-FEB-1993
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                                                                                         AAF60474;
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AAQ33731
                     AAF60474/c
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Matches
RESULT 160
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15-JAN-1991;

15-JAN-1992; 06-AUG-1992.

WO9213102-A1

Bos taurus

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of
                                                                                                                                                                                                                                                                                                                                           Oligo-dC primer P12 (see AAQ27542) was used with primer P6(2) (see AAQ27540) in a PCR amplification on a dG-tailed TKF coding sequence. A second round of PCR was performed on the product, this time using primer P12 with primer TKF1 to isolate a new Protein-Tyrosine-Kinase-Sequence. See AAQ27539-Q27544
                                                                                                                                                                                                                   New tyrosine kinase receptor protein related to FGF receptor proteins and corresponding DNA sequences, used in treatment and diagnosis of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                     Strebhardt K, Ruebsamen-Waigmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26.4; DB 1; Length 28; Pred. No. 1.2e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28 BP; 6 A; 10 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                            (GEOR-) GEORG-SPEYER-HAUS CHEMOTHERAPEUTISCHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microsatellite sequence from clone TGLA424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1632 TGCCCGCAATGTGCTGGTGACCGAGGAC 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 TGCCCGCAATGTGCTGGTGACTGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Table 7; Page 341; 517pp; English.
                                                                                                                                                                                                                                                                                                                  Example 2; Page 11; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ34027 standard; DNA; 28 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.7%;
Best Local Similarity 96.4%;
Matches 27; Conservative (
                91DE-04104240.
                                                         91DE-04104240
                                                                                                                                              Holtrich U, Braeuninger A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-284684/34.
                                                                                                                                                                                        WPI; 1992-277527/34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1991;
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02-FEB-1993
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                12-FEB-1991;
                                                           12-FEB-1991;
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                                                                                                                                                                                                                                                                                    tumours.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ34027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of a bovine microsatellite sequence obtd. by

C screening a library of bovine Mbol DNA fragments of between 250 and 500

C bp with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50

C clones cross-hybridised. Assuming independent distribution of

C clones cross-hybridised. Assuming independent distribution of

C microsatellites and Mbol sites, the frequency of (TG)n >9 microsatellites

C in the bovine genome is estimated at >100, 000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the

C specification and indexed herein (see below). The sequences upstream and

C specification and indexed herein (see below). The sequences upstream and

C downstream of the microsatellite sequence waset to generate the

C caquired PCR primers for in vitro amplification of the corresp.

C microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellity individuals, for parentage testing, and in the genetic

C used to identify individuals, for parentage testing, and in the genetic

C mapping of economic trait loci, or genes involved the determinism of

C conformically important traits sep. in cattle, to allow selective

C breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                  PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 0.7%; Score 26.6; DB 1; Length 33; Best Local Similarity 87.9%; Pred. No. 1.4e+02; Matches 29; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR Primer TKF1 corresponds to TKF receptor nts. 675-648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33 BP; 3 A; 0 C; 13 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2316 rerererererererererererererer 2348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TATATATGTGTGTGTGTGTGTGTGTGTGT 33
                                Microsatellite sequence from clone TGLA149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Table 7; Page 222; 517pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                            Georges M, Massey JM;
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                                                                                                                                                                                                                                                                                                                                                                (GENM-) GENMARK.
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DE4104240-A 13-AUG-1992

Synthetic.

AAQ27543;

RESULT 162

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Gaps

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microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the
                                 specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic economically important traits sep. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; 88.
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                                                                                                                                                                                           Score 26.4; DB 1; Length 28; Pred. No. 1.2e+02;
                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                  Sequence 28 BP; 0 A; 0 C; 14 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                2318 TGTGTGTGTGTGTGTGTGTGTGTGTG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                               Microsatellite sequence from clone TGLA45.
                                                                                                                                                                                                                                                            1 TGTGTGTGTGTGTGTGTGTGTGTG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                       AAQ34074 standard; DNA; 28 BP.
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                                                                                                                                                                                             0.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                       Local Similarity 96.4 les 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                          (revised)
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                                                                                                                                                                                              Query Match
                                                                                                                                           field.)
                                                                                                                                                                                                                                                                                                               RESULT 164
                                                                                                                                                                                                                      Matches
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comparteam of the microsatellite sequence waset to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
inconsidently individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
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breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct
field.)
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                                                                                                                                Gaps
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Pred. No. 1.2e+02;
                                                                                               Score 26.4; DB 1; Length 28;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                Indels
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                                                               Sequence 28 BP; 1 A; 0 C; 14 G; 13 T; 0 U; 0 Other;
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                                                                                                                              0; Mismatches
                                                                                                                                                                2322 TGTGTGTGTGCGTGTGTGTGTGTGTG 2349
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                                                                                                                                                                                   1 TGTGTGTGTGAGTGTGTGTGTGTG 28
                                                                                                                                                                                                                                                                                                                                                                                                Microsatellite sequence from clone MTGT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rable 7; Page 187; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mapping, and selective breeding.
                                                                                                                                                                                                                                                                                 ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92WO-US000340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.7%;
                                                                                              ch 0.7%;
il Similarity 96.4%;
27; Conservative
                                                                                                                                                                                                                                                                                 AAQ33645 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 **Ouery Match Similarity 96.4*
Best Local Similarity 96.4*
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-284684/34.
                                                                                               Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30s taurus.
                                                                                                                                                                                                                                                                                                                  AAQ33645;
                                                                                                                                                                                                                                                 RESULT 165
                                                                                                                                                                                                                                                                   AAQ33645
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 ollgonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and domonstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective

Table 7; Page 360; 517pp; English.

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The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MooI DNA fragments of between 250 and 500

CC clones cross-hybridised. Assuming independent distribution of 50

CC clones cross-hybridised. Assuming independent distribution of 50

CC clones cross-hybridised. Assuming independent distribution of 50

CC clones genome is estimated at >100, 000. The sequence information 50

CF cr ca. 230 such bovine microsatellites is summarised in the 50

CF or ca. 230 such bovine microsatellites is summarised in the 50

CF or ca. 230 such bovine microsatellite sequence waset to generate the 50

CF or ca. 230 such bovine microsatellite sequence waset to generate the 50

CF or ca. 230 such bovine microsatellite sequence waset to generate the 50

CF or ca. 230 such bovine microsatellite sequence waset or generate the 50

CF or ca. 230 such bovine microsatellite sequence waset or generate the 50

CF or ca. 230 such bovine microsatellite sequence was to generate the corresp. 50

CF or ca. 230 such bovine microsatellite sequence waset or generate the corresp. 50

CF or ca. 230 such bovine microsatellite sequence waset or generate the corresp. 50

CF or ca. 230 such bovine microsatellites may be 50

CF or ca. 230 such bovine microsatellites may be 50

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca. 230 such bovine microsatellites may be 60

CF or ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                          PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.7%; Score 26.4; DB 1; Length 28; 96.4%; Pred. No. 1.2e+02; ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28 BP; 0 A; 0 C; 14 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                           Sequence of a microsatellite from clone TGLA82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTCTCTCT 2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crerererererererererererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rable 7; Page 395; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ34035 standard; DNA; 28 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92WO-US000340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ilarity 96.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-00642342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2319 GTGTGTGTGTGTGTGCGG
AAQ34161 standard; DNA; 28
                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                         WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-1992.
                                                                                                        25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                       Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ34035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                       AAQ34161;
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The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MooI DNA fragments of between 250 and 500

CC screening a library of bovine MooI DNA fragments of between 250 and 500

CC clones cross-hybridised. Assuming independent distribution of

CC clones cross-hybridised. Assuming independent distribution of

CC cross-hybridised. Assuming independent distribution of

CC cross-hybridised. Assuming independent distribution of

CC cross-bovine genome is estimated at >100,000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the

CC specification and indexed herein (see below). The sequences upstream and

CC downstream of the microsatellite sequence were used to generate the

CC downstream of the microsatellite sequence were used to generate the

CC microsatellite (using the program OPTIPRIM). The microsatellites may be

CC used to identify individuals, for parentage testing, and in the genetic

CC used to identify individuals, for parentage testing, and in the genetic

CC used to identify individuals, for parentage testing, and in the genetic

CC used to identify individuals, for parentage testing, and in the genetic

CC used to identify individuals, for parentage testing, and in the genetic

CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN

Fight 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                    PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26.4; DB 1; Length 28;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat sequence found in the human chromosomal clone SW10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28 BP; 0 A; 0 C; 14 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2319 GIGIGIGIGIGIGIGIGIGIGIGI 2346
                                                    Microsatellite sequence from clone TGLA431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Grerererererererererererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Table 7; Page 345; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                   92WO-US000340.
                                                                                                                                                                                                                                                                                                         91US-00642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 96.4%;
hes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT66102 standard; DNA; 28
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(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                   Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                 (GENM-) GENMARK.
                                                                                                                                                                                                                                                                     .5-JAN-1992;
                                                                                                                                                                                                                                                                                                           15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
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25-MAR-2003
02-FEB-1993
                                                                                                                                                                                            W09213102-A1
                                                                                                                                                                                                                                 06-AUG-1992.
                                                                                                                                                        Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT66102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Gaps ö more tandemly repeated nucleotide

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acid (1) firm registes or feacue appealed including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer suitable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and core identifying chones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely a sesociated with the gene such that the SSR and the gene are such charted, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal species varieties, for testing the sSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profilling to establish the sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer;
                                                                                    New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                                                                                                                       The invention relates to a substantially purified or isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26.4; DB 1; Length 28;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human NOVX protein-related oligonucleotide probe SeqID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28 BP; 14 A; 14 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.4%; Pred. 1.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 rerererererererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome mapping; human; probe; ss.
                                                                                                                                                                                  Claim 6; Page 51; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-0372019P.
2002US-0374379P.
2002US-0384543P.
2002US-00160619.
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04-NOV-2002; 2002US-00287226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-2003; 2003WO-US010142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADK51120 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 96.4 Matches 27; Conservative
                                                     WPI; 2001-512563/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003083046-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2002;
08-APR-2002;
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03-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-OCT-2003
                   Forster JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADK51120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. The sequences AAT66084-T66107 represent repeat sequences of low informativeness found in specific human genes. This repeat sequence is found in the human chromosomal clone SW10. The sequence is amplified by primers AAT66103-4. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                                                                                                                                                                                                                                                                               Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.7%; Score 26.4; DB 1; Length 28; Best Local Similarity 96.4%; Pred. No. 1.2e+02; Matches 27; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28 BP; 14 A; 14 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIV ADELAIDE.
INT MAIZE & WHEAT IMPROVEMENT CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2319 GTGTGTGTGTGTGTGTGTGTGTGT 2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 crerererererererererererer
                                                                                                                                                                                                                                                                                                                                                                       Example 9; Col 61-62; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simple sequence repeat, SSR, #8.
                                                                                                           94US-00222177
                                                                                                                                              89US-00341562
91US-00754351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-2001; 2001NZ-00509193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-1999; 99AU-00004906
04-MAY-2000; 2000AU-00007310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS13711 standard; DNA; 28
                                                                                                                                                                                                    (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                         WPI; 1997-042299/04.
   Homo sapiens
                                                                                                             04-APR-1994;
                                                                                                                                                21-APR-1989;
                                                                                                                                                                 05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-2001.
                                    US5582979-A
                                                                         10-DEC-1996
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                                                                                                                                                                                                                                          Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS13711;
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(VICT-) (
(UYAD-) (
(ITMA-)
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AAS13711/c
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Gaps

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Indels

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                             ADKŠ1123;
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                ADK51123
                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                     셤
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                                                                                                                                                             This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NoVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of an oligonucleotide probe which was used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Furtak K;
Spytek KA;
                                                                                                                ö
                                       Casman SJ, Furtak K;
MP, Li L, Spytek KA;
Patturajan M;
                                                                                                              New NOVX polypeptide, useful for preparing a composition for treating
                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W, Bento P, Boldog FL, Burgess CE, Casman SJ, Gould-Rothberg BE, Gunther E, Heyes MP, Li L,
                                                                                                                                                                                                                                                                                       ch 0.7%; Score 26; DB 1; Length 26; 1 Similarity 100.0%; Pred. No. 1.2e+02; 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOVX protein-related oligonucleotide probe SeqID.
                               corman L, Gould-Rothberg BE, Gunther E, Heyes Stone DJ, Zhong M, Malyankar UM, Edinger SR, Isothenberg ME, Smithson G;
                                                                                                                                                                                                                                                                      Sequence 26 BP; 9 A; 9 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                          preventing e.g. cancer or for chromosome mapping
                                                                                                                                             Example C; SEQ ID NO 141; 433pp; English.
                                                                                                                                                                                                                                                                                                                                  714 CGCTAACACCACCGACAAGGAGCTAG 739
                                                                                                                                                                                                                                                                                                                                                CGCTAACACCACCGACAAGGAGCTAG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome mapping; human; probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-2002; 2002US-0370349F.
08-APR-2002; 2002US-0370969F.
12-APR-2002; 2002US-0370969F.
30-MAY-2002; 2002US-0374739F.
30-MAY-2002; 2002US-00166619.
15-AUG-2002; 2002US-00403748F.
04-NOV-2002; 2002US-00287226.
31-MAR-2003; 2003US-00403161.
                                                                                                                                                                                                                                                                                                                                                                                                         ADK51126 standard; DNA; 26 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-2003; 2003WO-US010142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002US-00115479
  31-MAR-2003; 2003US-00403161
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                            WPI; 2003-812539/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003083046-A2
                                                                                                                                                                                                                                                     the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gorman L,
                                                                                                                                                                                                                                                                                                                                                                                                                              ADK51126;
                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 171
ADK51126
                                                                                                                                                                                                                                                                                                                Matches
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This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NOVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of an oligonucleotide probe which was used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer; chromosome mapping; human; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New NOVX polypeptide, useful for preparing a composition for treating or
                                                                                                                                               or
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Spytek KA;
                                                                                                                                            New NOVX polypeptide, useful for preparing a composition for treating preventing e.g. cancer or for chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Edinger SR, Patturajan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Casman SJ,
MP, Li L,
Patturajan N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOVX protein-related oligonucleotide probe SeqID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 BP; 10 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson DW, Bento P, Boldog FL, Burgess CE, Gorman L, Gould-Rothberg BE, Gunther E, Heyes Stone DJ, Zhong M, Malyankar UM, Edinger SR, Rothenberg ME, Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.7%; Score 26; DB 1; Lo
100.0%; Pred. No. 1.2e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                         Example C; SEQ ID NO 147; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1306 AAAGACGATGCCACTGACAAGGACCT 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAAGACGATGCCACTGACAAGGACCT 26
Stone DJ, Zhong M, Malyankar UM,
Rothenberg ME, Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-APR-2002; 2002US-00115479.

05-APR-2002; 2002US-0370349P.

08-APR-2002; 2002US-0370969P.

12-APR-2002; 2002US-0372019P.

22-APR-2002; 2002US-0374379P.

30-MAY-2002; 2002US-0374379P.

31-AUG-2002; 2002US-00160619.

15-AUG-2002; 2002US-0403748P.

04-NOV-2002; 2002US-0403748P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADK51123 standard; DNA; 26 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2003; 2003US-00403161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-812539/76.
                                                                                          WPI; 2003-812539/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003083046-A2.
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The present invention describes a method for the inspection of flat epithelial cells in which it is judged that flat epithelial cancer when the separated from an organism can proceed to flat epithelial cancer when the class has been in fibroblast growth factor receptor (FGFR) gene of the cells is mutated from guanine to thymine. Also described is a method for screening treating or preventive agents for flat epithelial cancers in which a candidate substance of treating gent for flat epithelial cancer is applied to flat epithelial cancer cells producing FGFR protein in which the 2128th (exon 17) amino acid in FGFR3 gene is mutated from guanine to thymine or the 697th amino acid is mutated from gyanine to thymine candidate substance is selected by using the facts that the 2128th base in the flat epithelial call FGFR3 gene after the capilication returned to guanine and that the 697th amino acid of FGFR3 protein produced returned to glycine as the indices. The method is used
                                                                        This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NOVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of an oligonucleotide probe which was used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inspection of flat epithelial cell, screening of treating or preventive agents for flat epithelial cancers, the treating or preventive agents for flat epithelial cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, fibroblast growth factor 3, FGF3, flat epithelial cell, cancer;
flat epithelial cell cancer; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                                                                                                                                                                         y Match 0.7%; Score 26; DB 1; Length 26; Local Similarity 100.0%; Pred. No. 1.2e+02; hes 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human fibroblast growth factor 3 PCR primer SEQ ID NO:1.
                                                                                                                                                                                                                                                                                         Sequence 26 BP; 9 A; 9 C; 6 G; 2 T; 0 U; 0 Other;
preventing e.g. cancer or for chromosome mapping
                                      SEQ ID NO 144; 433pp; English
                                                                                                                                                                                                                                                                                                                                                                                                               714 CGCTAACACCACCGACAAGGAGCTAG 739
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGCTAACACCACCGACAAGGAGCTAG 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZERI ) ZERIA SHINYAKU KOGYO KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACC79666 standard; DNA; 29 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-2001; 2001JP-00083352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                  the invention
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                                        Example C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACC79666;
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                          Matches
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for the inspection of flat epithelial cells. The present sequence represents a PCR primer for human FGFR3, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      including autoimmune diseases, degenerative nervous system diseases, graft versus host disease, hypersensitivity diseases, infectious diseases and neoplastic diseases. Autoimmune diseases include Addison's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atrophic gastritis. Degenerative nervous system diseases include multiple sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; T-cell associated disease; Vbeta; autoimmune disease; degenerative nervous system disease; graft versus host disease; Apperensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastritis, disease; atrophic gastritis, disease; type I hypersensitivity disease; type I hypersensitivity; doodpasture's syndrome; type II hypersensitivity; doodpasture's syndrome; type IV hypersensitivity; doodpasture's syndrome; type IV hypersensitivity; parasitic infections disease; viral infection; fillaria; bacterial infection; Mycobacterium; neoplastic disease; linaria; bacterial infection; Hymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Voeta gene, VbetaRNA or CDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a kit for diagnosing and treating T-cell
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                                                                                                              0.7%; Score 25.8; DB 1; Length 29; 93.1%; Pred. No. 1.46+02; tive 0; Mismatches 2; Indel8
                                                                               Sequence 29 BP; 8 A; 9 C; 6 G; 6 T; 0 U; 0 Other
                                                                                                                                                                                            1049 TGGAGTCCAACGCGTCCATGAGCTCCAAC 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 665; 164pp; English.
                                                                                                                                                                                                                     1 TGGAATTCAACGCGTCCATGAGCTCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Vbeta gene repeat sequence #261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00309335.
95US-00531241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00263959
                                                                                                                                                                                                                                                                                                                        ADH70471 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                       Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-059052/06
                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        breast cancer; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROWE/) ROWEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002150891-A1.
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19-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                               ADH70471;
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                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                     RESULT 174
ADH70471
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TGTGTGTGTGTGTGTGTGTGTGTGT 2346

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The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AAZ98483-514 represent sequences from Haliotis discus, used in the method
                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
               allergies, Type II hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infectious diseases include viral infections caused by viruses such as HVV, fungal infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Wheta gene repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Satellite sequence, DNA fragmentation; microsatellite DNA; DNA marker;
                                                                                                                                                                                                                                                                           Gaps
hypersensitivities such as contact with allergens that lead to
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                   0.7%; Score 25.8; DB 1; Length 29; 93.1%; Pred. No. 1.4e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30 BP; 15 A; 13 C; 0 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                 Sequence 29 BP; 0 A; 0 C; 14 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                          Local Similarity 93.1%;
nes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ98502 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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The sequence is that of a bovine microsatellite sequence obtd. by creening a library of bovine MboI DNA fragments of between 250 and 500 screening a library of bovine MboI DNA fragments of between 250 and 500 comparing the an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and specification and indexed herein (see below). The sequences upstream and comparizem of the microsatellite sequence were used to generate the microsatellite (using the program OPTIPRIM). The microsatellites may be microsatellity individuals, for parentage testing, and in the genetic conspicually important trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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0.7%; Score 25.4; I
Best Local Similarity 96.3%; Pred. No. 1.5e
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                        Microsatellite sequence from clone TGLA435.
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             30 rgrcrcrcrcrcrcrcrcrcrcrcrcrcr
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                                                                                                           AAQ34044 standard; DNA; 27 BP.
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                                                                                                                                                                                              (first entry)
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AAQ33678
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Score 25.8; DB 1; Length 30; Pred. No. 1.5e+02; 0; Mismatches 2; Indels

0; Mismatches

Query Match
Best Local Similarity 93.1%;
Matches 27; Conservative

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonuclectide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence information
c specification and indexed herein (see below). The sequence upstream and
compartneam of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTPRRM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
ceonomically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                   Polymorphic bovine DNA markers - mapping, and selective breeding.
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(first entry)
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02-FEB-1993
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The microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                             PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                      Microsatellite sequence from clone TGLA12.
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RESULT 178 AAQ33804

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Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                          Microsatellite sequence from clone TGLA417.
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     Маввеу ЈМ;
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02-FEB-1993
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      Georges M,
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cc by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of 50 clones cross-hybridised. Assuming independent distribution of 6 clones cross-hybridised. Assuming independent distribution of 6 clones cross-hybridised. Assuming independent distribution of 6 clones cross-hybridised. Assuming independent of 160 n. 9 microsatellites at >100, 000. The sequence information in the bovine genome is estimated at >100, 000. The sequence information comparison of the microsatellite sequence below). The sequence upstream and specification and indexed herein (see below). The microsate the required PCR primers for in vitro amplification of the corresp.

The microsatellite (using the program OPTIPRIM). The microsatellites may be microsatellite (using the program OPTIPRIM). The microsatellites may be committy individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of connecting see also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN 8\$8888888888888888**8** The sequence is a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an Library of bovine Mbol DNA fragments of between 250 and 500 bp with an comparing the sequence of the contes cross. The frequency of (76) is a microsatellites and Mbol stees, the frequency of (76) is microsatellites in the bovine genome is stemated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein see below). The sequences upstream and downstream of the microsatellite sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primars for in vitro amplification of the corresp. microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals; for parentage testing, and in the genetic mapping of economic trait sets for cattle, to allow selective breeding. See also AAQ31501-34437. (Updated on 250 25-MAR-2003 to correct PN field.) Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding. Gaps ; 0.7%; Score 25.4; DB 1; Length 27; 96.3%; Pred. No. 1.5e+02; rive 0; Mismatches 1; Indels Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other; 2318 TGTGTGTGTGTGTGTGTGTGTGT 2344 rererererererererererer Table 7; Page 403; 517pp; English. AAQ34012 standard; DNA; 27 (revised)
(first entry) Query Match 0.7 Best Local Similarity 96.3 Matches 26; Conservative

Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.
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0.7%; Score 25.4; DB 1; Length 27; 96.3%; Pred. No. 1.5e+02; tive 0; Mismatches 1; Indels
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02-FEB-1993
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on 25-MAR-2003 to correct PN field.)
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17-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-1996
                                                                                                                                                                                                                                                                                                  AAT65733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * Best Loca
                                                                                                                                                                                                                                RESULT 183
                                                                                                                                                                                                                                                   AAT65733/
                                                                                                                                                                                                                                                                 SXS
                                                                                                                                          ઠે
                                                                                                                                                                          g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents an oligonucleotide clamp which was used to bind a target sequence comprising a segment of the HIV pol and nef genes in single stranded or double stranded forms. This molecule forms a loop-and-branch comfigurartion. An oligonucleotide clamp is a compound capable of forming a covalently closed macromolecule or a stable circular complex after specifically binding to the target polymucleotide. Oligonucleotide clamps generally comprise one or more oligonucleotide moieties capable of specific binding to the target molecule and one or more pairs of binding moieties covalently linked to the oligonucleotide moieties. Upon annealing of the oligonucleotides moieties to the target polymucleotide, the binding moieties of a pair are bought into juxtaposition so that they form a stable covalent or non-covalent linkage or complex. The interaction of the binding moieties effectively clamps the specifically annealed oligonucleotide moieties to the target polymucleotide. (Updated
                                                                                                                                                                             ö
                                                     ď
used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthesis of branched polymers and novel branched polymeric structures used as molecular probes esp. for detecting poly-nucleotide(s).
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide clamp 1, containing loop-and-branch forming region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
                                                                                                                                                                             ..
0
                                                                                                                                     Score 25.4; DB 1; Length 27;
Pred. No. 1.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/note= "Modified with -OP(O-) (=O)S"
                                                                                                        Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "Modified with SP(O-) (=0)-"
                                                                                                                                                                                                            2318 TGTGTGTGTGTGTGCGTGTGTGTGT 2344
                                                                                                                                                                                                                                1 TGTGTGTGTGTGTGTGTGTGTGTGT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Page 33; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-US007557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYNX-) LYNX THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-00087386.
                                                                                                                                         0.78;
                                                                                                                                                                                                                                                                                                                                     AAQ83951 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                           26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-060944/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified_base
                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
04-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gryaznov SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                        AAQ83951;
                                                                       field.)
                                                                                                                                                                                                                                                                                                    RESULT 182
AAQ83951/c
                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of polymorphic genetic markers of the form (dC-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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16.3%; Pred. No. 1.5e+02;
ve 0; Mismatches 1; Indels '
                                                                    Score 25.4; DB 1; Length 27; Pred. No. 1.5e+02;
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat sequence from polymorphic marker clone Mfd31.
Sequence 27 BP; 13 A; 14 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 BP; 14 A; 13 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                              Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                     2319 GTGTGTGTGTGTGTGTGTGTGTGTG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2318 TGTGTGTGTGTGTGTGTGTGTGT 2344
                                                                                                                                                                                                                                                                                          27 drerererererererererere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89US-00341562.
91US-00754351.
                                                                        0.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT65733 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                Query Match
Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 96.3
Les 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
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RESULT 185

27 TGTGTGTGTGTGTGTGTGTGTGT 1

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The invention relates to compositions for the treatment of cancers, comprising purified hyaluronic acid (HA) and a second antineoplastic comprising purified hyaluronic acid (HA) and a second antineoplastic agent such as Mycobacterium phile! DNA, and you a synthetic wall complex, a cytotoxic chemotherapeutic drug or a synthetic cationer of the cytoxines interleakine, (IL-6) and IL-12 by immune system cells. In combination, HA and the second antineoplastic agent of the composition act synergistically to potentiate each other's ability to inhibit act syneightically to potentiate each other's ability to inhibit brownen the HA and the second antineoplastic agent, a reduced standard composition and induce apoptosis in cancer cells. Due to the synergy complexed the second antineoplastic agent can be used without compromising the therapeutic effectiveness of the cancer treatment of drug complexed composition in cose helps to reduce adverse side-effects and the development of drug cresistance or immunosensitisation, thereby improving the quality of life commotherapeutic drugs are expensive, the combined use of HA and a chemotherapeutic drugs are expensive, the combined use of the ancer treatment. The increase in dose effectiveness, decrease in toxicity and composition in the change of the increase in dose effectiveness, decrease in toxicity and content of the increase in dose effectiveness, decrease in toxicity and content of the content of the mannals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             decrease in cost address provide important benefits for mammals, including humans. The present sequence represents a synthetic antineoplastic oligonucleotide which was used in a composition with HA in an exemplification of the invention
                                                                                                                                                                                       Antineoplastic oligonucleotide; hyaluronic acid; HA; cytokine production; interleukin; IL-6; IL-12; synergistic action; standard dose reduction; side-effect reduction; drug resistance reduction; immunosensitisation reduction; cancer; tumour; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synergistic compositions comprising hyaluronic acid and Mycobacterium phlei DNA and cell walls, useful for treating cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                               Synthetic antineoplastic oligonucleotide, SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27 BP; 0 A; 0 C; 14 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BION-) BIONICHE LIFE SCI INC.
                     AAH24300 standard; DNA; 27 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-2000; 2000WO-CA001562.
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Matches 26; Conservative
                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Filion MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-408766/43.
                                                                                                                                                                                                                                                                                                                                                            WO200147561-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phillips NC,
                                                                                                         21-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2001.
                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                 AAH24300;
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The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 invention. The invention relates to a composition, comprises multiple base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple base 3'-OH, 5'-OH synthetic oligonucleotide which compositions of the part of dinucleotides auch as GT, TG, etc., according to specific compositions of the are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour of necrosis factor (TNF) alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, and secondary sarcoma cancer. The compositions induce apoptosis independent of Fas, p53/p21, p21,waf-1/CIP, p15(ink4), drug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                      Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNP; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27 BP; 0 A; 0 C; 14 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BION-) BIONICHE LIFE SCI INC.
             AAH46017 standard; DNA; 27 BP.
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29-AUG-2000; 2000US-0228925P.
                                                                                                                                                                                                                                                                                                                                                                   12-DEC-2000; 2000WO-CA001467.
                                                                                                                         Synthetic oligonucleotide 17.
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                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phillips NC, Filion MC;
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                                                                                                                                                                                                                                                                                             WO200144465-A2.
                                                                                       12-SEP-2001
                                                                                                                                                                                                                          lymphoma; ss
                                                                                                                                                                                                                                                                                                                                  21-JUN-2001.
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                                                                                                                                                                                                                                                            Synthetic.
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                                                  AAH46017;
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AAH46017
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12-DEC-2000; 2000WO-CA001467.

WO200144465-A2.

Synthetic.

21-JUN-2001

99US-0170325P.

13-DEC-1999;

BION-) BIONICHE LIFE SCI INC 29-AUG-2000; 2000US-0228925P.

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The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3 -044, 5 -04 synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT. TG, etc., according to specific composition and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, cytokines such as interleukin (IL) -1 beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNP) -alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis resistance, caspase 3, transforming growth factor (TGP) -beta 1 receptor and hormone dependence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                             Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                               Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic oligonuclectide; dinuclectide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25.4; DB 1; Length 27;
Pred. No. 1.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27 BP; 0 A; 0 C; 14 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2319 GTGTGTGTGTGTGTGTGTGTGTGTGTG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 16; 77pp; English.
                 Synthetic oligonucleotide 1.
                                                                                                                                                                                                                                                                                                                           (BION-) BIONICHE LIFE SCI INC
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                                                                                                                                                                                                                                                                        13-DEC-1999; 99US-0170325P.
29-AUG-2000; 2000US-0228925P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic oligonucleotide 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH46005 standard; DNA; 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 96.3
nes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                           Filion MC;
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-398150/42.
                                                                                                                                                                      WO200144465-A2.
                                                                                                                                                                                                                                                                                                                                                         Phillips NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lymphoma; ss.
                                                                                                     lymphoma; ss
                                                                                                                                                                                                      21-JUN-2001.
                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH46005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caspases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3 - OH, 5'-OH synthetic oligonucleotide which comprises multiple crepeats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspasses and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNF) alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
                                                                                                                                                                                                                                                                             Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.7%; Score 25.4; DB 1; Length 27; 96.3%; Pred. No. 1.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318 TGTGTGTGTGTGTGTGTGTGTGTGT 2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 rerererererererererererer 27
                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 16; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF60473 standard; DNA; 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide clamp #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide clamp; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Conservative
                                                                                                                                                                                                                   Phillips NC, Filion MC;
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The present invention relates to a method for synthesising a branched or multiply connected macromolecular structure, comprising oligonucleotide clamps (OC). The macromolecular structure is capable of specifically binding to a target molecule, and can therefore be used as probes. At least one OC comprises a target binding sequence that binds specifically and stably with the target molecule, and at least two OCs comprise signal generation moieties capable of generating a detectable signal in the presence of the target molecule. In addition the OCs are connected to one present sequence is an OC used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; T-cell associated disease; Vbeta; autoimmune disease; hypersensitivity disease; infectious disease; neoplastic disease; hypersensitivity disease; infectious disease; neoplastic disease; degenerative nervous system disease; multiple sclerosis; disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; allergy; type II hypersensitivity; Goodpasture's syndrome; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                                                Synthesizing branched nucleic acids useful as diagnostic and molecular probes, involves combining first units having haloalkylamino groups and second units having thiol or phosphorothicate groups.
                                                                                                                                                                                                                                                                                                                                                                                                       Score 25.4; DB 1; Length 27; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                         Sequence 27 BP; 13 A; 14 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2319 GTGTGTGTGTGTGCGTGTGTGTGTG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Vbeta gene repeat sequence #366.
                                                                                                                                                                   Disclosure; Col 29-30; 20pp; English.
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95US-00531241.
                                                                                                                                                                                                                                                                                                                                                                                                           0.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Conservative
                                                                          WPI; 2001-201911/20
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                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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Ε
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             (FARB ) BAYER CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROWE/) ROWEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2002150891-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                           Horn T;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers consciented diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Voete gene. Obseration and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, including autoimmune diseases, infectious diseases and neoplastic diseases. Autoimmune diseases influde Addison's disease. Controphic gastritis. Degenerative nervous system diseases include multiple atrophic gastritis. Degenerative nervous system diseases include multiple controphic gastritis. Degenerative nervous system diseases include multiple controphic gastritis and halpingues. Hypersensitivity diseases include Type contact with allergens that lead to allergies, Type II hypersensitivities such as those contact with allergens that lead to contact with allergens that set those caused by viruses such as Huy. Importantial infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by contact with allergens such as those caused by hycobacterium. Neoplastic diseases include lymphoproliferative diseases contact sequence. The present sequence represents a Voeta gene repeat sequence.
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                                      Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.7%; Score 25.4; DB 1; Length 27;
96.3%; Pred. No. 1.5e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (dC-dA)n.(dG-dT)n polymorphic repeat sequence #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2318 rejerererererecerererer 2344
                                                                                                                                           Disclosure; SEQ ID NO 770; 164pp; English.
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ID AAT66066 standard; DNA; 30 BP.
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              WPI; 2004-059052/06
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-1994;
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18-JUN-1997
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Gaps ö

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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. The repeats, when canalysed, fall into 4 categories: 1) perfect repeats which are alternating tandem CA repeats with no interruptions and without adjacent repeats of another sequence; 2) imperfect repeats which are defined as 2 or more runs of uninterrupted CA repeats separated by no more than 3 consecutive non-repeat bases; 3) compound perfect repeats which are runs of CA separated by no more than 3 consecutive non-repeat bases; 3 compound perfect repeats which are repeats from a run of at least 5 uninterrupted dinucleotide or least 10 uninterrupted mononucleotides; and 4) imperfect compound repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 runs of CA are interrupted. This sequence is an example of an imperfect repeat sequence of structure: (CA)5G(ACA)G(AC)7A. (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; T-cell associated disease; Wheta, autoimmune disease; degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease, atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzhaimer's disease, hypersensitivity disease; type I hypersensitivity; doodpasture's syndrome; type II hypersensitivity; doodpasture's syndrome; type IV hypersensitivity; leprosy; infectious disease; viral infection; HIV; fungal infection, Candida; parasitic infection; schiktosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                                                        Detection of polymorphic genetic markers of the form (dC-dA) n(dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which are defined as for the perfect compound repeats except that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.7%; Score 25.2; DB 1; Length 30; 00.0%; Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30 BP; 15 A; 13 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
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                                                                                                                                                                                  Example 8; Col 57-58; 186pp; English
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95US-00531241.
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Matches 27; Conservative
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to correct PF field.)
WPI; 1997-042299/04
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ADH70406
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DT 25-WAR
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DE Human;
XW human;
XW human;
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Gaps

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The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers pecifically priming and allowing amplification of each Vbeta gene, VbetaRNA or CDNA. The kit is useful for diagnosing organ transplant respection and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, infectious diseases, and neoplastic diseases. Autoimmune diseases include Addison's disease, arrophic gastritis. Degenerative nervous system diseases include multiple atrophic gastritis begenerative nervous system diseases include multiple of arrophic gastritis and cases. Hypersensitivity diseases include Type I hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those caused by arranses such as HIV, fungal infections such as those caused by the yeast genus Candida, parasitic infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                      Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibroblast growth factor 3 receptor; FGFR3; mutant; detection; cancer; carcinoma; lung cancer; breast cancer; colon cancer; skin cancer; bladder; cervix; human; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25.2; DB 1; Length 30; Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30 BP; 1 A; 1 C; 13 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                               Disclosure; SEQ ID NO 600; 164pp; English.
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 90.0 Matches 27; Conservative
                                                                    WPI; 2004-059052/06
(ROWE/) ROWEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200068424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2001
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                                  Hood LE,
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1011 CAAGATCTCCCGCTTCCCGCTCAAG 1035
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                                 Example 4; Page 14; 41pp; English.
                                                                                                                                                                                                                                                                  (CURI-) INST CURIE.
(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                              04-MAY-2000; 2000WO-EP004591.
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                                                                                                                                                        AAA54586 standard; DNA; 25
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                Chopin D,
                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                           WPI; 2001-016103/02.
    WPI; 2001-016103/02
                                                                                                                                                                                                                            WO200068424-A2
                                                                                                                                                                                                                                                        05-MAY-1999;
                                                                                                                                                                                                                                                                                 Cappellen D,
                                                                                                                                                                            11-APR-2001
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                                                                                                                                                                                                                   Synthetic
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                                                                                                    Query Match
                                                                                                              tches
                                                                                                                                               RESULT 19
AAA54586/
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The present invention describes a method for determining if an individual has a tumour cell or site of angiogenesis, or if a treatment is effective in changing angiogenesis or changing a status of a set of target cells, comprising determining if a sample of the subject has an expression product of at least one marker gene. Also described is a compound capable of altering the expression or activity of Keratin 14, TIE 1, Salioadhesin or Siglec in a cell. Peripheral blood mononuclear cell (PBMC)-expressed Keratin 14, TIE 1, Salioadhesin or Siglec, and kits containing them from the present invention can be used in a diagnostic method, particularly as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an indicator of angiogenesis or to determine presence of a tumour cell. The method of the invention is suitable to determine within a few days if a certain treatment against Kaposi's Sarcoma is successful. ABQ81851 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a certain treatment against Kaposi's Sarcoma is successful. ABQ81851 to ABQ82006 represent nucleotide sequence used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining presence of a tumor cell or angiogenesis, and the effectiveness of treatment, by detecting the presence of marker genes is useful to detect and monitor treatment of Karposi's Sarcoma.
of FGFR3 and so have an anti-proliferation effect on carcinomas can be used to treat cancer. Two primers (AAA54429, AAA54586) were used in PCR reactions on urine samples to detect the G372C mutation in FGFR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Kaposi's sarcoma; tumour; angiogenesis; PCR primer; ss.
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                                                                                                                                                                 Length 25;
                                                                                                                                                                                                                   0; Indels
                                                                                                         Sequence 25 BP; 5 A; 4 C; 11 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                           0.7%; Score 25; DB 1; Lu
100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaposi's Sarcoma TAG PCR primer SEQ ID NO:105.
                                                                                                                                                                                                                                                                        1011 CAAGAICTCCCGCTTCCCGCTCAAG 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; Page 23; 38pp; English.
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28-SEP-2001; 2001US-0325722P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                             Local Similarity 100.
nes 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1225233-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABQ81955;
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 194
                                                                                                                                                                                                  Best Loc
Matches
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                                                                                                                                                                                                                                            The identification of fibroblast growth factor receptor 3 (FGFR3) mutations in a biological sample such as tissue, bone marrow or body fluid e.g. urine, from a warm-blooded animal, preferably human is useful for diagnosing carcinomas such as human bladder and cervix carcinomas, or cancers associated with lung, breast, colon and skin. The pharmaceutical preparations comprising agents which inhibit the synthesis and expression of FGFR3 and so have an anti-proliferation effect on carcinomas can be used to treat cancer. Two primers (AAA54430, AAA54587) were used in PCR reactions on urine samples to detect the Y375C mutation in FGFR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing carcinoma e.g. bladder or cervix carcinomas in a biological sample such as tissue, bone marrow or body fluid, preferably from animal or human, by identifying fibroblast growth factor receptor 3 mutations.
                                                                                      Diagnosing carcinoma e.g. bladder or cervix carcinomas in a biological sample such as tissue, bone marrow or body fluid, preferably from animal or human, by identifying fibroblast growth factor receptor 3 mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer used for detecting mutant fibroblast growth factor receptor 3. \dot{\ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fibroblast growth factor 3 receptor; FGFR3; mutant; detection; cancer; carcinoma; lung cancer; breast cancer; colon cancer; skin cancer; bladder; cervix; human; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 0.7%; Score 25; DB 1; Length 25; 1 Similarity 100.0%; Pred. No. 1.5e+02; 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 5 A; 4 C; 11 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Radvanyi F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGATCTCCCGCTTCCCGCTCAAG 1
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1648 GTGACCGAGGACAACGTGATGAAGA 1672

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OPTIPRIM; breeding; cattle; parentage; amplification; ss.

Microsatellite sequence from clone TGLA255.

PCR; selection; primers; genetic mapping; traits;

WO9213102-A1

Bos taurus.

06-AUG-1992.

(first entry)

(revised)

25-MAR-2003 02-FEB-1993

AAQ33843;

92WO-US000340. 91US-00642342

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The invention relates to a novel method for determining whether a treatment is effective in changing a status of a certain set of target cells in an individual. The method comprises obtaining a sample from an individual after initiation of the treatment; and determining whether the sample comprises an expression product of at least one marker gene. The marker gene and a proteinaceous molecule (which can bind to the protein derived from the marker gene of the invention) are useful for determining whether a treatment is effective in counteracting a tumour in an individual, especially Kaposi's Sarcoma. Peripheral blood mononuclear cell in (PBMC) expressed Keratin 14, TIE I, Salioadhesin, or Siglec I sequences or a fully defined sequence given in the specification, or their analogues are useful as indicators for angiogenesis and for their analogues are useful as indicators for angiogenesis and for product of a gene comprising a marker gene of the invention is useful as a drug target. The compound is useful for preparing a medicament. This polymucleotide sequence represents a PCR primer of a Kaposi's Sarcoma tag
                                                                                                                                                                                                                                                                                             marker gene; tumour; Kaposi's Sarcoma; peripheral blood mononuclear cell; PBMC; expressed keratin 14; TIE 1; Salioadhesin; Siglec 1; angiogenesis; drug target; tag; SAGE library; KS3; KS4; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining whether a treatment is effective in changing a status of a certain set of target cells in an individual comprises determining whether the sample comprises an expression product of at least one marker
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                        Kaposi's sarcoma tag PCR primer, SEQ ID No 107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 107; 94pp; English.
                          GTGACCGAGGACAACGTGATGAAGA 25
Van Der Kuyl AC, Cornelissen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-2001; 2001EP-00203703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-2001; 2001EP-00203703
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                                                                                                                              ADC13440 standard; DNA; 25
                                                                                                                                                                                                               18-DEC-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                          EP1298221-A1
                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                     ADC13440;
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Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

Georges M, маввеу JM;

(GENM-) GENMARK. .5-JAN-1991; 15-JAN-1992;

WPI; 1992-284684/34.

Table 7; Page 267; 517pp; English.

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 and and a (TC)15 and an (AC)15 and a (TC)15 and an (AC)10 and a (TC)15 and an (AC)10 and a (TC)10 and a (
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28 BP; 0 A; 1 C; 13 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2319 GTGTGTGTGTGTGTGTGTGTGTGT 2346
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Best Local Similarity
Matches 26; Conservat
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02-FEB-1993
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Gaps ;

1648 GIGACCGAGGACAACGIGAIGAAGA 1672

Local Similarity 100. nes 25; Conservative

Matches

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GTGACCGAGGACAACGTGATGAAGA 25

AAQ33843 standard; DNA; 28 BP.

RESULT 196 AAQ33843 ID AAQ3

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The sequence is that of a bovine microsatellite sequence obtd. by

creening a library of bovine MboI DNA fragments of between 250 and 500

creening a library of bovine MboI DNA fragments of between 250 and 500

creening an intervent of a (TC)15 oligonucleotide probe. One out of 50

clones cross-hybridised. Assuming independent distribution of

microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

control of the microsatellites is summarised in the sequence information

for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequence upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

concoratellite (using the program OPTIPRIM). The microsatellites may be microsatellite (using the program OPTIPRIM). The microsatellites may be mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 24.4; DB 1; Length 26; 96.2%; Pred. No. 1.8e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2319 GTGTGTGTGTGTGTGTGTGTGTGT 2344
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                                                                                                                                                             Table 7; Page 203; 517pp; English
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                                            Georges M, Massey JM;
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                                                                              WPI; 1992-284684/34.
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Best Local Similarity
               (GENM-) GENMARK.
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02-FEB-1993
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screening a library of bovine MboI DNA fragments of between 250 and 500
c by with an (ACI)5 and a (TC)15 oligomuclecide probe. One out of 50
c lones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
c required genome is estimated at >100, 000. The sequence information
c specification and indexed herein (see below). The sequence upstream and
downstream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program oPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
c mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 26;
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Pred. No. 1.8e+02;
0; Mismatches 1;
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Best Local Similarity 96.2%
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                                                                                                                                                                              (GENM-) GENMARK.
                                                                                                               .5-JAN-1992;
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02-FEB-1993
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                 Bos taurus.
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                            The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonuclectide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (TG)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine ganome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and
                                                                                                                                                specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required FCR primers for in vitro amplification of the corresp.

microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economic traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 24.4; DB 1; Length 26; 96.2%; Pred. No. 1.88+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
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Table 7; Page 211; 517pp; English.
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02-FEB-1993
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Matches
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downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                    0; Mismatches
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Best Local Similarity 96.2
Matches 25; Conservative
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(first entry)

29-JUL-2004

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
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                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
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   Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26 BP; 12 A; 12 C; 2 G; 0 T; 0 U; 0 Other;
0.6%; Score 24.4; DB 1;
96.2%; Pred. No. 1.8e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2319 GTGTGTGTGTGTGTGTGTGTGTGT 2344
                                                                                                                                     2318 TGTGTGTGTGTGTGTGTGTGTGTG 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
                                                                                                                                                                                                    1 rerererererererererere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 19; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JAN-2001; 2001NZ-00509194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-DEC-1999; 99AU-00004907
28-MAR-2000; 2000AU-00006520
                                                                                                                                                                                                                                                                                                                                                                            AA164469 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                   Local Similarity 96.2
nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koelliker R, Forster JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-431058/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSR motif #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NZ509194-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI64469;
          Query Match
                                                                                                                                                                                                                                                                                                  RESULT 202
AAI64469/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                      Matches
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ADO81053 standard; DNA; 26 BP

RESULT 203
ADO81053/c
ID ADO8109
XX
AC ADO8109

ADO81053;

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The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DNA region of (I) that includes PML, using as template a DNA sample containing at least one segment of (I); and determining the length of the resulting amplicon(s). Also described are: a method of determining (M2) microsatellite markers (MM) for predisposition to a disease, associated with a gene that includes one or more PML, and prediagnosis (M3) of diseases associated with gene that include PML. The method is used to identify microsatellite markers, in a include PML. The method is used to identify microsatellite markers, in a conclude PML. The method is used to identify microsatellite markers, in a conclude PML. The method is used to identify microsatellite markers, in a conclude PML. The method is used to identify microsatellite markers, in a conclude PML. The method is such diseases, especially prion diseases but also cystic fibrosis, malignant hyperthermia syndrome in pigs and method of season of seasons in the method is simpler, quicker and particularly less expensive than known methods based on sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the cow prion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                    gene typing; polymorphic microsatellite loci; PML; disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; cow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence represents a primer used to genotype a region of th
protein (PrP) comprising a polymorphic microsatellite locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24.4; DB 1; Length 26;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26 BP; 13 A; 13 C; 0 G; 0 T; 0 U; 0 Other;
                                                     Cow prion protein microsatellite locus primer #65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microsatellite sequence from clone TGLA15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2318 IGTGTGTGTGTGTGTGTGTGTG 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 rererererererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 27; 64pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Han Y;
                                                                                                                                                                             microsatellite; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%;
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                                                                                                                                                                                                                                                                                                                                     09-AUG-2002; 2002DE-01036711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 96.2
Matches 25; Conservative
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02-FEB-1993
                                                                                                                                                                                                                                                                                               26-FEB-2004.
                                                                                                                                                                                                                   Bos taurus.
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                                                                                                                                                                                                                                                        The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MooI DNA fragments of between 250 and 500 by this and (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at .>100,000. The sequence information of a pecification and indexed herein (see below). The sequence information commistream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The propriet of the microsatellite sequence were used to generate the microsatellite (using the program OPTTRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                     Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Local Similarity 96.2%; Pred. No. 2.5e+02;
Les 25; Conservative 0; Mismarchan
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34 BP; 0 A; 0 C; 17 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsatellite sequence from clone GBPRLGR.
           genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rGTGCGTGTGTG 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 rererererererererererere 26
                                                                                                                                                                                                                                       Table 7; Page 223; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ33630 standard; DNA; 29 BP
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                                                                                             92WO-US000340
                                                                                                                   91US-00642342
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                                                                                                                                                              Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2318 TGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                   WPI; 1992-284684/34.
                                                                                                                                        GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9213102-A1.
                                                                                                                   15-JAN-1991;
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                                                    WO9213102-A1
                                                                                             15-JAN-1992;
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02-FEB-1993
                                                                         06-AUG-1992
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                               Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (ACI)5 and a (TCI)5 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 210 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence information
for ca. 210 such bovine microsatellite sequence water used to generate the
specification and indexed herein (see below). The sequences upstream and
commercem of the microsatellite sequence water used to generate the
microsatellite (using the program opplied). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genese involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibroblast growth factor receptor; FGFR3; achondroplasia; antagonist; malignant cell transformation; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer used in generation of FGFR3 G380R achondroplasia mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening assay for antagonists of fibroblast growth factor receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24.2; DB 1; Length 29;
Pred. No. 2.2e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 29 BP; 1 A; 0 C; 13 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2315 GTCTGTGTGTGTGTGTGTGTGTG 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reznitsky D, Ben-Levy R;
                                                                                                                                                                                                                                                                                                                                                                                                                              Table 7; Page 181; 517pp; English
                                                                                                                                                                                                                                                                                                                                                         mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (YEDA ) YEDA RES & DEV CO LTD. (PROC-) PROCHON BIOTECH LTD.
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91US-00642342.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.7%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA72753 standard; DNA; 29
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                                                                                                                                                       Georges M, Massey JM;
                                                                                                                                                                                                                                 WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-514956/46.
                                                                         (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200046343-A2.
15-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fayon A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA72753;
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This invention relates to an in vitro screening assay for an antagonist of fibroblast growth factor receptor (FGFR)-mediated malignant cell transformation. The assay comprises: (a) providing a stable cell line corresponding a stable cell line and proper stable cell line corresponding to the FGFR, or 3, where the malignant potential of he cell line is modulated by the FGFR, (b) condidate antagonist; and (c) measuring an FGFR downstream signalling event, where an antagonist. The present sequence represents a PCR primer downstream signalling event. The FGFR3 achondroplasia G380R mutant. The cresulting DNA encoding mutant FGFR3 a schondroplasia G380R mutant. The cresulting DNA encoding mutant FGFR3 is used in the construction of a cell line for use in the assay of the invention. The method is useful for in vivo and in vitro screening of antagonist of FGFR-mediated malignant cell transformation and tumor formation and progression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention concerns an anti-Tie (Tyrosine kinase-Immunoglobulin like domain-EGF (epidermal growth factor) homology domain) monoclonal antibody (MAb) which specifically recognises the Tie extracellular domain, and a hybridoma producing it. The MAb can be used in the diagnosis of leukaemia and also in separation and concentration of haematopoietic stem cells. The MAb can also be used to detect and determine levels of (soluble) Tie. AAT33121-22 are primers used to amplify a 160 bp probe based on a
mediated malignant cell transformation and tumor formation, by using stable cell lines expressing recombinant or wild type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-Tie monoclonal antibody and hybridoma producing it - useful in diagnosis of leukaemia and detection of haematopoietic stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-Tie monoclonal antibody; extracellular domain; hybridoma; Tyrosine kinase-Immunoglobulin like domain-EGF homology domain; pedidermal growth factor; leukaemia; diagnosis; separation; haematopoietic stem cells; detection; primer; probe; PCR; amplify; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 29 BP; 6 A; 7 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24.2; DB 1;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5' primer to amplify 160 bp probe for Tie gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 896 CAGGCATCCTCAGCTACGGGGTGGGCTTC 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 caddaarrcrcadcracaddaddadacrrc 29
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                                                                 Disclosure; Page 22; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YAMA ) YAMANOUCHI PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT33121 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94JP-00308249.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 89.7 es 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-318959/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JUN-1996.
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT3312
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                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing carcinoma e.g. bladder or cervix carcinomas in a biological sample such as tissue, bone marrow or body fluid, preferably from animal or human, by identifying fibroblast growth factor receptor 3 mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                        Fibroblast growth factor 3 receptor; FGFR3; mutant; detection; cancer; carcinoma; lung cancer; breast cancer; colon cancer; skin cancer; bladder; cervix; human; primer; s8.
tyrosine kinase domain, to detect the human Tie gene from a UT-7 cDNA library. A 3933 bp cDNA clone, ptk-1, was identified, encoding a 1138 amino acid residue protein
                                                                                                                                                                                                                                                                                                                                                                                        Primer used for detecting mutant fibroblast growth factor receptor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                        Gaps
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                                                                                                 0.6%; Score 24; DB 1; Length 24; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 4 A; 7 C; 6 G; 7 T; 0 U; 0 Other;
                                                                     Sequence 24 BP; 3 A; 8 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ricol D,
                                                                                                                                                                          1622 GGGACCTGGCTGCCGCAATGTGC 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               597 CIGCAAGGIGTACAGIGACGCACA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Radvanyi F,
                                                                                                                                                                                             1 GGGACCTGCCCGCAATGTGC 24
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                           AAAS4427 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                          Query Match
Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chopin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-016103/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                  11-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                  AAA54427;
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                                                                                                                                                                                                                                                                 RESULT 208
                                                                                                                                                                                                                                                                                   AAA54427,
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Length 29;

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has a tumour cell or site of anglogenesis, or if a treatment is effective in changing anglogenesis or changing a status of a set of target cells, comprising determining if a sample of the subject has an expression product of at least one marker gene. Also described is a compound capable of altering the expression or activity of Keratin 14, TIE 1, Salioadhesin or Siglec in a cell. Peripheral blood monomuclear cell (PBMC)-expressed Keratin 14, TIE 1, Salioadhesin or Siglec, and kits containing them from the present invention can be used in a diagnostic method, particularly as an indicator of anglogenesis or to determine presence of a tumour cell. The method of the invention is suitable to determine within a few days if a certain treatment against Kaposi's Sarcoma is successfull. ABQBISI to ABQB2006 represent nucleotide sequence used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    marker gene; tumour; Kaposi's Sarcoma; peripheral blood mononuclear cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining presence of a tumor cell or angiogenesis, and the effectiveness of treatment, by detecting the presence of marker genes is useful to detect and monitor treatment of Karposi's Sarcoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for determining if an individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                  Human; Kaposi's sarcoma; tumour; angiogenesis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 24; DB 1; Length 24; 00.0%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 5 A; 4 C; 7 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaposi's sarcoma tag PCR primer, SEQ ID No 108.
                                                                                                                                 Kaposi's Sarcoma TAG PCR primer SEQ ID NO:106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. nv.
                                                                                                                                                                                                                                                                                                                                                                                                          (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1933 ACACACGACCTGTACATGATCATG 1956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 10; Page 23; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Der Kuyl AC, Cornelissen M;
                               ABQ81956 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                     23-JAN-2001; 2001EP-00200228.
28-SEP-2001; 2001EP-00203703.
28-SEP-2001; 2001US-0325722P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC13441 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                       23-JAN-2002; 2002EP-00075264
                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-668396/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention
                                                                                                                                                                                                                                     EP1225233-A2.
                                                                                                 19-NOV-2002
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2003
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                                                                 ABQ81956;
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The invention relates to a novel method for determining whether a treatment is effective in changing a status of a certain set of target cells in an individual. The method comprises obtaining a sample from an individual after initiation of the treatment; and determining whether the sample comprises an expression product of at least one marker gene. The marker gene and a proteinaceous molecule (which can bind to the protein derived from the marker gene of the invention) are useful for determining whether a treatment is effective in counteracting a tumour in an individual, especially Kaposi's Sarcoma. Peripheral blood mononuclear cell (PBMC) expressed keratin 14, TIE 1, Salioadhesin, or Siglec 1 sequences or a fully defined sequence given in the specification, or their analogues are useful as indicators for angiogenesis and for their analogues are useful as indicators for angiogenesis and for product of a gene comprising a marker gene of the invention is useful as a drug target. The compound is useful for preparing a medicament. This polynucleotide sequence represents a PCR primer of a Kaposi's Sarcoma tag
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                                                                                                                                                                                                                                                                                                                                            Determining whether a treatment is effective in changing a status of a certain set of target cells in an individual comprises determining whether the sample comprises an expression product of at least one marker
PBMC; expressed keratin 14; TIE 1; Salioadhesin; Siglec 1; angiogenesis;
drug target; tag; SAGE library; KS3; KS4; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; 88.
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100.0%; Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microsatellite sequence from clone TGLA47.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 108; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1933 ACACACGACCTGTACATGATCATG 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 ACACACGACCTGTACATGATCATG
                                                                                                                                                                                                                                                                        Cornelissen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР
                                                                                                                                                              28-SEP-2001; 2001EP-00203703.
                                                                                                                                                                                                28-SEP-2001; 2001EP-00203703.
                                                                                                                                                                                                                                    (PRIM-) PRIMAGEN HOLDING BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ34077 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                           WPI; 2003-589342/56.
                                                                                                                                                                                                                                                                        Van Der Kuyl AC,
                                                    Unidentified
                                                                                      EP1298221-A1
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02-FEB-1993
                                                                                                                          02-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                    gene.
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The probe was used to screen a human placental lambda gt11 cDNA library for the gene encoding baaic FGF receptor. It was designed from the partial cDNA clone published by Ruta et al, 1988. See also AAQ13308-Q13311. (Updated on 25-MAR-2003 to correct PA field.)
     Extracellular form of human fibroblast growth factor receptor treat tumours, abnormal angiogenesis e.g. diabetic retinopathy, rheumatoid arthritis and arteriosclerosis and as contraceptives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2316 TCTGTGTGTGTGTGTGCGTGTGTGTGTG 2345
                                                           Example 1; Page 11; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                                                                                                                                                                                    29-JUL-2004
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Matches
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XFFFXXXX0000X8
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                                                                                                                                                                                                            The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 correcting a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50 cones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information correction in the bovine microsatellite see below). The sequences upstream and specification and indexed herein (see below). The sequences upstream and commistream of the microsatellite sequence were used to generate the microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                    - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23.8; DB 1; Length 27; Pred. No. 2.38+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 BP; 1 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Basic fibroblast growth factor; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2319 GIGIGIGIGIGIGIGIGIGIGIGIG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe OAB984 for bFGF receptor DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FARM ) FARMITALIA ERBA SRL CARLO
                                                                                                                                                                                            rable 7; Page 362; 517pp; English.
                                                                                                                                                      Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90GB-00001466
                           92WO-US000340
                                                     91US-00642342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ13309 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                       Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-252611/34.
                                                                                                                                 WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                              GENM- ) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JAN-1990;
                              15-JAN-1992;
                                                      15-JAN-1991;
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28-OCT-1991
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   06-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ13309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant expression cassette comprising a promoter that is functional in plants, operably linked with a coding sequence and a non-plant 3' termination sequence, useful for gene expression in plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heterologous gene; expression cassette; gene expression; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer, UplCA used to construct heterologous 3'-termination DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                   / Match 0.6%; Score 23.6; DB 1; Length 30; Local Similarity 86.7%; Pred. No. 2.7e+02; Local 26; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33 BP; 4 A; 1 C; 11 G; 17 T; 0 U; 0 Other;
Sequence 30 BP; 5 A; 8 C; 11 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                           1963 TGCTGGCATGCCGCGCCCTCCCAGAGGCCC 1992
                                                                                                                                                                                                         30 TGCTGGCATGCAGTGCCTCACAGAGACCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; SEQ ID NO 62; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bertain S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                  BP
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                                                                                                                                                                                                                                                                                                                                                                                  ADO39641 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mcbride K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WILK/) WILKINSON J Q. (MCBR/) MCBRIDE K. (BERT/) BERTAIN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-374960/35.
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AAQ33918

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vivlemore401-10.rng

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
by with an (ACI)5 and a (TCI)5 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence information
for ca. 210 such bovine microsatellite sequence were used to generate the
sequired PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                          PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.6%; Score 23.4; DB 1; Length 25; Best Local Similarity 96.0%; Pred. No. 2.3e+02; Matches 1; Indels Matches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microsatellite sequence from clone TGLA354.
                                                                 Microsatellite sequence from clone MTGT13B.
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                     (first entry)
  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Georges M, Massey JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-284684/34.
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25-MAR-2003
02-FEB-1993
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02-FEB-1993
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                                                                                                                                                                                    Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (APO)15 and a (TC)15 oligonuclectide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence upstream and
downstream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTTRRIM). The microsatellites may be
cloned to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                            PCK; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;
                     rcrargrargrergrerrrergrergre 33
                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA327.
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                                                                                                                                    AAQ33918 standard; DNA; 25 BP
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                                                                                                                                                                                                                             (revised)
(first entry)
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus.
                                                                                                                                                                                  AAQ33918;
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Bos taurus

AAQ33642

AAQ33642 ID AAQ3 XX AC AAQ3 XX

RESULT 215

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Best Loca Matches

92WO-US000340

15-JAN-1992;

06-AUG-1992

WO9213102-A1

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 c. by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information concar, 230 such bovine microsatellites is summarised in the sequence information concar. 230 such bovine microsatellites sequence were used to generate the sequence Ack primers for in vitro amplification of the corresp.

The microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic microsatellite crait loci, or genes involved the determinism of economic traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23.4; DB 1; Length 25;
Pred. No. 2.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                           Table 7; Page 315; 517pp; English.
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1 Similarity 96.0%;
24; Conservative
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(first entry)
                                                                                                                                                     Massey JM;
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Best Local Similarity
                                                                                                                                                                                 WPI; 1992-284684/34.
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                                                                                                                       (GENM-) GENMARK
                                                                                         15-JAN-1991;
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02-FEB-1993
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Gaps

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleocide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites microsatellites microsatellites for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of
                                                                                                                                                                                                                                                                                                                                                                                        economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                    Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 0.6%; Score 23.4; DB 1; Length 25; 1 Similarity 96.0%; Pred. No. 2.3e+02; 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25 BP; 0 A; 0 C; 13 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2319 GTGTGTGTGTGTGTGTGTGTGTG 2343
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                                                                                                                          Table 7; Page 274; 517pp; English
                                                                                         mapping, and selective breeding.
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91US-00754351.
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(first entry)
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Georges M, Massey JM;
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Best Local Similarity
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05-SEP-1991;
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17-JUN-1997
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Disclosure; Col 9-10; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dG-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly (dG-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf32 which contains the repeat sequence is from formula: (AC)12A. (Updated on 25-MAR-2003 to correct PF field.) 0.6%; Score 23.4; DB 1; Length 25; 96.0%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels Sequence 25 BP; 13 A; 12 C; 0 G; 0 T; 0 U; 0 Other; 2318 TGTGTGTGTGTGTGTGTGTGT 2342 25 rerererererererererererer AAH38303 standard; DNA; 25 14-AUG-2001 (first entry) Local Similarity 96.0 108 24; Conservative WO200129262-A2. 15-OCT-1999; Homo sapiens 26-APR-2001. AAH38303; Query Match Matches RESULT 219 AAH38303 ઠે 셤

BP

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Gaps

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Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenemiarentecta; autoimmune disease; acute intermittent porphyria; rhoumacoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss. New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic SNP specific SNPE primer SEQ ID 1099. Claim 1; Page 55; 83pp; English. (ORCH-) ORCHID BIOSCIENCES INC. 13-OCT-2000; 2000WO-US028436. 99US-0160096P Picoult-Newburg L, Pohl M; WPI; 2001-290930/30. acid sample.

Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by

conting a single-nucleotide primer extension reaction. The coligonucleotides are useful for determining the presence, absence of identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus. Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, craits also include symptoms of or susceptibility to multifactorial cisease of which a component is or may be genetic such as autoimmune ciseases, including, rheumatoid arthritis, multiple sclerosis, confirmantion, cancer, nervous system diseases and infection by pathogenic inflammation, cancer, nervous system diseases and infections and conformation is or may be genetic investigations and microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a single nucleotide primer extension (SNPE) primer specific for a human SNP containing DNA ö The sequences given in AAQ47176-77 represent triplex forming oligonicleotides which bind to the mRNA sequence of the MRC diass II locus DR A structural gene at positions 851-86. The sequences given in AAQ47178-80 represent control oligomers which contain base compositions similar to that around this DR A region but not containing the correct sequences. DR A is a transplantation antigen. Binding of this sequence to the DR A gene inhibits antigen production. This method may be used for treating MHC; major histocompatability complex; class II; control oligomers; DR A; transplantation; antigen; autoimmune disease; 88. Depletion of transplantation antigens in donor cells - using anti-sense or triplex-forming oligonucleotide(s), used for treating auto-immune disease and in transplants. Gaps ö Score 23.4; DB 1; Length 25; Pred. No. 2.3e+02; Indels Sequence 25 BP; 0 A; 0 C; 13 G; 12 T; 0 U; 0 Other; Weiss TL, Garovoy MR, Hunt A, Huey B, Tam S; 0.6%; Scc. No. c.. 96.0%; Pred. No. c.. 2319 GTGTGTGTGTGTGCGTGTGTGT 2343 MHC DR A intron binding oligomer GTcon. 1 grererererererererere 25 Example; Page 22; 71pp; English. BP. 93WO-US000797. 92US-00830427. AAQ47179 standard; DNA; 26 (first entry) Matches 24; Conservative (REGC) UNIV CALIFORNIA. (revised) WPI; 1993-258367/32. Best Local Similarity 25-MAR-2003 25-JAN-1994 WO9314769-A1 29-JAN-1993; 31-JAN-1992; 14-SEP-1992; 05-AUG-1993 Synthetic. AAQ47179; Query Match RESULT 220 AAQ47179 \$ 셤 ઠે

Gaps

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Indels

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Mismatches

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Conservative
                                                                                                                                                                   25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                       Bos taurus.
         27;
                                                                                                                                             AAQ33933;
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                                                                                               RESULT 222
         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Glones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. Those clones where the repeat sequence has by primers AAT65798-T6647. Those clone where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf97 which contains the repeat sequence having the formula: CTCTCTCT(CA)11.5. (Updated on 25-MAR-2003 to correct PP
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expression of a transplantation antigen. It may also be used to produce cells which are more easily transplanted into a recipient. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of polymorphic genetic markers of the form (dG-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                               Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.6%; Score 23.4; DB 1; Length 33; 81.8%; Pred. No. 3.2e+02;
                                                                                               0.6%; Score 23.4; DB 1; Length 26; 96.0%; Pred. No..2.4e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33 BP; 11 A; 17 C; 0 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd97.
                                                                        Sequence 26 BP; 0 A; 0 C; 14 G; 12 T; 0 U; 0 Other;
                                                                                                                                                    2319 GIGIGIGIGIGIGIGIGIGIG 2343
                                                                                                                                                                         2 drdrdrdrdrdrdrdrdrdrdrd 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Col 11-12; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           hybridisation; chromosome; ds
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91US-00754351.
                                                                                                                                                                                                                                           AAT65770 standard; DNA; 33
                                                                                                                                                                                                                                                                                            (revised)
(first entry)
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                                                                                                       Query Match
Best Local Similarity 96.0
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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17-JUN-1997
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Best Local Similarity

Query Match

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The sequence is that of a bovine microsatellite sequence obtd. by

C screening a library of bovine MboI DNA fragments of between 250 and 500

C closes cross-hybridised. Assuming independent distribution of

C closes cross-hybridised. Assuming independent distribution of

C closes cross-hybridised. Assuming independent distribution of

C closes across-hybridised. Assuming independent distribution of

C closes across-hybridised. Assuming independent distribution of

C closes cross-hybridised. Assuming independent distribution of

C cross-230 such bovine microsatellites is summarised in the

C specification and indexed herein (see below). The sequences upstream and

C compacted pcR primers for in vitro amplification of the corresp.

C downstream of the microsatellite sequence wased to generate the

microsatellite (using the program OPTIPRIM). The microsatellites may be

C used to identify individuals, for parentage testing, and in the genetic

C used to identify individuals, for parentage testing, and in the genetic

C capping of economic trait loci, or genes involved the determinism of

C connomically important traits esp. in cattle, to allow selective

C breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.6%; Score 23.2; DB 1; Length 28; Best Local Similarity 89.3%; Pred. No. 2.8e+02; Matches 25; Conservative 0; Mismatches 3; Indels
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2319 GIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIGIG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2311 TTTGGTCTGTGTGTGTGTGTGTGTGT 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic mapping; traits; amplification; 88.
                                                                             33 Grererererererererereadadadadad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microsatellite sequence from clone TGLA339.
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                                                                                                                                                                                                                                                                                 AAQ33933 standard; DNA; 28
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ID AAO9
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vivlemore401-10.rng

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genetic mapping; traits; amplification; ss.
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                                                                                                                                                                     (GENM-) GENMARK.
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                                                                                                             15-JAN-1992;
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                                                     WO9213102-A1
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                                                                                  06-AUG-1992
                            Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of a poly(GT) sequence found in the promoter of the gene encoding the natural resistance-associated macrophage protein (NRAMP) from mice (AAAQ2294) or humans. The NRAMP protein controls the response of macrophages to pathogenic microorganisms. The DNA sequence encoding the NRAMP was isolated and cloned into plasmid pBabe lambda 8.1 which can be used for gene transfer to haematopoietic cells, especially in vitro to bone marrow or progenitor cells, in cases of NRAMP deficiency such as cancer. The full-length murine DNA can be used to isolate the human analogue from a yeast artificial chromosome library (see AAQ92942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New natural resistance associated macrophage protein - with N-terminal region contg. SH3 binding domain, also related nucleic acid, vectors, primers, antibodies etc., useful for diagnosis and treatment e.g. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                  26. .27
/*tag= a
/note= this pair of nucleotides can be repeated any
number of times"
                                                                                                Natural resistance-associated macrophage protein; phage lambda 8.1; gene therapy; plasmid pBabe lambda 8.1; retro virus; therapy, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23.2; DB 1; Length 28;
Pred. No. 2.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28 BP; 2 A; 2 C; 12 G; 12 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2322 TGTGTGTGTGTGTGTGTGTGTGTG 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TGTGTGTGTACGTGTGTGTGTACGTG 28
                                                                                                                                                                                                                                                                                                                                                                                                                 Blackwell JM;
                                                                   NRAMP promoter poly(GT) sequence #2.
                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 24; Page 57; 72pp; English
                                                                                                                                                                                                                                                                                                                95WO-GB000095
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I Similarity 89.3%;
25; Conservative (
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                                         01-APR-1996 (first entry)
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                White JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     (LYNX-) LYNXVALE LTD
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                                                                                                                                                                                                                                                                                                                19-JAN-1995;
                                                                                                                                                                                                                                                                                                                                            19-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                           31-OCT-1994;
                                                                                                                                                                                  misc feature
                                                                                                                                                                                                                                                        WO9520044-A1
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02-FEB-1993
                                                                                                                                                                                                                                                                                  27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                 Barton CH,
                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ34149;
              AAQ92939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer.
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ID AAQ3
XX
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AZ AAQ3
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DT 25-P
DT 02-F
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by with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 500 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibroblast growth factor 3 receptor; FGFR3; mutant; detection; cancer; carcinoma; lung cancer; breast cancer; colon cancer; skin cancer; bladder; cervix; human; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer used for detecting mutant fibroblast growth factor receptor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32 BP; 0 A; 0 C; 16 G; 16 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Table 7; Page 390; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphic bovine DNA markers - mapping, and selective breeding.
92WO-US000340
                                                                                91US-00642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 89.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA54428 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                             Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                         WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 25; Conserv
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and 500

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Gaps

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The invention relates to a method for stimulating a population of stem cells to differentiate into osteoblast cells by contacting the population cells to differentiate into osteoblast growth factor receptor 3 (FGFR3) expression or activity, where increase in FGFR3 protein expression or activity, where increase in FGFR3 protein expression or activity, westults in differentiation of the stem cells into osteoblast cells. The method is useful for stimulating the population of stem cells concreasing bone density. The method is useful for screening the agent increases bone density. The method is useful for screening the agent concreases bone density, or ameliotes the effects of osteoporosis. The method is useful for diagnosing a condition characterised by abnormal condition. Bone density or rate of osteoplast formation and treating a patient with a condition characterised by an abnormal rate of osteoblast formation. Sequence is a probe used for human FGFR3 expression in human tissues
                                                                                                                                                                                                                                                                            Sequence 23 BP; 5 A; 4 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                   3727 AAACCGGCAGGTGCGATTTTGTT 3749
                                                                                                                                                                                                                                                                                                                                                                                  1 NAACCGGCAGGTGCGATTTTGTT 23
                      Example 3; Page 58; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1239/c
ABZ70239 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
nes 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABZ70239;
                                                                                                                                                                                                                                                                                                                Query Match
activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 227
                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                            The identification of fibroblast growth factor receptor 3 (FGFR3) mutations in a biological sample such as tissue, bone marrow or body fluid e.g. urine, from a warm-blooded animal, preferably human is useful cor diagnosing carcinomas such as human bladder and cervix carcinomas, or cancers associated with lung, breast, colon and skin. The pharmaceutical preparations comprising agents which inhibit the synthesis and expression of FGFR3 and so have an anti-proliferation effect on carcinomas can be used to treat cancer. Two primers (AAA5428, AAA5458) were used in PCR reactions on urine samples to detect the K652B mutation in FGFR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stimulating a population of stem cells to differentiate into osteoblast cells useful for treating osteoporosis, by contacting the cells with agent which increases fibroblast growth receptor 3 expression or
                                                                                                                           Diagnosing carcinoma e.g. bladder or cervix carcinomas in a biological sample such as tissue, bone marrow or body fluid, preferably from animal or human, by identifying fibroblast growth factor receptor 3 mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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osteoblast cell; bone density; osteoporosis; osteopathic; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cook JS, Axelrod DW;
                                                                                                                                                                                                                                                                                                                                                                                         / Match 0.6%; Score 23; DB 1; Length 23; Local Similarity 100.0%; Pred. No. 2.3e+02; Indels tes 23; Conservative 0; Mismatches 0; Indels
                                                                          Thiery J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe used for FGFR3 expression in human tissues.
                                                                                                                                                                                                                                                                                                                                                                 Sequence 23 BP; 6 A; 4 C; 9 G; 4 T; 0 U; 0 Other;
                                                                          Ricol D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ji D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1646 TGGTGACCGAGGACAACGTGATG 1668
                                                                            Radvanyi F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mertz L,
                                                                                                                                                                                           Example 4; Page 13; 41pp; English.
                                   (CURI-) INST CURIE.
(CNRS ) CNRS CENT NAT RECH SCI
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24-APR-2001; 2001US-0285691P.
23-JUL-2001; 2001US-0306879P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENE LOGIC INC. (PROC ) PROCTER & GAMBLE CO.
         99US-0132705P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                               Chopin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-519881/55
                                                                                                          WPI; 2001-016103/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jaiswal N,
                                                                               Cappellen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-2002
         05-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD40533;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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0.6%; Score 23; DB 1; Length 23; 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0; Indels

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The present invention relates to murine tricarboxylic acid carrier 13.53 (see ABP59163). The protein is useful for treating various diseases, such as malignant tumours, haemopathy, HIV infection, immunological diseases and various inflammations. The present sequence is a PCR primer, which was used in an example from the invention
                                                            Murine, tricarboxylic acid carrier 13.53; tumour; cytostatic; haemopathy; HIV infection; anti-HIV; immunological disease; inflammation; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide murine tricarboxylic acid carrier 13.53 polymucleotides encoding this polypeptide.
Murine tricarboxylic acid carrier 13.53 PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 10 A; 12 C; 2 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-DEC-2000; 2000CN-00136313
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Best Local Similarity
                                                                                              GENM-) GENMARK
                         WO9213102-A1.
                                                                            15-JAN-1991;
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                                                           15-JAN-1992;
                                          06-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1992
         Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ34158;
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                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to human p70 ribosomal S6 kinase 13.97 (see ABB3103). The kinase and its coding sequence can be used for treating diseases such as cancer and HIV infection. The present sequence is a PCR primer, which was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                 Polypeptide-human P70 ribosome S6 kinase 13.97 and polynucleotide for
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                          Human; p70 ribosomal S6 kinase 13.97; enzyme; cancer; HIV infection;
cytostatic; anti-HIV; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22.6; DB 1; Length 32;
Pred. No. 3.8e+02;
 DB 1; here,
0, 2,4e+02;
0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 32 BP; 12 A; 17 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                          Human p70 ribosome S6 kinase 13.97 PCR primer #4
                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 18 (Disclosure); 34pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 0.6%; Score 22.6; D
Local Similarity 86.2%; Pred. No. 3.8e
es 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2326 TGTGTGTGTGTGTGTGTGTGTGTGCAC 2354
       Query Match 0.6%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 2.4 Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsatellite sequence from clone TGLA382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 TGTGTGTGTGTGTGTGTGTGTGTGGGAGCTC 4
                                                                                                                                                                                                                                                                                              (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                          2319 GIGIGIGIGIGIGIGIGIG 2341
                                                    23 GTGTGTGTGTGTGCGTGTGTG 1
                                                                                          26-JUN-2000; 2000CN-00116750
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(first entry)
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02-FEB-1993
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Matches
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comparream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
consomically important trait loci, or genes involved the determinism of
connectant see also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
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92WO-US000340.
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                                                                                                                                                                                                                               Georges M, Massey JM;
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02-FEB-1993 (first en
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Query Match
Best Local S:
Matches 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                         by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Molo sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100. 000. The sequence information in the bovine genome microsatellites is summarised in the specification and indexed herein (see below). The sequence upstream and specification and indexed herein (see below). The sequence upstream and committed by the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The equired PCR primers for in vitro amplification of the corresp.

The microsatellite (using the program OPTIPRIM). The microsatellites may be microsatellite (using the program OPTIPRIM). The microsatellites may be mapping of economic trait loci, or genes involved the determinism of conomically important traits esp. in cattle, to allow selective conomically important traits esp. in cattle, to allow selective the correct PN (L0) and the correct PN (L0) an
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                                                                                                                                                                - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                          sequence is that of a bovine microsatellite sequence obtd. by sening a library of bovine Mbol DNA fragments of between 250 at
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                                                                                                                                                                                                                                                 Table 7; Page 394; 517pp; English.
                                                                                                                                                                          Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ33909 standard; DNA; 24 BP
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(first entry)
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                                                                              Georges M, Massey JM;
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                                                                                                                            WPI; 1992-284684/34.
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Best Local Similarity
Matches 23; Conserv
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                                 (GENM-) GENMARK.
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02-FEB-1993
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The sequence is that of a bovine microsatellite sequence obtd. by

conservating a library of bovine MboI DNA fragments of between 250 and 500

conservation and (AC)15 and a (TC)15 oligonucleotide probe. One out of 50

conservation and (AC)15 oligonucleotide probe. One out of 50

conservation and MboI sites, the frequency of (T6)n >9 microsatellites

microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

conservation and indexed herein (see below). The sequence information

conservation and indexed herein (see below). The sequences upstream and

constream of the microsatellite sequence waset to generate the

constream of the microsatellite sequence waset to generate the

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite (using the program OPTIPRIM). The microsatellites may be

concomically important trait loci, or genes involved the determinism of

economically important traits esp. in cattle, to allow selective

breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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95.8%; Pred. No. 2.9e+02;
ve 0; Mismatches 1; Indels
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rable 7; Page 293; 517pp; English.
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23; Conservative
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02-FEB-1993
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The sequence is that of a bovine microsatellite sequence obtd, by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (ACL)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellite sequence were used to generate the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the microsatellite (using the program OPTTRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loid, or genes involved the determinism of economic trait loid, or genes involved the determinism of breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                        Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                          Score 22.4; DB 1;
Pred. No. 2.9e+02;
                                                                                                                                                                                                                                               0; Mismatches
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(first entry)
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Best Local Similarity 95.8
Matches 23; Conservative
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02-FEB-1993
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Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
constant an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (TG)n >9 microsatellites
control bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence information
confict on the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
concomically important trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
first.

breeding. See also AAQ31501-34437. (Updated on 25-WAR-2003 to correct PN
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                                  Gaps
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Length 24;
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Pred. No. 2.9e+02;
                                  Indels
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   DB 1;
Score 22.4; DB 1;
Pred. No. 2.9e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                Microsatellite sequence from clone TGLA131.
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                                                                2318 TGTGTGTGTGTGTGTGTGTG 2341
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 Query Match
Best Local Similarity 95.8%;
Matches 23; Conservative
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Local Similarity 95.8%;
nes 23; Conservative
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                                                                                                                                                                                                                                                                 (first entry)
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02-FEB-1993
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                                                                                                                                                                                                                 AAQ33707;
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Matches
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Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating caspases.
                                                                                                                                                  (BION-) BIONICHE LIFE SCI INC.
                                                                                         2-DEC-2000; 2000WO-CA001467.
                                                                                                               13-DEC-1999; 99US-0170325P.
29-AUG-2000; 2000US-0228925P.
                                                                                                                                                                        Phillips NC, Filion MC;
                                                                                                                                                                                                WPI; 2001-398150/42.
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Best Local Similarity
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                                             WO200144465-A2
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lymphoma; ss
                                                                    21-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH46016;
                       Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. The sequences AAT66084-T66107 represent repeat sequences of low informativeness found in specific human genes. This repeat sequence is found in the human chromosomal clone UM42. The sequence is amplified by primers AAT66097-8. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                              Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                          Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols, as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%; Score 22.4; DB 1; Length 24;
95.8%; Pred. No. 2.9e+02;
ive 0; Mismatches 1; Indels
                                                                                                          Repeat sequence found in the human chromosomal clone JW42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24 BP; 12 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318 rerererererererere 2341
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; Col 61-62; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH46015 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic oligonucleotide 15.
                            AAT66096 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                 94US-00222177
                                                                                                                                                                                                                                                                                        89US-00341562
                                                                                                                                                                                                                                                                                                   91US-00754351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                           (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 95.8 Matches 23; Conservative
                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-042299/04
                                                                                                                                                                                                                                                                  04-APR-1994;
                                                                                                                                                                                                                                                                                         21-APR-1989;
05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2001
                                                                          25-MAR-2003
18-JUN-1997
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                    JS5582979-A.
                                                                                                                                                                                                                                            10-DEC-1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH46015;
                                                                                                                                                                                                                                                                                                                                                    Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                     AAT66096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 236
                  AAT66096,
       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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The present sequence is that of a synthetic oligonuclectide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH synthetic oligonuclectide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonuclectide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, are useful for sapases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour or encrosis factor (TNF)-alpha by immune system calls, in an animal having and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4), idrug resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 22.4; DB 1; Length 24; 95.8%; Pred. No. 2.9e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318 TGTGTGTGTGTGTGCGTGTG 2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
Example 4; Page 17; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH46016 standard; DNA; 24 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Conservative
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response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostimulatory nucleic acids can be such immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpssviridae, retroviridae, and/or orthomyxoviridae), bacterial antigens (e.g. horpssviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                      Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simple Sequence Repeat, SSR, clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
                                                                                                                                                                                                                                                                      invention relates to a method for stimulating an immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22.4; DB 1; Length 24; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2318 TGTGTGTGTGTGTGCGTGTGTG 2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGTGTGTGTGTGTGTGTGTGTG 24
                                                                                                                                                                                                                          Claim 101; Page 59; 338pp; English.
                                                                    Vollmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2001; 2001NZ-00509194.
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(IOWA ) UNIV IOWA RES FOUND. (COLE-) COLEY PHARM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA164467 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.6
Best Local Similarity 95.8
Matches 23; Conservative
                                                                 Schetter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koelliker R, Forster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-431058/46.
                                                                                                         WPI; 2001-273485/28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-DEC-1999;
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                                                                                                                                                                                                                                                                           present
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                                                                    Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA164467;
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                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT, TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour encrosis factor (TNP)-alpha by immune system cells, in an animal having and secondary sarcoma such as primary carcinoma, primary sarcoma and secondary sarcoma, secondary carcinos, presst, prostate, olorectal, ovarian or bone cancer. The compositions induce apoptosis independent of Eas, p53/p21, p21/waf-1/CIP, p15/ink48), p16/ink4), drug resistance, caspase 3, transforming growth factor (TGP)-beta 1 receptor
                                                                                                                                                                                                                                                                    Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour; viral infection, bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunostimulatory nucleic acid #978.
                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 17; 77pp; English.
                                                                                                                                     (BION-) BIONICHE LIFE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР
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99US-0156135P.
2000US-0227436P.
                         12-DEC-2000; 2000WO-CA001467.
                                                                    99US-0170325P
                                                                                         29-AUG-2000; 2000US-0228925P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and hormone dependence
                                                                                                                                                                                                                            WPI; 2001-398150/42
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27-SEP-1999;
23-AUG-2000; 2
                                                                    13-DEC-1999;
                                                                                                                                                                               Phillips NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-2001
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                                                                                                                                                                                                                                                                                                                                             caspases.
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Gaps

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neovascularisation, telangiectasia, haemophiliac joints, angiofibroma
                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to inhibiting angiogenesis in a subject, comprising
                                  The present invention relates to Simple Sequence Repeats (SSR8) from clover species. SSR8, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs may are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anglogenesis inhibitor; ss; anglogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                            Score 22.4; DB 1; Length 24;
Pred. No. 2.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                              Sequence 24 BP; 11 A; 11 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiogenesis inhibitory oligonucleotide #1068.
                                                                                                                                                                                                                                                                                             2321 GTGTGTGTGTGTGTGTGTGT 2344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 38; 276pp; English.
             Example 1; Page 19; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-DEC-2001; 2001WO-US048458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-2000; 2000US-0255534P.
                                                                                                                                                                                                                                  0.68;
                                                                                                                                                                                                                                               95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                         ABS78584 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                 23; Conservative
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                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABS78584;
                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; zinc finger protein 9.46; recombinant production; gene therapy; malignant tumour; cancer; blood disease; human immunodeficiency virus; HIV infection; immune disorder; inflammatory condition; cytostatic; antiinflammatory; immunomodulator; reverse transcription-PCR; RT-PCR;
wound granulation, intestinal adhesions, atheroscierosis, scleroderma hypertrophic scars. The present sequence is an antiangiogenic nucleic
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                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human zinc finger protein 9.46 RT-PCR primer, SEQ ID NO:3.
                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                    0.6%; Score 22.4; DB 1; Length 95.8%; Pred. No. 2.9e+02; Live 0; Mismatches 1; Indels
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                                                                                                               Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 16 (Disclosure); 31pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2327 GTGTGTGCGTGTGTGTGTGTGT 2350
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                                                                                                                                                                                                                                                                                      2318 TGTGTGTGTGTGTGTGTGTG 2341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-DEC-2000; 2000CN-00136331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ57678 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                    Conservative
                                           hypertrophic scars. The acid of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein 9.46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CN1361165-A.
                                                                                                                                                                                                                                       23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer; ss.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
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WPI; 2004-215730/21.
                                                                                                                       (PETE/) PETERSEN (FOUR) FOURON Y.
                             US2003087848-A1.
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                                                  08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovis aries
          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO81094;
                                                                                                              BRAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 244
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                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic context dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                            Treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis inflammatory bowel disease; ulcerative colitis; crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22.4; DB 1;
Pred. No. 2.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2318 TGTGTGTGTGTGTGTGTGTGTG 2341
                                                                                                             Immunostimulatory nucleic acid #1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGTGTGTGTGTGTGTGTGTG 24
 GTGTGTGGGTGTGTGTGTGTGTGT 24
                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 36; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunostimulatory nucleic acid #978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.6%;
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                                                                                                                                                                                                                                               29-MAR-2002; 2002US-00112653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB37364 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-2003 (first entry)
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Conservative
                                                  ACH03377 standard; DNA;
                                                                                                                                                                                                                                                                                                                                          WPI; 2003-521815/49
                                                                                                                                                                                                                                                                                                                      Krieg AM, Berg DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                        (KRIE/) KRIEG A M. (BERG/) BERG D J.
                                                                                                                                                                                                        US2003050268-A1
                                                                                        25-SEP-2003
                                                                                                                                                                                                                            13-MAR-2003
                                                                                                                                                                                   Synthetic.
                                                                     ACH03377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB37364;
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The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                               Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene typing; polymorphic microsateillite marker; prion disease; disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk nrotein; hormone; transcription factor; pl7-blue-vector; sheep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22.4; DB 1; Length 24;
Pred. No. 2.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sheep prion protein microsatellite locus primer #65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2318 TGTGTGTGTGTGTGCGTGTG 2341
                                                                                                                                                                                                                                                                Fouron Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 20; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 rerererererererererere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   milk protein, hormone, transcri;
microsatellite, PCR, primer, ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP,
02-FEB-2001; 2001US-00776479.
                                                                03-FEB-2000; 2000US-0179991P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2002; 2002DE-01036711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2002; 2002DE-01036711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.6%;
Best Local Similarity 95.8%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO81094 standard; DNA; 24
                                                                                                                                                                                                                                                                Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geldermann H, Preuss S,
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                                                                                                                              BRATZLER R L.
PETERSEN D M.
                                                                                                                                                                                                                                                                                                                          WPI; 2003-657977/62.
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Geldermann H, Preuss S,
                                                     ADO81099;
                                            24
                                   Query Match
  dentify
 Typing
                                                RESULT 245
                                      Matches
                                                 ADO81099/
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The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR camplification of at least one DNA region of (I) that includes PML, using amplification of at least one beginn of (I) that includes PML, using ca template a DNA sample containing at least one segment of (I); and catermining the length of the resulting amplicon(s). Also described are: cample containing (M2) microsatellite markers (MM) for predisposition to a disease, associated with a gene that includes one or predisposition to a disease, associated with a gene that includes one or include PML. The method is used to identify microsatellite markers, in a include PML. The method is used to identify microsatellite markers, in a consense and for predisposis of such diseases, especially prion diseases of diseases and for predisposis of such diseases, especially prion diseases of the tanscription factors. The method is simpler, quicker and hormones or transcription factors. The method is simpler, quicker and continually less expensive than known methods based on sequencing. This sequence represents a primer used to genotype a region of the sheep prion content (PFP) comprising a polymorphic microsatellite locus. genes that contain polymorphic microsatellite loci, useful for tying predisposition to disease, by amplification and determining Example 3; Page 30; 64pp; German. length of amplicons.

0.6%; Score 22.4; DB 1; Length 24; llarity 95.8%; Pred. No. 2.9e+02; Conservative 0; Mismatches 1; Indels Sequence 24 BP; 12 A; 12 C; 0 G; 0 T; 0 U; 0 Other; 2318 TGTGTGTGTGTGTGTGTGTG 2341 Local Similarity nes 23; Conserv

Sheep prion protein microsatellite locus primer #70. ADO81099 standard; DNA; 24 BP (first entry) 29-JUL-2004

gene typing; polymorphic microsatellite loci; PML; disease; disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; sheep; microsatellite; PCR; primer; ss.

DE10236711-A1 Ovis aries.

09-AUG-2002; 2002DE-01036711. 26-FEB-2004

09-AUG-2002; 2002DE-01036711.

(UYHO-) UNIV HOHENHEIM:

WPI; 2004-215730/21.

Han Y;

Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.

Example 3; Page 30; 64pp; German.

Sequence 24 BP; 12 A; 12 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö 0.6%; Score 22.4; DB 1; Length 24; 95.8%; Pred. No. 2.9e+02; ive 0; Mismatches 1; Indels 23; Conservative Similarity Query Match Best Local S: Matches 23,

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2318 TGTGTGTGTGTGTGTGTGTGTG 2341 24 referererererererererer 셤

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Gaps

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ADO81051 standard; DNA; 24 ADO81051/ RESULT

AD081051;

ВP

(first entry) 29-JUL-2004

Cow prion protein microsatellite locus primer #63.

gene typing; polymorphic microsatellite loci; PML; disease; predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; cow; microsatellite; PCR; primer; ss

Bos taurus

DE10236711-A1.

09-AUG-2002; 2002DE-01036711. 26-FEB-2004.

09-AUG-2002; 2002DE-01036711.

(UYHO-) UNIV HOHENHEIM

Han Y; Preuss S, Geldermann H,

WPI; 2004-215730/21.

Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.

Example 3; Page 27; 64pp; German.

The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DNA region of (I) that includes PML, using as template a DNA sample containing at least one segment of (I); and determining the length of the resulting amplicon(s). Also described are:

predisposition to a disease, associated with a gene that includes one or more PML; and predisposition to a disease, associated with a gene that include with and prediagnosis (M3) of diseases associated with gene that disclude PML. The method is used to identify microsatellite markers, in a diseases-related gene, that are associated with a predisposition to but also cystic fibrosis, malignant hyperthermia syndrome in pigs and metabolic diseases; also to type genes that encode milk proteins, hormones or transcription factors. The method is simpler, quicker and particularly less expensive than known methods based on sequencing. This sequence represents a primer used to genotype a region of the cow prion protein (PrP) comprising a polymorphic microsatellite locus. method of determining (M2) microsatellite markers (MM) Sequence 24 BP; 12 A; 12 C; 0 G; 0 T; 0 U; 0 Other; Score 22.4; DB 1; Pred. No. 2.9e+02; 0; Mismatches 2318 TGTGTGTGTGTGTGCGTGTGTG 2341 0.6%; 23; Conservative Query Match Best Local Similarity Matches 88888888888888888888888888 ઠે

Gape ö Length 24; 1; Indels

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24 rererererererererere 1

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RESULT 247 AAH40163/c

AAH40163 standard; DNA; 25

AAH40163;

(first entry) 14-AUG-2001 SNP specific SNPE primer SEQ ID 2959.

Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss.

Homo sapiens

WO200129262-A2.

26-APR-2001.

13-OCT-2000; 2000WO-US028436

15-OCT-1999; 99US-0160096P.

(ORCH-) ORCHID BIOSCIENCES INC.

Picoult-Newburg L, Pohl M;

WPI; 2001-290930/30

New genotyping oligonucleotide, useful for detecting the presence, † absence or identity of single polynucleotide polymorphism in a nucleic acid sample.

Claim 1; Page 65; 83pp; English.

Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to

assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNBs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a single nucleotide primer extension (SNPE) primer specific for a human SNP containing DNA seguence

Sequence 25 BP; 12 A; 12 C; 1 G; 0 T; 0 U; 0 Other;

Gaps ; 0 Score 22.4; DB 1; Length 25; Pred. No. 3e+02; 0; Mismatches 1; Indels 0.6%; Query Match 0.6 Best Local Similarity 95.8 Matches 23; Conservative

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2319 GTGTGTGTGTGTGTGTGTGT 2342 24 drerererererererererer g ઠે

RESULT 248 AAI64452/

AAI64452 standard; DNA; 32

AA164452;

(first entry) 23-NOV-2001

SSR motif #12.

Simple Sequence Repeat; SSR; clover; microsatellite; genome mappir trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.

Unidentified.

NZ509194-A.

03-JAN-2001; 2001NZ-00509194. 25-MAY-2001.

99AU-00004907 24-DEC-1999;

28-MAR-2000; 2000AU-00006520.

(AGRI-) AGRIC VICTORIA SERVICES PTY LTD

Koelliker R, Forster JW;

WPI; 2001-431058/46.

Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.

Claim 6; Page 35; 52pp; English.

clover species. SSRs, also called microsatellites, rere based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs may be purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention The present invention relates to Simple Sequence Repeats (SSRs) from

Sequence 32 BP; 16 A; 10 C; 6 G; 0 T; 0 U; 0 Other;

Query Match

S

Matches

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32

RESULT 249 AAD34805 AAD34805;

Mus sp.

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Compounds that modulate the activity of a multiple lineage kinase protein treating a cell that contains MLK with a test compound and determining it the decreases or increases the activity of MLK and promotes cell survival or death. Compounds identified as having MLK modulating activity have applications as anti-neurodegenerative agents, antiinflammatory agents and anticancer agents and are potentially useful for treatment of neurodegenerative diseases (e.g. Alzheimer's, Huntington's and Parkinson's diseases, amyotrophic lateral sclerosis, ischaemia etc.) and amalignant cell growth. DLK was cloned for its use in pFLAG-DLK by using degenerate primers derived from the highly conserved VID and IX subdomains of PTK polypeptides. Two primers (AAZ93406, AAZ93407) were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying compounds that modulate multiple lineage.kinase proteins, useful e.g. for treating neurodegeneration or cancer, from their effect on survival or death of kinase-expressing cells.
                                                                                                                                                                                              Multiple linkage kinase; MLK; PYK; modulation; antiinflammatory;
anticancer; Alzheimer's disease; Huntington's disease; primer;
Parkinson's disease; amyotrophic lateral sclerosis; ischaemia; ss
                                                                                                                                                          Degenerate conserved sequence of PTK domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 19; Page 50; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used in the amplification reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dionne CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Forward PCR primer for FGFR3.
                                  AAZ93407 standard; DNA; 31 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US018864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0097980P.
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                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maroney A, Walton KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CEPH-) CEPHALON INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-282953/24.
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                        MO200013015-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                              18-AUG-1999;
                                                                                                                        24-JUL-2000
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                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                                                 AAZ93407;
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RESULT 250
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                    4AZ93407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an animal model for chondrodysplasia, more particularly, to a transgenic mouse model for achondroplasia. This transgenic mouse contains a fibroblast growth factor receptor 3 (FGFR3) gene including a G to A point mutation changing Gly to Arg in codon 380 in its genome. The transgenic mouse is useful as a model for FGFR-associated chondrodysplasia, particularly FGFR3 achondroplasia, e-g. shortening of the limbs, midface hypoplasia and large skull. This model may be exploited to gain better understanding of the disease and as an experimental model with which experimental therapy to chondrodysplasias can be exercised. The transgenic mouse is particularly useful as a tool for screening, developing and evaluating drugs with a potential of relieving or abolishing chondrodysplasia syndromes and/or symptoms. The present sequence is a PCR primer used to detect mouse FGFR3 allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New transgenic mice having a genetically modified fibroblast growth factor receptor gene, useful as a model for human chondrodysplasia, e.g. achondroplasia characterized by shortening of the limbs, midface hypoplasia or large skull.
                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; chondrodysplasia; achondroplasia; transgenic mouse; therapy; fibroblast growth factor receptor 3; FGFR3; limb; midface hypoplasia; large skull; drug screening; drug development; transgenic; PCR; primer;
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                                             Gaps
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81.2%; Pred. No. 4e+02;
tive 0; Mismatches 6; Indels
Score 22.4; DB 1; Length 32;
Pred. No. 4e+02;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32 BP, 5 A, 9 C, 11 G, 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 GGCCCTTACTGGACACGGCCCGAGCGGATGG 253
                                                                                          2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTG 2347
                                                                                                                                                                                                                                                                                                                                                                          Mouse FGFR3 allele detecting sense PCR primer.
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                                                                                                                                                                                                                                                BP.
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    ch 0.6%;
1 Similarity 81.2%;
26; Conservative
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(PROC-) PROCHON BIOTECH LTD.
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Best Local Similarity 81.2
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                    (first entry)
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                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-1999;
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Glicksman MA;

Knight E,

Neff N,

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                                      0.6%; Score 22.2; DB 1; Length 31; 70.4%; Pred. No. 4.1e+02; ative 7; Mismatches 1; Indels
Sequence 31 BP; 7 A; 6 C; 6 G; 5 T; 0 U; 7 Other;
                                                                                                                                1740 GCTCCCCGTGAAGTGGATGCCGCCTGA 1766
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GCTTCCYRTSAAGTGGAYSGCVCCYGA 31
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A method for increasing the differentiation of undifferentiated central nervous system (CNS) cells in culture. This novel method involves culturing the cells in low ambient oxygen conditions. Differentiated CNS cells can be used to treat neurodegenerative diseases such as Parkinson's disease. In order to determine the differentiated phenotype messenger RNA levels can be measured using reverse transcription PCR. This involves using PCR primers specific to certain genes. The present sequence is the reverse PCR primer used to monitor the message level of FGFR3
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                            Low oxygen culturing of central nervous system progenitor cells useful in treatment of neurodegenerative disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Culturing of neural crest stem cells useful for treatment of neurodegenerative disorders comprises culturing in low ambient oxygen conditions.
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; cell differentiation; neurodegenerative disorder; stroke; brain injury; spinal cord injury; Alzheimer's disease; epilepsy; Huntington's disease; Parkinson's disease; neurological disorder; cell transplantation; FGFR3; fibroblast growth factor receptor 3; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                             Score 22; DB 1; Length 22;
Pred, No. 2.9e+02;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         22 GAGAACAAGITIGGCAGCAICC 1
                                                                                       Example 1; Page 36; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                       466 GAGAACAAGTTTGGCAGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВЪ.
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Best Local Similarity 100.
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGFR3 mRNA PCR primer #1.
WPI; 2000-387772/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      A method for increasing the differentiation of undifferentiated central nervous system (CNS) cells in culture. This novel method involves culturing the cells in low ambient oxygen conditions. Differentiated CNS cells can be used to treat neurodegenerative diseases such as Parkinson's disease. In order to determine the differentiated phenotype messenger RNA levels can be measured using reverse transcription PCR. This involves using PCR primers specific to certain genes. The present sequence is the forward PCR primer used to monitor the message level of FGFR3.
                                                                                                                                                                                                                                                                                                                                                                 Low oxygen culturing of central nervous system progenitor cells useful in treatment of neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkinson's disease; neurodegenerative disorder; PCR primer; FGFR3; fibroblast growth factor R3; ss.
Parkinson's disease; neurodegenerative disorder; PCR primer; FGFR3;
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Pred. No. 2.9e+02;
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                                                                                                                                                                                                                                                                                            Studer L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 0.6%; Score 22; DB 1 Similarity 100.0%; Pred. No. 2.5 22; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                            Mckay R,
                                                                                                                                                                                                                                                        (CALY ) CALIFORNIA INST OF TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCCTCGGGAGATGACGAAGAC 22
                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 36; 80pp; English.
                  fibroblast growth factor R3; ss
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99US-00425462
                                                                                                                                                                                                                                                                                          Wold BJ,
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99US-00425462
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22-OCT-1999;
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                                                       Rattus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The present sequence is a PCR primer for the fibroblast growth factor receptor gene (FGFR3). It was used in reverse transcription PCR to determine expression patterns of the FGFR3 gene in cultured cells. These cells had been grown in low oxygen conditions, and had differentiated to form various types of neuronal cell. The different expression patterns can be used to determine which set of conditions promotes the used for tissue transplantation, to treat disorders such as stroke, brain and spinal cord injury, Alzheimer's disease, Huntington's disease, other neurodegenerative disorders, epilepsy, Parkinson's disease, neurological
used for tissue transplantation, to treat disorders such as stroke, brain and spinal cord injury, Alzheimer's disease, Huntington's disease, other neurodegenerative disorders, epilepsy, Parkinson's disease, neurological disorders and psychiatric disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Culturing of neural crest stem cells useful for treatment of neurodegenerative disorders comprises culturing in low ambient oxygen conditions.
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; cell differentiation; neurodegenerative disorder; stroke; brain injury; spinal cord injury; Alzheimer's disease; epilepsy; Huntington's disease; Parkinson's disease; neurological disorder; cell transplantation; FGFR3; fibroblast growth factor receptor 3;
                                                                                                                                               ;
                                                                                                               Score 22; DB 1; Length 22;
Pred. No. 2.9e+02;
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                                                                                Sequence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                       0.6%; Scc...
100.0%; Pred. No. ...
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                                                                                                                                                                               162 ATCCTCGGGAGATGACGAAGAC 183
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99US-00425462.
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                   Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         FGFR3 mRNA PCR primer #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer;
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The present invention relates to a method for identifying a genetic marker for spider lamb syndrome (SLS). The method comprising, obtaining a sheep DNA sample, and analysing the sample DNA with a probe to determine the presence or absence of a polymorphism in fibroblast growth factor receptor 3 (FGRN. The invention is used for diagnosting if sheep carry the gene for SLS, used to eliminate carriers of the syndrome from a flock. SLS or hereditary chondrodysplasia is a semi-lethal congenital disorder in sheep causing severe skeletal abnormalities. The present sequence is a PCR primer used to amplify sheep FGRR3 gene. The FGFR3 gene is located on chromosome 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a genetic marker for spider lamb syndrome, used to diagnose if sheep carry a gene for the syndrome, involves analyzing sheep DNA samples for mutations in fibroblast growth factor receptor 3.
                                                                                                                                                                                                                             Sheep, spider lamb syndrome, SLS; fibroblast growth factor receptor 3; FGFR; hereditary chondrodysplasia; semi-lethal congenital disorder; severe skeletal abnormality; genetic marker; PCR primer; chromosome 6;
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/note= "Represented in the specification as M in sequence shown in column 24 of the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 BP; 3 A; 5 C; 8 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                     Sheep FGFR3 gene amplifying PCR primer #2.
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                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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              22 GAGAACAAGTTTGGCAGCATCC
GAGAACAAGTTTGGCAGCATCC
                                                                                                           ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beever JE;
                                                                                                           AAD21621 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-662278/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
ses 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                       19-MAR-2002
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                                                                                                                                         AAD21621;
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Matches
                                                                              RESULT 255
                                                                                              AAD21621,
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ВР.

AAI67714 standard; DNA; 22

RESULT 256

AAI67714 ID AAI6

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Gaps

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0; Indels

0.6%; Score 22; DB 1; Length 22; .00.0%; Pred. No. 2.9e+02;

Query Match 0.6%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 2.9 Matches 22; Conservative 0; Mismatches

Pred. No. 2.9e+02;

Best Local Similarity

particularly for serotonin and dopamine, neuronal cell survival, and the electrophysicochemical properties of differentiated neuronal cells. Sequences AAI67692-721 represent gene-specific PCR primers for CNS and dopaminergic specific regulatory genes, used for examining the developmental progression of ES cells Lee S, 8XCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCX

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The invention provides a method of culturing cells. The method involves expanding a culture of undifferentiated embryonic stem (ES) cells, cancural ing embryoid bodies (EB), culturing the bodies to select for central nervous system (CMS) precursor cells (PC), culturing PC in an expansion medium comprising a neurologic factor, and differentiating and culturing the expanded PC to form a culture of differentiated neuronal cells. The method is useful for culturing undifferentiated neuronal cells. The method is useful for culturing undifferentiated neuronal cells which are useful for treating a neurological disorder, especially Parkinson's disease in a patient. A gene product such as tyrosine hydroxylase, nerve growth factor (MDNF), brain derived neurorsphic factor (BDNF), bFGF, glial derived growth factor (GDNF) will a useful for culturing doppainergic and servicencegic neuronal cells. The differentiated neuronal cells are useful for treating neurological disorders such as Huntington's disease, alliance service disorders cincluding epilepsy, familial dysauchonomia as well as injury or trama to the nervous system such as neurotoxic injury or disorders cuch as stroke and CNS disorders resulting from aging. Assays are useful for developing drugs capable of regulating the survival, proliferation or developing drugs capable of regulating the survival, proliferation or developing drugs capable of regulating the survival, and a dispersive disorders of domains or neuronal cells and to screen for antagonist of for developing drugs capable of regulating the survival, and of and domain drugs capable of regulating the survival, and a disponders con the survival and contains the domain of and domain of the survival and contains the domain of the domain 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Culturing cells such as neuronal cells for use in treating neurological disorders, comprises generating embryoid bodies from undifferentiated embryonic stem cells, selecting precursor cells, expanding and differentiating them.
                                                                                                                                                                                                                                                                                                                                                                      dopaminergic, cholinergic, serotonergic, antiparkinsonian, nootropic, neuroprotective, anticonvulsant, tranquilizer, vulnerary, neuroleptic, cerebroprotective, cell therapy, gene therapy, CNS, PCR primer, ss.
                                                                                                                                                                                                                                                                                                                              Cell culturing; embryonic stem; ES; central nervous system; FGFR3;
                                                                                                                                                                                                            Receptor FGFR3 cDNA amplifying forward primer.
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                                                                                                27-FEB-2002 (first entry)
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MCKA/) MCKAY R D G.
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AAI67714;
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(LEES/)
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(STUD/)
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Seguence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

0.6%; Score 22; DB 1; Length 22;

Query Match

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The invention provides a method of culturing cells. The method involves expanding a culture of undifferentiated embryonic stem (ES) cells, generating embryoid bodies (EB), culturing the bodies to select for central nervous system (CNS) precureor cells (PC), culturing PC in an expanded PC to form a culture of differentiated neuronal cells. The method is useful for culturing undifferentiated neuronal cells. The method is useful for culturing undifferentiated ES cells to corn differentiated neuronal cells which are useful for treating a neurological disorder. especially Parkinson's disease in a patient. A gene product such as tyrosine hydroxylase, nerve growth factor (NGF), brain derived neurotrophic factor (BDNF), bFGF, glial derived growth factor. (GDNF) NT-3, and NT-4/5 can be introduced into a brain of a subject. The method is useful for culturing dopaminergic, cholinergic and subject. The method is useful for culturing dopaminergic, cholinergic for treating neuronal cells. The differentiated neuronal cells are useful for culturing dopaminergic, cholinergic for treating neurological disorders such as Hultiple sclerosis, severe seizure disorders including epilepsy, familial dysautonomia as well as injury or trauma to the nervous system such as neurotoxic injury or disorders of mood and behavior such as addiction and schizophrenia, cerebrovascular disorders such as stroke and CNS disorders resulting from aging. Assays are useful for developing drugs capable of regulating the survival, proliferation or genesis of neuronal cells and to screen for antagonist or agonist of dopamine or serotonin. Cell cultures comprising 50%-85% neurons which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Culturing cells such as neuronal cells for use in treating neurological disorders, comprises generating embryoid bodies from undifferentiated embryonic stem cells, selecting precursor cells, expanding and
                                                                                                                                                                                                                                                                                                                                                                     Cell culturing; embryonic stem; ES; central nervous system; FGFR3; dopaminergic; cholinergic; serotonergic; and notropic; neuroprotective; anticonvulsant; tranquiliaer; vulnerary; neuroleptic; cerebroprotective; cell therapy; gene therapy; CNS; PCR primer; se.
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                         Indels
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                         0; Mismatches
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                                                               183
                                                                                    1 ATCCTCGGGAGATGACGAAGAC 22
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                                                               162 ATCCTCGGGAGATGACGAAGAC
                                                                                                                                                                                                         AAI67715 standard; DNA; 22 BP.
100.08;
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                         22; Conservative
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LEE S.
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MCKAY R D G.
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                       Matches
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AAI67715/c
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research
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comprise 20-40% dopaminergic neurons and 1-3% astrocytes are useful for studying the mechanism of neurotransmitter synthesis and release, particularly for serotonin and dopamine, neuronal cell survival, and the electrophysiochemical properties of differentiated neuronal cells. Sequences AAI67699-721 represent gene-specific PCR primers for CNS and dopaminergic specific regulatory genes, used for examining the developmental progression of ES cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; PCR; probe; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                           Score 22; DB 1; Length 22;
Pred. No. 2.9e+02;
                                                                                                                                                                                                             0; Indels
                                                                                                                                           Sequence 22 BP; 4 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                               Local Similarity 100.0%; Pred. No. 2.5 hes 22; Conservative 0; Mismatches
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/note= "TAMRA labelled"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human FGFR-3 DNA specific PCR probe.
                                                                                                                                                                                                                                                   487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                   466 GAGAACAAGTTTGGCAGCATCC
                                                                                                                                                                                                                                                                                                                                                                       AAD55414 standard; DNA; 22 BP.
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mod_base=
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                                                                                                                                                                                                                                                                                                                                                                                                             AAD55414;
                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                      Matches
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The present invention relates to a method of inducing differentiation of mammalian embryonic stem cells into functioning cells, which comprises culturing embryonic stem cells in a medium comprising leukaemia inhibitor culturing embryonic stem cells in a medium comprising leukaemia inhibitor factor and basic fibroblast growth factor. In particular, the invention comprises to the differentiation of murine embryonic stem cells. The method is useful for inducing differentiation of mammalian embryonic stem cells is useful for inducing discrete in pancreatic function, and in nerve function. Comparison particular parts of the present comparison of the present dispersely in neuronal degeneration (e.g. Alzheimer's disease and cells are useful not only for cell transplant therapy, but for in vitro colls are useful not only for cell transplant therapy, but for in vitro colls are useful or only for cell transplant therapy, but for in vitro cells are useful not safety evaluation of new drugs. The present sequence is function, and for safety evaluation of the invention
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reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is human FGFR-3 DNA specific PCR probe. This probe is used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inducing differentiation of mammalian embryonic stem (ES) cells into functioning cells, for treating e.g. diabetes, comprises culturing ES cells in a medium containing leukemia inhibitor factor and basic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Embryonic stem cell; ES cell; mouse; differentiation; nerve cell; pancreatic islet cell; cell transplant therapy; antidiabetic; neuroprotective; nootropic; PCR; primer; 88.
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                                                                                                                                                                             0.6%; Score 22; DB 1; Length 22;
ilarity 100.0%; Pred. No. 2.9e+02;
Conservative 0; Mismatches 0; Indels
                                                                                                                                          Sequence 22 BP; 4 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine embryonic cell line FGFR3R PCR primer #1.
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                                                                                                                                                                                                                                                              1271 CCGCCAAGCCTGTCACCGTAGC 1292
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                                                                                                                                                                                                                                                                                   1 CCGCCAAGCCTGTCACCGTAGC 22
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fibroblast growth factor
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nes 22; Conserva
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                                                                                                                 of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s MP, Li L, Spytek KA;
Patturajan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g. cancer or for chromosome mapping.
                                                                                                                                       Gaps
                                                                                                                                    ö
                                                           Query Match 0.6%; Score 22; DB 1; Length 22; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 22; Conservative 0; Mismatches 0; Indels
   BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson DW, Bento P, Boldog FL, Burgess CB, Gorman L, Gould-Rothberg BE, Gunther E, Heyes Stone DJ, Zhong M, Malyankar UM, Edinger SR, Rothenberg ME, Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 6 A; 8 C; 1 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NOVX protein-related PCR primer SegID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example C; SEQ ID NO 148; 433pp; English
                                                                                                                                                                                                  162 ATCCTCGGGAGATGACGAAGAC 183
                                                                                                                                                                                                                                                                 1 ATCCTCGGGAGATGACGAAGAC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-APR-2002; 2002US-0370969P.
12-APR-2002; 2002US-0372019P.
22-APR-2002; 2002US-0374379P.
30-MAY-2002; 2002US-0384543P.
31-US-2002; 2002US-040160619.
15-AUG-2002; 2002US-0403748P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002US-00115479.
2002US-0370349P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-2003; 2003WO-US010142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2003; 2003US-00403161
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADK51127 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-812539/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2002;
Sequence 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK51127;
                                                                                                                                                                                                                                                                                                                                                                      RESULT 260
                                                                                                                                                                                                                                                                                                                                                                                                  ADK511277

110 ADK5

AC ADK5

XX ADK5

XX ADK5

XX ADK5

XX CAPPO

BE HUMB

BE HORO

XX BOS-A

BY 02-A

BY 03-A

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The invention relates to a method for inducing differentiation of mammalian embryonic stem (ES) cells into functioning cells. The method is useful for inducing differentiation of mammalian ES cells into functioning cells. The pancreatic islet-like cell clusters induced from alloganic ES cells are useful for treating a mammalian patient having disorders in pancreatic islet function, such as when the patient is a type I diabetic patient. The nerve-like cells induced from alloganic ES cells can be used for treating a mammalian patient having disorders in nerve function. The method is a lso useful in cell therapy. The present sequence is a reverse transcription (RT). PCR primer used to amplify mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inducing mammalian embryonic stem (ES) cell differentiation into functioning cells, for treating e.g. diabetes, by culturing mammalian ES cells in a medium having leukemia inhibitory factor and basic FGF to give
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibroblast growth factor receptor (FGF 3R) cDNA. This sequence is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                      Embryonic stem cell; BS cell; pancreatic islet-like cell; type I diabetis; nerve-like cell; nerve function; cell therapy; reverse transcription; RT; PCR; primer; mouse; ss; cell differentiation; fibroblast growth factor receptor; FGF 3R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                        Mouse FGF 3R cDNA amplifying RT-PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; SEQ ID NO 47; 30pp; English.
1343 TGTCTGAGATGGAGATGAA 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 ATCCTCGGGAGATGACGAAGAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATCCTCGGGAGATGACGAAGAC 22
                22 TGTCTGAGATGGAGATGATGAA 1
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                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-2003; 2003US-00626772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2002; 2002US-00054789.
                                                                                                                    ADN03543 standard; DNA; 22
                                                                                                                                                                                      01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.6
Best Local Similarity 100.
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-328577/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              embryonic bodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INOU/) INOUE K.
(KIMD/) KIM D.
                                                                                                                                                                                                                                                                                                                                                                              US2004072344-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GUYY/) GU Y.
(ISHI/) ISHII M.
                                                                                                                                                                                                                                                                                                                                                                                                                15-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inoue K,
                                                                                                                                                    ADN03543;
                                                                                                                                                                                                                                                                                                                                              Mus sp.
                                                                                                     ADN03543
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RESULT 262 AAV44045/c

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Gaps

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0.6%; Score 22; DB 1; Length 22; 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0; Indels

Query Match 0.6 Best Local Similarity 100. Matches 22; Conservative

WO200264732-A2

22-AUG-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANY44043-V44045 are PCR primers used to amplify a murine basic fibroblast growth factor (bFGF) which is a member of the heparin-binding growth factor receptor family. This protein is used in a method which assays the ability of a substance to bind to a high-affinity heparin-binding growth factor (HBGF) receptor. The assay screens for potential antitumour agents that inhibit binding of HBGF to high-affinity receptors, or for potential wound healing agents that promote such binding. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                       Assays for high-affinity heparin-binding growth factor receptor ligands -using receptor-overexpressing cells or cell-free system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potassium channel alpha subunit; K+alphaMI; pathological condition; neuronal disorder; Addison's disease; male reproductive disorder; infertility; metabolic disorder; diabetes; cardiac disease; congestive heart failure; wound; human; single nucleotide polymorphism; SNP; K+alphaMI.v2; ds.
                                                                                                                      Basic fibroblast growth factor receptor; bFGF; heparin binding; murine; antitumour agent; inhibitor; wound healing; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                    Klagsbrun M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28 BP; 6 A; 11 C; 1 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                       Ornitz DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human K+alphaMl.v2 SNP polynucleotide #4.
                                                                                                Mouse bFGF receptor DNA PCR primer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1348 GAGATGGAGATGATGAGATGA 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 GAGATGGAGATGATGAAGATGA 7
                                                                                                                                                                                                                                                                                                                                                                       Leder P, Yayon A, Flanagan JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Col 7; 38pp; English.
                                                                                                                                                                                                                                                                                                                              (HARD ) HARVARD COLLEGE.
(CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABS64553, standard; DNA; 31 BP
                                                                                                                                                                                                                                                                                                 90US-00631717.
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AAV44045 standard; DNA; 28
                                                        (revised)
(first entry)
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                                                                                                                                                                                                                                                                          14-DEC-1993;
                                                                                                                                                                                                                                                                                                      20-DEC-1990;
                                                        25-MAR-2003
                                                                                                                                                                                                                  US5789182-A
                                                                                                                                                                                                                                               04-AUG-1998
                                                                    01-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS64553;
                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                              AAV44045;
                                                                                                                                                                                        Mus sp.
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                                                                                                                                                                                                                                  New polynucleotide encoding a potassium channel alpha subunit polypeptide or its variants, useful for diagnosing, preventing or treating a pathological condition e.g. diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potassium channel alpha subunit; K+alphaM1; pathological condition; neuronal disorder; Addison's disease; male reproductive disorder; infertility; metabolic disorder; diabetes; cardiac disease; congestive heart failure; wound; human; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                             Jackson D, Ramanathan C, Siemers N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 31 BP; 11 A; 4 C; 16 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human K+alphaM1 SNP polynucleotide #3.
                                                                                                                                                                                                                                                                                                     Disclosure; Page 73; 465pp; English.
                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-NOV-2000; 2000US-0245383P.
21-DEC-2000; 2000US-0257780P.
20-FEB-2001; 2001US-0269854P.
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                                                                             02-NOV-2000; 2000US-0245383P.
21-DEC-2000; 2000US-0257780P.
20-FEB-2001; 2001US-0269854P.
                                                 01-NOV-2001; 2001WO-US045385.
                                                                                                                                                                      Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS64526 standard; DNA; 31
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                                                                                                                                                                                                                WPI; 2002-636623/68.
                                                                                                                                                                      Lee LM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
                                                                                                                                                                        Feder JN,
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                                                                                                                                                                                        Chang H;
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channel alpha subunit (K+alphaMI) polypeptide. The K+alphaMI polymucleotides, polypeptides and antibodies are useful for diagnosing, preventing, treating or ameliorating a pathological condition or a susceptibility to a pathological condition such as neuronal disorders e.g. Addison's disease, male reproductive disorders e.g. infertility, metabolic disorders e.g. cardiac diseases e.g. congestive heart failure, or wounds. The present nucleic acid sequence represents a single nucleotide polymorphism (SNP) oligonucloeitde, as described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking sites of single mucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch.Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss.
                                                                        The present invention relates to a new polynucleotide encoding potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                   tch 0.6%; Score 22; DB 1; Length 31; al Similarity 83.3%; Pred. No. 4.3e+02; 25; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                        Seguence 31 BP; 11 A; 4 C; 16 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 GATGACGAAGACGGGGAGGACGAGGCTGAG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GAAGACGAAGACGGGGAGGAGGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP specific SNPE primer SEQ ID 2955.
                        Disclosure; Page 54; 465pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH40159 standard; DNA; 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200129262-A2
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                                                                                                                                                                                                                                                                                                          invention
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH40159,
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                                                                                                                                                                                                                                                                                                                          The present invention relates to a new polynucleotide encoding potassium channel alpha subunit (K+alphaM1) polypeptide. The K+alphaM1 polypeptide. The K+alphaM1 polynucleotides, plypeptides and antibodies are useful for diagnosing, preventing, treating or ameliorating a pathological condition or a susceptibility to a pathological condition such as neuronal disorders e.g. Addison's disease, male reproductive disorders e.g. infertility, metabolic disorders e.g. diabetes, cardiac diseases e.g. congestive heart failure, or wounds. The present nucleic acid sequence represents a single nucleotide polymorphism (SNP) oligonuclocitde, as described in the
                                                                                                                                                                        New polynucleotide encoding a potassium channel alpha subunit polypeptide or its variants, useful for diagnosing, preventing or treating a pathological condition e.g. diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potassium channel alpha subunit; K+alphaMI; pathological condition; neuronal disorder; Addison's disease; male reproductive disorder; infertility; metabolic disorder; diabetes; cardiac disease; congestive heart failure; wound; human; single nucleotide polymorphism; SNP; K+alphaMI.v1; ds.
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                                                  Siemers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 0.6%; Score 22; DB 1; Length 31; 1 Similarity 83.3%; Pred. No. 4.3e+02; 25; Conservative 0; Mismatches 5: Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ramanathan C,
                                                Ramanathan C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31 BP; 11 A; 4 C; 16 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 GATGACGAAGACGGGGAGGACGAGGCTGAG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGACGAGGGGGGGGGGGACCAG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human K+alphaM1.v1 SNP polynucleotide #4.
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                                                Jackson D,
                                                                                                                                                                                                                                                                             Disclosure, Page 34; 465pp; English.
(BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BRIM ) BRISTOL-MYERS SQUIBB CO
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21-DEC-2000; 2000US-0257780P.
20-FEB-2001; 2001US-0269854P.
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                                                  Chen J,
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                                                                                                                          WPI; 2002-636623/68
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Best Local Similarity
                                                  Lee LM,
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                                                Feder JN,
Chang H;
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ABS64541;

RESULT 265 ABS64541

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Matches

Feder JN,

HANDER BERKER STANDER
Chang

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identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits aspected of being agammaglobulinaemia, diabetes insplains, lesch-Nyhan syndrome, muscular detrophy, familial hypercholesterolaemia, polycystic kidney disease, detrophy, familial hypercholesterolaemia, polycystic kidney disease, costeogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptomes of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune configuration, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and microorganism. The method is also useful in forensic investigations and configuration (SNPE) primer specific for a human SNP containing DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the apportification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR, selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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0
                                                                                                                                                                                                                                                                                                                                Score 21.8; DB 1; Length 25;
Pred. No. 3.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                 Sequence 25 BP; 11 A; 12 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microsatellite sequence from clone TGLA40.
                                                                                                                                                                                                                                                                                                                                                                                                            rable 7; Page 330; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
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                                                                                                                                                                                                                                                                                                                                         0.6%;
Local Similarity 92.0%;
nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ34000 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Georges M, Massey JM;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ34000;
                                                                                                                                                                                                                                                                                                                                             Query Match
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The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine Mbo! DNA fragments of between 250 and 500

cc bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50

cc clones cross-hybridised. Assuming independent distribution of

cc clones cross-hybridised. Assuming independent distribution of

cc microsatellites and Mbo! sites, the frequency of (T6)n >9 microsatellites

in the bovine genome is estimated at >100,000. The sequence Information

cc process 230 such bovine microsatellite is summarised in the

cp specification and indexed herein (see below). The sequences upstream and

cp specification and indexed herein (see below). The sequences upstream and

cc specification and indexed herein (see below). The microsatellites may be

cc cromated pcr primers for in vitro amplification of the corresp.

cc microsatellite (using the program OPTIPRIM). The microsatellites may be

cc used to identify individuals, for parentage testing, and in the genetic

cc mapping of economic trait loci, or genes involved the determinism of

cc economically important traits esp. in cattle, to allow selective

cc breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - used in genetic identification, gene
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                  Length 28;
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;
                                                                                                               Sequence 28 BP; 2 A; 5 C; 12 G; 9 T; 0 U; 0 Other;
                                                                                                                                                   Score 21.6; DB 1;
Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA110.
                                                                                                                                                                                                                           2328 TGTGTGCGTGTGTGTGTGTGTGCACA 2355
                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                           rgrigrgrgrgrgrgrgrgcgcgcgcaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Table 7; Page 195; 517pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                       AAQ33663 standard; DNA; 23 BP.
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                                                                                                                                                     0.6%;
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                                                                                                                                                                                              24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
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Best Local Similarity
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Best Local Similarity
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                  AAQ33663;
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Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                     Microsatellite sequence from clone TGLA304.
                                                                                                                                                                                                                                                                                Georges M, Massey JM;
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                                                                                                                                                                                                                                                         (GENM-) GENMARK.
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                                  25-MAR-2003
02-FEB-1993
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                                                                                                                                  Bos taurus.
            AAQ33885;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of a bovine microsatellite sequence obtd. by
                                                                                                                                                                                                                   PCR, selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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Pred. No. 3.6e+02;
0; Mismatches 1; Indels
 Indels
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Mismatches
                        2318 TGTGTGTGTGTGTGTGTGT 2340
                                               1 rerererererererererer 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Page 239; 517pp; English
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                                                                                                          BP.
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Best Local Similarity 95.7%;
Matches 22; Conservative
                                                                                                         AAQ33773 standard; DNA; 23
                                                                                                                                                         (revised)
(first entry)
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Georges M, Massey JM;
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                                                                                                                                                                                                                                                                                                                                                        15-JAN-1991;
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02-FEB-1993
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                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                  AAQ33773;
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                                                                                   RESULT 269
AAQ33773
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92WO-US000340. 91US-00642342.

(first entry) (revised)

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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine ganome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information for ca. 230 such bovine microsatellite sequence were used to generate the sequence PR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat sequence found in the human chromosomal clone SW13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23 BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318 TGTGTGTGTGTGTGTGTGT 2340
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Table 7; Page 283; 517pp; English.
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Gaps

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2318 TG

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AAQ33885 standard; DNA; 23 BP

RESULT 270 AAQ33885 ID AAQ3388

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Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

cytochrome CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

cytochrome CYP4501A2; cytochrome CYP47; Cathepain S; CTSS;

cytochrome CYP4501A2; cytochrome CYP47; DB1; haematological;

cytochrome CYP4501A2; cytochrome CYP47; cytochrome CYP47;

cytochrome CYP4501A2; cytochrome CYP47; cytochrome CYP47;

cytochrome CYP47; cytochrome CYP47; cytochrome CAPA;

cytochrome CYP47; cytochrome CYP47; cytochrome CYP47;

cytochrome CYP47; cytochrome CYP47; cytochrome CAPA;

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                                                                                                                                                   The present invention relates to a method for synthesising a branched or multiply connected macromolecular structure, comprising oligonuclectide clamps (OC). The macromolecular structure is capable of specifically binding to a target molecule, and can therefore be used as probes. At least one OC comprises a target binding sequence that binds specifically and stably with the target molecule, and at least two OCs comprises signal generation molecules capable of generation adetectable signal in the presence of the target molecule. In addition the OCs are connected to one another by thioalkylamino, or thiophosphorylakylamino bridges. The present sequence is an OC used in the present invention
                              Synthesizing branched nucleic acids useful as diagnostic and molecular probes, involves combining first units having haloalkylamino groups and second units having thiol or phosphorothioate groups.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #44.
                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 21.4; DB 1; Length 23; 95.7%; Pred. No. 3.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23 BP, 11 A, 12 C, 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2319 GTGTGTGTGTGTGCGTGTGT 2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crererererererererere
                                                                                                                        Example 7; Col 19; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-2000; 2000US-00724389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-2001; 2001WO-US044838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABS97836 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Conservative
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WPI; 2001-201911/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guida M, Hall J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200257410-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DNAS-) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABS97836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABS97836/c
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      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. The sequences AAT66084-T66107 represent repeat sequences of low informativeness found in specific human genes. This repeat sequence is found in the human chromosomal clone SW13. The sequence is amplified by primers AAT66106-7. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of polymorphic genetic markers of the form (dG-dA) n (dG-dT) n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
      linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%; Score 21.4; DB 1; Length 23; 95.7%; Pred. No. 3.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23 BP; 12 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318 TGTGTGTGTGTGTGTGTGT 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 9; Col 61-62; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 rerererererererererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF60472 standard; DNA; 23 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-00787321
                                                                                                                                                                                                   94US-00222177.
                                                                                                                                                                                                                                               89US-00341562.
91US-00754351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide clamp #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide clamp; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6
Best Local Similarity 95.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                            (MARS-) MARSHFIELD CLINIC
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6180777-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-1997;
                                                                                                                                                                                                                                                                       05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001
                                                                                   Homo sapiens
                                                                                                                                                                                                         04-APR-1994;
                                                                                                                                                                                                                                                 21-APR-1989;
                                                                                                                          US5582979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF60472;
                                                                                                                                                                                                                                                                                                                                                        Weber JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Horn T;
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Gaps

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This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2), cytochrome P450 O2E1 (CYP4501A1), cytochrome P450 O2E1 (CYP5), cytochrome CYP5), cytochrome CYP5), cytochrome P450 O2E1 (CYP5), cytoc
                      Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 11 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymorphic DNA sequence of the invention
                                                                                                                                                           Example 16; Page 131; 714pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nervous system function.
                                                                                                        disorder-related traits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral
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The sequence of a poly(GT) sequence found in the promoter of the gene encoding the natural resistance-associated macrophage protein (NRAMP) from mice (AAQ92940) or humans. The NRAMP protein controls the response of macrophages to pathogenic microorganisms. The DNA sequence encoding the NRAMP was isolated and cloned into plasmid pBabe lambda 8.1 which can be used for gene transfer to haematopoietic cells, specially in vitro to bone marrow or progenitor cells, in cases of NRAMP deficiency such as cancer. The full-length murine DNA can be used to isolate the human

analogue from a yeast artificial chromosome library (see AAQ92942)

Sequence 26 BP; 2 A; 2 C; 11 G; 11 T; 0 U; 0 Other;

New natural resistance associated macrophage protein - with N-terminal region contg. SH3 binding domain, also related nucleic acid, vectors, primers, antibodies etc., useful for diagnosis and treatment e.g. of

region contg. SH3 binding primers, antibodies etc.,

cancer.

Claim 24; Page 57; 72pp; English

Blackwell JM;

Barton CH, White JK, (LYNX-) LYNXVALE LTD

31-OCT-1994;

WPI; 1995-269457/35

95WO-GB000095. 94GB-00000929.

19-JAN-1995;

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Gaps

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1; Indels

Score 21.4; DB 1; Length 26; Pred. No. 4.1e+02;

Query Match
0.6%; Score 21.4; Di
Best Local Similarity 95.7%; Pred. No. 4.1e
Matches 22; Conservative 0; Mismatches

2322 TGTGTGTGTGTGTGTGTGT 2344

1 rerererereracerererer 23

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AA164470 standard; DNA; 26

RESULT 275 AAI64470/c AA164470;

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Gaps
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0.6%; Score 21.4; DB 1; Length 24; 95.7%; Pred. No. 3.7e+02;
                               1; Indels
                                 0; Mismatches
                                                               2322 TGTGTGTGTGTGTGTGTGT 2344
                                                                                           23 rérarérérérécérérérérer 1
 Query Match
Best Local Similarity 95.7
Matches 22; Conservative
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Natural resistance-associated macrophage protein; phage lambda 8.1; gene therapy; plasmid pBabe lambda 8.1; retro virus; therapy, ss.
                                                                                          NRAMP promoter poly(GT) sequence.
                       AAQ92938 standard; DNA; 26 BP.
                                                                    01-APR-1996 (first entry)
                                             AAQ92938;
RESULT 27
AAQ92938
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WO9520044-A1

Synthetic.

Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds. (AGRI-) AGRIC VICTORIA SERVICES PTY LTD 03-JAN-2001; 2001NZ-00509194. 24-DEC-1999; 99AU-00004907. 28-MAR-2000; 2000AU-00006520. 23-NOV-2001 (first entry) Coelliker R, Forster JW; WPI; 2001-431058/46. SSR motif #20. Unidentified 25-MAY-2001. NZ509194-A.

The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNa. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs may are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches. Gaps ; 0 Score 21.2; DB 1; Length 26; Pred. No. 4.3e+02; Indels Sequence 26 BP; 11 A; 12 C; 3 G; 0 T; 0 U; 0 Other; 0; Mismatches 2319 GTGTGTGTGTGTGTGTGTGTGT 2344 Example 1; Page 19; 52pp; English ch 0.6%; 1 Similarity 88.5%; 23; Conservative Local Similarity Query Match Matches ð

26 셤

AAQ33740 standard; DNA; 27 AAQ33740; RESULT 276

BP

Microsatellite sequence from clone TGLA154. (revised)
(first entry) 25-MAR-2003 02-FEB-1993

selection; primers; OPTIPRIM; breeding; cattle; parentage;

genetic mapping; traits; amplification; 88.

Bos taurus.

WO9213102-A1 06-AUG-1992 92WO-US000340 15-JAN-1992; 91US-00642342 15-JAN-1991;

(GENM-) GENMARK.

WPI; 1992-284684/34.

Georges M, Massey JM;

Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

Table 7; Page 226; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the appecification and indexed herein (see below). The sequences upstram and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

ö used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN Gaps ö Length 27; 3; Indels Sequence 27 BP; 2 A; 0 C; 12 G; 13 T; 0 U; 0 Other; Score 21.2; DB 1; Pred. No. 4.5e+02; 0; Mismatches 3; 2318 TGTGTGTGTGTGTGTGTGTGTG 2343 rgrgrgrgrgrgrgratardrgrg 26 0.6%; 23; Conservative Query Match Best Local Similarity field.) Matches 셤 ន្តដ្ឋឧទ្ធន្ឋន ò

Microsatellite sequence from clone TGLA2. BP AAQ33789 standard; DNA; 21 (first entry) (revised) 25-MAR-2003 02-FEB-1993 AAQ33789; AAQ33789

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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

WO9213102-A1

15-JAN-1992; 06-AUG-1992

92WO-US000340. 91US-00642342 15-JAN-1991;

Georges M, Massey JM; (GENM-) GENMARK.

WPI; 1992-284684/34.

Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.

Table 7; Page 245; S17pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by

C screening a library of bovine Mbo! DNA fragments of between 250 and 500

C of Date across-hybridised. Assuming independent distribution of

C olones cross-hybridised. Assuming independent distribution of

C in the bovine genome is estimated at >100, 000. The sequence information

C for ca. 210 such bovine microsatellites is summarised in the

C specification and indexed herein (see below). The sequences upstream and

C specification and indexed herein (see below). The sequences upstream and

C downstream of the microsatellite sequence waset to generate the

C microsatellite (using the program OPTIPRIM). The microsatellites may be

Microsatellity individuals, for parentage testing, and in the genetic

C used to identify individuals, for parentage testing and in the genetic

C connomically important traits esp. in cattle, to allow selective

C breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN

Sequence 21 BP; 0 A; 1 C; 10 G; 10 T; 0 U; 0 Other;

Score 21; DB 1; Length 21; Pred. No. 3.6e+02; 0.6%; S 100.0%; Query Match Best Local Similarity

Matches

ò 유 RESULT 278

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGP) receptor 3 (also known as FGFR-3. ACH, JTF4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is human exemplification of the invention
                                                           Human, antisense, fibroblast growth factor receptor 3; prophylaxis; developmental disorder; hyperproliferative disorder; antisense therapy; FGFR-3; ACH; JTK4; CEK2; cancer; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stem cell; dental follicle; tooth; membrane structure; periodontal ligament; pluripotent mesenchymal stem cell; osteopathic; antiinflammatory; stem cell therapy; tissue replacement; tissue repair; transplantation; periodontal tissue; periodontitis; dental cementum; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibroblast growth factor receptor 3-IIIC forward PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%; Score 21; DB 1; Length 21; 100.0%; Pred. No. 3.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 3 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
                      Human FGFR-3 DNA specific reverse PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 13; Page 76; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1297 AAGATGCTGAAAGACGATGCC 1317
                                                                                                                                                                                                                                                                                                                                10-SEP-2001; 2001US-00953047.
                                                                                                                                                                                                                                                                                     06-SEP-2002; 2002WO-US028549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC64705 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                     Monia BP, Wyatt JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-313244/30.
                                                                                                                                                                                              WO2003023004-A2.
                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC64705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC64705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for identifying a genetic marker for spider lamb syndrome (SLS). The method comprishing, obtaining a sheep DNA sample, and analysing the sample DNA with a probe to determine the presence or absence of a polymorphism in fibroblast growth factor receptor 3 (FGFR). The invention is used for diagnosing if sheep carry the gene for SLS, used to eliminate carriers of the syndrome from a flock. SLS or hereditary chondrodysplasia is a semi-lethal congenital disorder in sheep causing severe skeletal abnormalities. The present sequence is a PCR primer used to amplify sheep FGFR3 gene. The FGFR3 gene is located on chromosome 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a genetic marker for spider lamb syndrome, used to diagnose if sheep carry a gene for the syndrome, involves analyzing sheep DNA samples for mutations in fibroblast growth factor receptor 3.
                                                                                                                                                                                                                                                                                                                                                                       Sheep, spider lamb syndrome, SLS; fibroblast growth factor receptor 3; FGFR; hereditary chondrodysplasia; semi-lethal congenital disorder; severe skeletal abnormality; genetic marker; PCR primer; chromosome 6;
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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100.0%; Pred. No. 3.6e+02;
iive 0; Mismatches 0; Indels
  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 3 A; 4 C; 8 G; 6 T; 0 U; 0 Other;
  Mismatches
                                                                                                                                                                                                                                                                                                                                  Sheep FGFR3 gene amplifying PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1425 CCTGTACGTGCTGGTGGAGTA 1445
                                           2324 TGTGTGTGTGCGTGTGTGT 2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCTGTACGTGCTGGTGGAGTA 21
                                                                                    rerererecerererer 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Col 24; 24pp; English
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                                                                                                                                                                                                BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0050127P.
                                                                                                                                                                                              AAD21620 standard; DNA; 21
                                                                                                                                                                                                                                                                                     19-MAR-2002 (first entry)
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1es 21; Conservative
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UTAH ) UNIV UTAH STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cockett NE, Beever JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-662278/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6306591-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2001.
                                                                                                                                                                                                                                           AAD21620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD55413;
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AAD55413/C
1D AAD554
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AC AAD554
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DT 07-AUG
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AND 1620
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06-FEB-2002; 2002US-0354152P.
                                            (CAES-) STIFTUNG CAESAR
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05-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2-APR-2002;
                                                                                Schierholz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK51121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 282
ADK51121/c
                                                                                                                                                                   useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                     The present invention describes a stem cell (A) that is obtained from non cembryonic tissue isolated from the dental follicle of a (wisdom) tooth which can differentiate in vitro into a membrane structure that resembles connected that is a described; (I) a stem cell (Al), derived from periodontal ligament. Also described; (I) a stem cell (Al), derived from con-embryonic or post-natal animal cells or tissue, that is capable of con-embryonic or post-natal animal cells of endo-, ecto- or meso-dermal consideration and antinfilammatory activities, and can be used (A). (A) has osteopathic and antinfilammatory activities, and can be used considered from them, can be used to prevent or treat cellular. Confiferentiated from them, can be used to prevent or treat cellular. Configuration They can especially be used to rebuild periodontal cramplantation. They can especially be used to rebuild periodontal cramplantation of tooth extraction or skin lesions. They can also be used in a seaffold, for growing teeth (or associated bone) or attental expense or presents a por primer which is used in an example from the control or skin being the primer which is used in an example from the control or skin being the primer which is used in an example from the control or skin being the control or 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stem cell; dental follicle; tooth; membrane structure; periodontal ligament; pluripotent mesenchymal stem cell; osteopathic; antiinflammatory; stem cell therapy; tissue replacement; tissue repair; transplantation; periodontal tissue; periodontitis; dental cementum; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                          Morsczeck C;
                                                                                                                                                                                                                                       Pluripotent embryonic-like stem cells derived from dental follicle, useful e.g. for engineering teeth or dental tissue, and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 21; DB 1; Length 21; 0.00.0%; Pred. No. 3.6e+02; Pred. No. 3.6e+02; Pred. O; Mismatches 0; Indels
                                                                                                                                                                          Zeilhofer F, Hoffmann KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 4 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
0.6%; Score 21; DB
Best Local Similarity 100.0%; Pred. No. 3.6
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 AACGCCAGGGAGTTCCGCGGC 366
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                                                                                                                                                                                                                                                                                                               Example; Page 23; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC64703 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-FEB-2003; 2003WO-EP001131.
                                                                         05-FEB-2003; 2003WO-EP001131.
                                                                                                             06-FEB-2002; 2002US-0354152P
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                                                                                                                                                                                Schierholz J, Brenner N,
                                                                                                                                               (CAES-) STIFTUNG CAESAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention.
                                                                                                                                                                                                                WPI; 2003-663591/62.
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                                                                                                                                                                                                                                                                      useful e.g. for transplantation.
            WO2003066840-A2
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                                            14-AUG-2003
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The present invention describes a stem cell (A) that is obtained from non-
cembryonic tissue isolated from the dental follicle of a (wisdom) tooth
which can differentiate in vitro into a membrane structure that resembles
compendated ligament. Also described: (1) a stem cell (A1), derived from
compendated ligament. Also described: (1) a stem cell (A1), derived from
compendated and differentiation to cells of endo-, ecto- or meso-dermal
compendated and differentiation to cells of endo-, ecto- or meso-dermal
compendated (2) pluripotent mesonchymal stem cells (A2) obtained from
lineages; and (2) pluripotent mesonchymal stem cells (A2) obtained from
compendated (2) pluripotent mesonchymal stem cells (A2) obtained from
compendated from them, can be used to prevent or treat cellular
compendated from them, can be used to prevent or treat cellular
compendated from them, can be used to rebuild periodontal
compendated in cases of periodontitis) or dental cementum, and to improve
tissue (in cases of periodontitis) or dental cementum, and to improve
compendated from with a scaffold, for growing teeth (or associated bone) or
association with a scaffold, for growing teeth (or associated bone) or
present sequence represents a PCR primer which is used in an example from
the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compendation of the compenda
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Morsczeck C;
                                                                                                                                                                                Pluripotent embryonic-like stem cells derived from dental follicle, useful e.g. for engineering teeth or dental tissue, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
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100.0%; Pred. No. 3.6e+02;
tive 0; Mismatches 0; Indels
Zeilhofer F, Hoffmann KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 4 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NOVX protein-related PCR primer SeqID.
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2002US-0370969P.
2002US-0372019P.
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2002US-0384543P
2002US-00160619
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                    Brenner N,
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                                                                                                                    WPI; 2003-663591/62.
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                                                                                                                                                                                                                                                                 useful e.g. for transplantation.
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This primer and its 5' partner (AAQ52727) correspond to regions highly conserved among mouse BEK, human FLG and chicken fibroblast growth factor
                                                                                                                                                                                                        This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NOVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of a PCR primer which was used in the exemplification of the
                                                                                                                        New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g. cancer or for chromosome mapping.
 Casman SJ, Furtak K;
MP, Li L, Spytek KA;
Patturajan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cells having high-affinity heparin-binding growth factor binding sites are used for screening substances for e.g. anti-tumour agents or wound healing promoters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 21; DB 1; Length 21; 100.0%; Pred. No. 3.6e+02; tive 0; Mismatches 0; Indels
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   Anderson DW, Bento P, Boldog FL, Burgess CE, Gorman L, Gould-Rothberg BE, Gunther E, Heyes Stone DJ, Zhong M, Malyankar UM, Edinger SR, Rothenberg ME, Smittson G,
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse fibroblast growth factor 3' DNA primer.
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                                                                                                                                                                             Example C; SEQ ID NO 145; 433pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibroblast growth factor; DNA primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 7; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-404932/50.
                                                                                          WPI; 2003-812539/76
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                        nvention
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                             This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NoVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromesome mapping. The present sequence is that of a PCR primer which was used in the exemplification of the
                                                                                                          Furtak K;
Spytek KA;
                                                                                                                                                                                                                             New NOVX polypeptide, useful for preparing a composition for treating preventing e.g. cancer or for chromosome mapping.
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                                                                                                        Boldog FL, Burgess CE, Casman SJ, F.
19 BE, Gunther E, Heyes MP, Li L, Sj
yankar UM, Edinger SR, Patturajan M;
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100.0%; Pred. No. 3.6e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                   Anderson DW, Bento P, Boldog FL, Burgess CE, Gorman L, Gould-Rothberg BE, Gunther E, Heyes Stone DJ, Zhong M, Malyankar UM, Edinger SR, Rothenberg ME, Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NOVX protein-related PCR primer SegID
                                                                                                                                                                                                                                                                                  Example C; SEQ ID NO 142; 433pp; English.
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08-APR-2002; 2002US-03709699.

12-APR-2002; 2002US-03720199.

22-APR-2002; 2002US-03743799.

30-MAY-2002; 2002US-0384543P.

33-UN-2002; 2002US-0160619.

15-AUG-2002; 2002US-040748P.

04-NOV-2002; 2002US-0407226.
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15-AUG-2002; 2002US-0403748P.
04-NOV-2002; 2002US-002B7226.
31-MAR-2003; 2003US-00403161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-2002; 2002US-00115479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2003; 2003US-00403161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124/c
ADK51124 standard; DNA;
                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP
                                                                                                                                                                                             WPI; 2003-812539/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003083046-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADK51124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
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The invention relates to producing a Bur-Projucation of Academic acids (NAB) comprising contacting a NA sample from a physiological source, with a pool of 50 distinct gene specific primers under suitable confitions to enzymatically generate sub-population of NAB, where each cach labeled NA is generated using a single gene specific primer. The method is useful for producing a sub-population of Labeled NAB which is method is useful for analysing the differences in the RNA profiles between several different physiological sources, where the method comprises producing subpopulation of labeled NAB for the different physiological sources, comprising the populations for each physiological sources, comprising the population, where the comparison is preferably differences in the population, where the comparison is preferably differences in the population, where the comparison is preferably differences to an array of probe NAB stably associated with the surface of a substrate to produce a hybridisation pattern for each of the surface of a substrate to produce a hybridisation pattern for each of the surface of a substrate to produce a hybridisation pattern for each of the surface of a substrate to produce a normal tissue or. Gifferential gene expression assays are utilised in differential expression analysis of diseased a normal tissue or. Gifferential expression analysis of diseased a normal tissue or. Hoppen a sequence is a tissue, or different tissue or subtissue types. The present sequence is a the sequence data for this patent did not form part of the printed produce specification, but was obtained in electronic format directly from USPTO specification, but was obtained in electronic format
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing sub-population of labeled nucleic acids, useful for analyzing differences in RNA profiles between several different physiological sources, using set of distinct gene specific primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to producing a sub-population of labeled nucleic
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Primer; ss; DNA microarray; differential expression analysis; human.
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 21; DB 1; Length 30;
82.8%; Pred. No. 5.4e+02;
tive 0; Mismatches 5; Indels
Length 27;
                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 BP; 8 A; 11 C; 5 G; 6 T; 0 U; 0 Other;
                         4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification, but was obtained in electronic
0.6%; Score 21; DB 1;
100.0%; Pred. No. 4.8e+0
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bibilashvilli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; SEQ ID NO 172; 11pp; English
                                                                                                                                                                                                                                                                                                                                                                       Human gene specific PCR primer #172.
                                                                                       1349 AGATGGAGATGATGAAGATGA 1369
                                                                                                                                  2
                                                                                                                    27 AGATGGAGATGATGAAGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00225928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-00859998
                                                                                                                                                                                                                                              ABK66084 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                     02-JUL-2002 (first entry)
                                             21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chenchik A, Jokhadze G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CLON-) CLONTECH LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-314699/35
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS6352829-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-2002
                                                                                                                                                                                                                                                                                            ABK66084;
                                                  Matches
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Sequences AAH17205 - AAH40944 represent PCR primers, single nucleotide polymorphisms SNPs. The present invention sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the coliponucleotides are useful for genotyping a nucleic acid sample a SNP flanking sequence, the SNPB primer is used as a genotyping primer. SNP flanking sequence, the SNPB primer extension reaction. The coliponucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The cliponucleotides are useful for determining the presence, absence or identity of a SNP and for genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include disease e.g. caused by one or more SNPs. Phenotypic traits include disease e.g. caused by one or more SNPs. Phenotypic traits include disease e.g. cateogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis of patennic microorganism. The method is also useful in forensic investigations and perminer extension (SNPE) primer specific for a human SNP containing DNA containing may and containing perfective or a containing perfective or a containing DNA                                                                                                                                                                                                                                         Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypertholesterolaemia; polycystic kidney disease; osteogenesis imperfects; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 11 A; 11 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                 SNP specific SNPE primer SEQ ID 2951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 65; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ORCH-) ORCHID BIOSCIENCES INC
                                            AAH40155 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0160096P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-2000; 2000WO-US028436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Picoult-Newburg L, Pohl M;
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-290930/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200129262-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                  14-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2001.
                                                                                                AAH40155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seguence
RESULT
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0.5%; Score 20.8; DB 1; Length 25;

Query Match

Gaps

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Ouery Match Best Local Similarity 82.8 Matches 24; Conservative

bronchial hyperreactivity; ets family; transcription factor; splice variant; genetic predipposition; polymorphism; antibody; drug screening; prophylaxis; therapy; diagnosis; single nucleotide polymorphism; SNP; ss.

Location/Qualifiers replace(12. .17,TA) /*tag= a

variation

Homo sapiens

98US-00009913. 97US-0035663P. 97US-0051432P.

21-JAN-1998;

US6087485-A. 11-JUL-2000.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ84793, a new autosomal dominant spinocerebellar ataxia type 1 (SCA 1) nucleic acid. and its protein product (AAR71111) can be used to develop products, for the presymptomatic detection of a SCA 1 disorder. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New autosomal dominant spinocerebellar ataxia type 1 nucleic acid - us to develop prods. for detection or presymptomatic diagnosis of a SCA1 disorder.
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ95132 and M13U are a pair of primers for the PCR amplification of
                                                                                                                                                                                                                                           Spinocerebellar ataxia type 1; SCA 1; presymptomatic diagnosis;
                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 20.6; DB 1; Length 27; 85.2%; Pred. No. 5.3e+02;
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 BP; 10 A; 14 C; 2 G; 1 T; 0 U; 0 Other;
   Pred. No. 4.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                   Spinocerebellar ataxia type 1 BamCA PCR primer.
                                        2317 CTGTGTGTGTGTGTGTGTGT 2340
                                                        24 CCGTGTGTGTGTGTGTGTGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example I; Page 37; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                             94WO-US007336
                                                                                                                                                                                                                                                                                                                                                                                   93US-00084365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zoghbi HY
   91.78;
                                                                                                                            AAQ95132 standard; DNA; 27
                                                                                                                                                                                             (first entry)
               22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         (MINU ) UNIV MINNESOTA.
                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                        BamcA PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-061001/08
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chung M,
                                                                                                                                                                                                                                                                                                           WO9501437-A2
                                                                                                                                                                                                                                                                                                                                                            29-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                     29-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                  28-JUN-1994;
                                                                                                                                                                              25-MAR-2003
28-SEP-1995
                                                                                                                                                                                                                                                                                                                                    12-JAN-1995
                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                       AA095132
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orr HT,
                                                                                                                  AAQ95132,
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                                                           셤
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New nucleic acids other than naturally occurring chromosomes encoding ASTH1 protein, for e.g. screening compositions that modulate expression or function of ASTH1 proteins or as diagnostics for genetic predisposition to asthma.

Example; Col 41-42; 131pp; English.

Buckler A;

Cardon L,

Galvin M, Miller A, North M, Brooks-Wilson AR, Carey AH;

WPI; 2000-505109/45.

(AXYS-) AXYS PHARM INC.

01-JUL-1997; 21-JAN-1997;

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The invention relates to the ASTH1 locus on the short arm of human chromosome (11p). This locus comprises the ASTH1I and ASTH1I are not in trached in opposite directions with the ASTH1 locus, and have similar patterns of expression and common sequence motifs. They are both expressed in traches, lung and a sequence motifs. They are both expressed in traches, lung and several other tissues. ASTH1I and ASTH1I are novel members of the ets family of transcription factors, which have been implicated in the actionative to be important in the actiology of asthma. Both ASTH1I and ASTH1I mRNAs are alternatively spliced. Alternative splicing of transcripts has no effect on the open reading frame of ASTH1I and ASTH1I mRNAs are all 5' to the start codon in exon b. In contrast, alternative splicing of ASTH1I transcripts results in 3 different ASTH1I concleic acids are useful as diagnostics to identifying ASTH1 related genes, for identifying expression of the gene in a biological specific gene modifications that minic or modulate activity or expression of ASTH1I and and or ASTH1I and as a miniodises in drug screening for compositions that minic or modulate activity or expression of ASTH1I and anti-ASTH1I or ASTH1I conclude the agence of prophylactic and therapeutic purposes. The intext for modulate or reduce to prophylactic and therapeutic purposes. The intext ASTH1I or ASTH1I concluded by a proteins or active fragmence the intext ASTH1I or ASTH1I and anti-ASTH1I and anti-ASTH1I and anti-ASTH1I and anti-ASTH1I and anti-ASTH1I and altered fragmence within the identification of individual and hereapeutic purposes. The intext ASTH1I or ASTH1I or activity or expression of ASTH1I concluded with the id
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        represent polymorphic sites within the ASTH1J or ASTH1I genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20.6; DB 1; Length 27;
Pred. No. 5.3e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 27 BP; 1 A; 2 C; 13 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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Gaps

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0; Mismatches

Local Similarity 85.2 nes 23; Conservative

Matches

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Query Match

2335 GTGTGTGTGTGTGCACATCCGCG 2361

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27

AAA80358 standard; DNA; 27

(first entry)

22-NOV-2000

AAA80358;

2319 GTGTGTGTGTGTGTGTGTGTGTG 2345

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ASTH1 locus; ASTH11; ASTH1J; human; chromosome 11p; asthma; Human ASTH11 5' region polymorphic site, SEQ ID NO:103 (b)

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Human fibroblast growth factor 3 PCR primer SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                      Sequence 27 BP; 5 A; 12 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                             2180 GGGGCTCGCGGACGTGAAGGGCCACTG 2206
                                                                                                                                                                                                          Example; Page 7; 18pp; Japanese.
                                                                                                                                                       (ZERI ) ZERIA SHINYAKU KOGYO KK.
                                                                                                                             22-MAR-2001; 2001JP-00083352
                                                                                                                                          22-MAR-2001; 2001JP-00083352
                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ33810 standard; DNA; 22
            ACC79667 standard; DNA; 27
                                     27-AUG-2003 (first entry)
                                                                                                                                                                    WPI; 2003-345602/33
                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                     JP2002272474-A.
                                                                                  Homo sapiens.
Synthetic.
                                                                                                                  24-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33810;
                                                                                                                                                                                                                                                                                                                                                      Query Match
                         ACC79667;
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 290
                                                                                                                                                                                                                                                                                                                                                                  Matches
RESULT 289
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27 gegecreeceacereaacearrere 1

23;

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The sequence is that of a bovine microsatellite sequence obtd. by

conserving a library of bovine Mbol DNA fragments of between 250 and 500

conserving a library of bovine Mbol DNA fragments of between 250 and 500

conserving a (TC)15 and a (TC)15 oligonucleotide probe. One out of 50

conserving a (TC)15 oligonucleotide probe. One out of 50

conserving a genome is testimated at >100, 000. The sequence information of for ca. 230 such bovine microsatellites is summarised in the correspond of the microsatellite sequence where used to generate the required PCR primers for in vitro amplification of the correspond constream of the microsatellite sequence where used to generate the microsatellite (using the program OPTIPRIM). The microsatellites may be microsatellity individuals, for parentage testing, and in the genetic conserving of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective for the correct PN for the correct PN for a correct PN for the correct PN fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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0
                                                                                                                            PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 0.5%; Score 20.4; DB 1; Length 22; Local Similarity 95.5%; Pred. No. 4.4e+02; nes 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microsatellite sequence from clone TGLA117.
                                                                           Microsatellite sequence from clone TGLA214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2319 GTGTGTGTGTGTGTGTGT 2340
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(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENM-) GENMARK.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JĀN-1991;
   25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                          VO9213102-A1
                                                                                                                                                                                                                                                                                                                                                   36-AUG-1992.
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                                                                                                                                                                                                                                      30s taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for the inspection of flat

C epithelial cells in which it is judged that flat epithelial cells

c separated from an organism can proceed to flat epithelial center when the

CC 128th base in fibroblast growth factor receptor (FGFR) gene of the cells

CC is mutated from quanine to thymine. Also described is a method for

CC screening treating or preventive agents for flat epithelial cancers in

CC which a candidate substance of treating agent for flat epithelial cancer

CC which the 2128th (exon 17) amino acid in FGFR3 gene is mutated from

CC quanine to thymine or the 697th amino acid is mutated from glycine to

CC quanine to thymine or the 697th amino acid is mutated from glycine to

CC quanine to thymine and that epithelial cell FGFR3 gene after the

CC quanine to thymine and that the 697th amino acid of FGFR3

CC the 2128th base in the flat epithelial cell FGFR3 gene after the

CC application returned to glycine as the indices. The method is used

CC the inspection of flat epithelial cells. The present sequence

CC for the inspection of flat epithelial cells. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inspection of flat epithelial cell, screening of treating or preventive agents for flat epithelial cancers, the treating or preventive agents for flat epithelial cancer.
                                                                                                                                                                                                                                                                                                                                                                                                          Human; fibroblast growth factor 3; FGF3; flat epithelial cell; cancer; flat epithelial cell cancer; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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ilarity 85.2%; Pred. No. 5.3e+02;
Conservative 0; Mismatches 4; Indels
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
compatream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellite (using the program OPTIPRIM). The microsatellites may be
mapping of economic trait loci, or genes involved the determinism of
conomically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.5%; Score 20.4; DB 1; Length 22; larity 95.5%; Pred. No. 4.4e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microsatellite sequence from clone TGLA48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2318 IGTGTGTGTGTGTGTGTG 2339
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                                                                                                                                               Table 7; Page 346; 517pp; English.
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(first entry)
Маввеу ЈМ;
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                                        WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-284684/34.
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les 21; Conserv
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02-FEB-1993
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Georges M,
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Matches
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a
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                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the sequence information for ca. 230 such bovine microsatellite sequence were used to generate the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the microsatellite (using the program OPTIRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                   Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20.4; DB 1; Length 22; Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite sequence from clone TGLA432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2318 TGTGTGTGTGTGTGTGTG 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                  Table 7; Page 199; 517pp; English.
                                                                                                                                                                                                                                                                                                                       mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ34038 standard; DNA; 22 BP.
                                                                                  92WO-US000340
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(first entry)
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                                                                                                                                                                                                                  Georges M, Massey JM;
                                                                                                                                                                                                                                                        WPI; 1992-284684/34.
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                                                                                                                           15-JAN-1991;
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  WO9213102-A1
                                                                                     15-JAN-1992;
                                          06-AUG-1992.
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ34038;
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Matches

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cc by with an (AC115 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites and mboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information cross-point of the cross-point of the microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and commerce and the microsatellite sequence wased to generate the correspond of the microsatellite sequence wased to generate the microsatellite (using the program OPTIRRIM). The microsatellites may be compared to individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of cenomic ally important traits espon in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20.4; DB 1; Length 22; Pred. No. 4.4e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 0.5%;
1 Similarity 95.5%;
21; Conservative
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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                     Microsatellite sequence from clone TGLA39.
       22 BP
                               (first entry)
        AAQ33991 standard; DNA;
                         (revised)
                                                                      WO9213102-A1
                          25-MAR-2003
02-FEB-1993
                                                              Bos taurus
                 AAQ33991;
RESULT 294
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92WO-US000340
                                               91US-00642342.
                                                 15-JAN-1991;
                        15-JAN-1992;
06-AUG-1992
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(GENM-) GENMARK.

Georges M, Massey JM;

WPI; 1992-284684/34.

Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding. Table 7; Page 327; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the appecification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp.

The sequences given in AAQ83938, AAQ83952 and AAQ83940 are used in the construction of an oligonucleotide clamp. The clamp is a comb-type

Example 8; Page 33; 52pp; English.

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                                 to correct PN
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used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                    ppp = a linkage or monomer containing
functionality, and p = phosphodiester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pnp = a linkage or monomer containing functionality, and p = phosphodiester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pnp = a linkage or monomer containing
functionality, and p = phosphodiester
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                          HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss
                                                                                                                                                                                                                                                                                     Oligonucleotide clamp n, for producing comb-type brached polymer.
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                                                                                        Length 22;
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/note= "Modified with BrCH2(=0)CNH-"
                                                                 Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
                                                                                          Score 20.4; DB 1;
Pred. No. 4.4e+02;
                                                                                                                0; Mismatches
                                                                                                                                    2318 TGTGTGTGTGTGTGCGTGTG 2339
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                                                                                                                                                                                                                                                                                                                                                                                                                bromoacetylamino fulinkage"
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bromoacetylamino f
linkage"
                                                                                                                                                   1 TGTGTGTGTGTGTGTGTGTG 22
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/note= "C(pnp)A,
oromoacetylamino
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                                                                                                                                                                                                               AAQ83952 standard; DNA; 22 BP.
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                                                                                            0.5%;
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/*tag= b
/note= "C(
                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 95.5
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linkage
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                                                                                                                                                                                                                                                            (revised)
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                                                                                                                                                                                                                                                                                                                                                                      modified base
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04-OCT-1995
                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                        AAQ83952;
                                                     field.)
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branched polymer which has 3' termini and was used to bind a target sequence comprising a segment of the HIV pol and nef genes in single stranded or double stranded forms. An oligonucleotide clamp is a compound capable of forming a covalently closed macromolecule or a stable circular complex after specifically binding to the target polymucleotide. Glamps generally comprise one or more oligonucleotide or incular oligonucleotide clamps generally comprise one or more oligonucleotide moieties capable of specific binding to the target molecule and one or more pairs of binding moieties covalently linked to the oligonucleotide polymucleotide, the binding of the oligonucleotide so the target polymucleotide, the binding moieties of a pair are bought into juxtaposition so that they form a stable covalent or non-covalent linkage or complex. The interaction of the binding moieties effectively clamps the specifically annealed oligonucleotide moieties to the target the specifically annealed oligonucleotide moieties to the target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 20.4; DB 1; Length 22; 95.5%; Pred. No. 4.4e+02; tive 0; Mismatches 1; Indels
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91US-00754351
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(first entry)
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Matches 21; Conservative
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17-JUN-1997
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AAT65727/
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by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-797. This repeat sequence is from the marker clone Mdf25 which contains the repeat sequence having the formula: (AC)11. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                          Gaps
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                                                                                     Sequence 22 BP; 11 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
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28-MAR-2000; 2000AU-00006520.
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                                                                                                                                      Local Similarity
les 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         SSR motif #18.
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                                                                                                                       Query Match
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Matches
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AA164448

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The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 20.4; DB 1; Length 22; larity 95.5%; Pred. No. 4.4e+02; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                   24-DEC-1999; 99AU-00004907.
28-MAR-2000; 2000AU-00006520.
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nes 21; Conserva
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Unidentified.
                                                                                                                     25-MAY-2001.
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Matches
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28-MAR-2000; 2000AU-00006520
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                                                                                                           AA164448 standard; DNA; 22
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                                                                                                                                                                                                                                                                                                   SSR motif #8.
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RESULT 299 AAI64456,

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Gaps

vivlemore401-10.rng

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Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                                                                                                 The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter — as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene
                                                                                                                                   Claim 8; Page 9; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            TA repeat polymorphism
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0.5%; Score 20.4; DB 1; Length 22; 95.5%; Pred. No. 4.4e+02; Sequence 22 BP; 11 A; 0 C; 0 G; 11 T; 0 U; 0 Other; Best Local Similarity Query Match

2823 TATATACATATATATATA 2844 셤 ઠ

AAL50669 standard; DNA; 22

ВР

AAL50669;

16-JAN-2003 (first entry)

Human uridine diphosphate glucuronosyltransferase gene polymorphism #3.

Human, polymorphism, TA repeat, ds, UGT; thymidine-adenine repeat, uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1, drug dosage optimisation; xenobiotic sensitivity.

Homo sapiens

US2002115097-A1.

22-AUG-2002

01-FEB-2002; 2002US-00061693

99US-00251274. 16-FEB-1999;

(ARCH-) ARCH DEV CORP.

Ratain MJ; Rienzo AD, Iyer L,

WPI; 2002-740095/80.

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.

Claim 8; Page 9; 13pp; English.

The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter — as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful in oplymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that

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are glucuronidated by UGT. The present DNA sequence represents a UGT gene
                  TA repeat polymorphism
   SXXS
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Sequence 22 BP; 11 A; 0 C; 0 G; 11 T; 0 U; 0 Other;

Gaps ö Score 20.4; DB 1; Length 22; Pred. No. 4.4e+02; 0; Mismatches 1; Indels 0.5%; Query Match
Best Local Similarity 95.5
Matches 21, Conservative

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2823 TATATATATATATATATA 2844 셤 ठ

RESULT 302 ABS97834/c

BP ABS97834 standard; DNA; 22

ABS97834;

23-DEC-2002 (first entry)

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Gaps

.; 0

1; Indels

0; Mismatches

21; Conservative

Matches

Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #42.

rundari, us; Qr. Controll of the control of the con ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; single nucleotide polymorphism

Homo sapiens.

25-JUL-2002

28-NOV-2001; 2001WO-US044838.

28-NOV-2000; 2000US-00724389.

(DNAS-) DNA SCI LAB

Hall J; Guida M, WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genee e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 16; Page 131; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A2 (CYP4501A2), cytochrome P450 A2 (CYP4501A2), aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARNY), catheppsin S (CTSS), cyclooxygenaes 2 (COX), diazepam binding inhibitor (DBI), epoxide hydroxylase 2 (CPAX), classepam binding protein (FLAP), glutathione-S-transferase 12 (GFXI2), histamine-N-methyl

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transferase (NAWI), (NAILINIETH 1, NADEH QUIDONE OXIGOTEGUCCASE (NAC2), transferase (NAWI), NADEH QUIDONE OXIGOTEGUCCASE (NAC2), transferase (NAC2), transferase thermolabile (STM), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B4), UDP-glucuronosyl transferase (UGT2B1), urokinase receptor (URA), multidrug resistance associated protein (MRR1), lactorransferin (LTF), multidrug resistance associated protein (MRR1), lactorransferin (LTF), multidrug resistance associated protein (MRR1), orphan nuclear receptor (NRR12), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR3, CHMR3, CHMR4 or CHMR5) sequence cresponsible for specific traits within the genome and eventually definitying the genes responsible for a variety of disorder-related cortains as a result of their e-g., overexpression, constitutive and variety of disorder-related cand/or treating the disorders. The nucleic acid molecules comprising the cand/or treating the disorders. The nucleic acid molecules comprising the cand/or MDR3 are useful for screening individuals for altered drug contained in CYP4501A1, CYP4F01A1, CYP4501A1, CYP4F01A1, CYP4501A1, CYP4F01A1, CYP4501A1, CYP4F01A1, CYP4F01A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene typing; polymorphic microsatellite loci; PML; disease; disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; sheep;
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59.5%; Pred. No. 4.4e+02;
ve 0; Mismatches 1; Indels
transferase (HNWT), (kallikrein 2) KLK2, nicotinamide
transferase (NNWT), NADPH quinone oxidoreductase 2 (N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22 BP; 10 A; 10 C; 1 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymorphic DNA sequence of the invention
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Best Local Similarity
Matches 21; Conserv
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ADO81143/c
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The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DNA region of (I) that includes PML, using cas template a DNA sample containing at least one segment of (I); and cast template a DNA sample containing at least one segment of (I); and cast template a DNA sample containing at least one segment of (I); and cast template a DNA sample containing at least one segment of disease, associated with a gene that include PML. The method is used to identify microsatellite markers, in a disease related gene, that are associated with a predisposition to disease and for prediagnosis of such diseases, especially prion diseases but also cystic fibrosis, malignant hypethermia syndrome in pigs and bramones or transcription factors. The method is simpler, quicker and barticularly less expensive than known methods based on sequencing. This sequence represents a prion protein polymorphic microsatellite marker
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Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene typing; polymorphic microsatellite loci; PML; disease; disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; sheep;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Score 20.4; DB 1; Length 22; 95.5%; Pred. No. 4.4e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sheep prion protein microsatellite locus primer #69.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 BP; 11 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2318 TGTGTGTGTGTGTGTGTG 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 30; 64pp; German
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                                                                              German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 95.5
21; Conservative
                                                                                Claim 9; Page 50; 64pp;
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                                                                                                                                                                                                                                                                                                                                                                                       consensus sequence.
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The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DNA region of (I) that includes PML, using as template a DNA sample containing at least one segment of (I); and determining the length of the resulting amplicon(s). Also described are: a method of determining (M2) microsatellite markers (MM) for predisposition to a disease, associated with a gene that includes one or more PML, and prediagnosis (M3) of diseases associated with gene that include PML. The method is used to identify microsatellite markers, in a disease related gene, that are associated with a predisposition to diseases and for prediagnosis of such diseases, especially prion diseases but also cystic fibrosis, malignant hyperthermia syndrome in pigs and metabolic diseases; also to type genes that encode milk proteins, commons or transcription factors. The method is simpler, quicker and particularly less expensive than known methods based on sequencing. This sequence represents a primer used to genotype a region of the sheep prion protein (PrP) comprising a polymorphic microsatellite locus. ö The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter — as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is useful in optimising drug desages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter. Human uridine diphosphate glucuronosyltransferase gene polymorphism #4. Gaps Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity. ö 0.5%; Score 20.4; DB 1; Length 22; 5.5%; Pred. No. 4.4e+02; 1; Indels Seguence 22 BP; 11 A; 11 C; 0 G; 0 T; 0 U; 0 Other; 0; Mismatches 2318 TGTGTGTGTGTGTGCGTGTG 2339 22 TGTGTGTGTGTGTGTGTGTG 1 Claim 8; Page 9; 13pp; English Ratain MJ AAL50670 standard; DNA; 24 BP 01-FEB-2002; 2002US-00061693 95.5%; (first entry) 21; Conservative (ARCH-) ARCH DEV CORP. Rienzo AD, Iyer L, WPI; 2002-740095/80. Local Similarity US2002115097-A1 Homo sapiens .16-JAN-2003 22-AUG-2002 AAL50670; Query Match 305 Matches ઠ g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
are glucuronidated by UGT. The present DNA sequence represents a UGT gene
TA repeat polymorphism
                                                                                                                                                                                                                                                                                                                                                                                               Human uridine diphosphate glucuronosyltransferase gene polymorphism #4.
                                                                                                                                 Gaps
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                                                                                            0.5%; Score 20.4; DB 1; Length 24; 35.5%; Pred. No. 4.9e+02;
                                                                                                                                 1; Indels
                                                           Sequence 24 BP; 12 A; 0 C; 0 G; 12 T; 0 U; 0 Other;
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                                                                                                                                 0; Mismatches
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                                                                                                             Best Local Similarity 95.5%;
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                  Query Match
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RESULT 307

US2002115097-A1

Homo sapiens.

16-JAN-2003

AAL50671;

16-FEB-1999;

22-AUG-2002.

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The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine—edenine (TA) repeats in the promoter—as the number of TA repeats correlates with expression of the UGT gene promoter. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenoblotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene
                                                                                                                                                                                                                                                                    Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 0.5%; Score 20.4; DB 1; Length 26; al Similarity 95.5%; Pred. No. 5.4e+02; 21; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26 BP; 13 A; 0 C; 0 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "thiophosphate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
(CIST-) CISTEM BIOTECHNOLOGIES GMBH.
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1. .26
/*tag= a
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                                                                                                                                                                                                 Ratain MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZ24782 standard; RNA; 26 BP.
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                                                                                                                 99US-00251274.
                                                                         01-FEB-2002; 2002US-00061693.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TA repeat polymorphism
                                                                                                                                                        (ARCH-) ARCH DEV CORP
                                                                                                                                                                                                   Rienzo AD, Iyer L,
                                                                                                                                                                                                                                          WPI; 2002-740095/80.
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                                                                                                                     16-FEB-1999;
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                                    22-AUG-2002
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Best Local 3
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug desages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene TA repeat polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
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                                                                                                                                             Human uridine diphosphate glucuronosyltransferase gene polymorphism #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
uridine diphosphate glucuronosyltransferase gene promoter; UGTIA1;
drug dosage optimisation; xenobiotic sensitivity.
                                                                                                                                                                                  Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26 BP; 13 A; 0 C; 0 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratain MJ
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                            AAL50671 standard; DNA; 26
                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rienzo AD, Iyer L,
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Best Local Similarity
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Homo sapiens

AAL50671;

AALSO671/
ID AALS
XX AALS
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XX AALS
XX Hume
XX KW Hume
KW UTIC
KW UTIC
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RESULT 308

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Best Loca Matches

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Gaps

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AAL50672 standard; DNA; 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                             RESULT 311
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                                                                                                         The present sequence is that of a thiosubstituted oligodeoxynucleic acid (ODN) molecule, ODN 21, including deoxyuridine monophosphates. The invention is based on the discovery that ODNs containing deoxyuridine residues (U-ODNs) have an immunostimulatory effect comparable to, or in many instances greater than, ODNs containing CpG motifs, producing higher numbers of specific T cells to a given antigen. The U-ODNs do not induce the systemic production of pro-inflammatory cytokines and, in contrast to CpG ODNs, are not dependent on a specific motif or a palindromic combining the U-ODN with an antigen strongly increases the potential of the antigen to raise the protection/immune response of a vaccinated individual. An example of the invention demonstrated the generation of a specific immune response against a melanoma-derived peptide (see
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New oligodeoxynucleic acid molecules useful for the preparation of
                                                 New oligodeoxynucleic acid molecules useful for the preparation of
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                                                                                                                                                                                                                                                                                                                                        0.5%; Score 20.4; DB 1; Length 26;
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                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                Sequence 26 BP; 13 A; 0 C; 0 G; 0 T; 13 U; 0 Other;
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(CIST-) CISTEM BIOTECHNOLOGIES GMBH.
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1. .26
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 Schmidt
                                                                                     Example 7; Page 31; 57pp; English
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Schellack C,
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                       WPI; 2003-183880/18
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modified_base
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 Lingnau K,
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The present sequence is that of a thiosubstituted oligodeoxynucleic acid (ODN) molecule, ODN 21, including deoxyuridine monophosphates. The invention is based on the discovery that ODNs containing deoxyuridine residues (U-ODNs) have an immunostimulatory effect comparable to, or in many instances greater than, ODNs containing CpG motifs, producing higher numbers of specific r cells to a given antigen. The U-ODNs do not induce the systemic production of pro-inflammatory cytokines and, in contrast to CpG ODNs, are not dependent on a specific motif or a palindromic Combining the U-ODN with an antigen strongly increases the potential of the antigen to raise the protection/immune response of a vaccinated the antigen terzongly increases the generation of a specific immune response against a melanoma-derived peptide (see ABPSB360) by injection of mice with the peptide in combination with ODN
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uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
drug dosage optimisation; xenobiotic sensitivity.
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Example 7; Page 31; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.5%;
Best Local Similarity 95.5%;
Matches 21; Conservative
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SKSSS

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The present invention relates to identifying a rice variety as amplification genetic marker and identifying whether test rice variety is any one of the 32 rice varieties e.g., Kasalath, breath which came or Alayamasari, Italica Livorno, Dunghan Shali, Arroz Da Terra, Fany, USSR22, Nihonbare. The method is useful for identifying rice variety and identifies excellent rice variety. The present sequence represents a base containing SSR sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying rice variety using base sequence containing SSR sequence and amplifying genetic marker.
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                                                                                                                                                                              rice variety; amplification genetic marker; ds.
                                                                                                                                                                                                                                                                                                                                                                                                               (HOKU-) HOKUREN NOGYO KYODO KUMIAI.
(HOKK-) HOKKAIDO GREEN BIO KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 50; SEQ ID NO 13; 30pp; Japanese.
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                                                                                                                                             Base containing SSR sequence #13
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                                ADK61709 standard; DNA; 28
                                                                                                           (first entry)
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                                                                                                                                                                                                                              Oryza sp.
                                                                        ADK61709;
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RESULT 313
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                      4DK6170
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individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene TA repeat polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human uridine diphosphate glucuronosyltransferase gene polymorphism #6.
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                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity.
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                                                                                                                 Query Match
0.5%; Score 20.4; DB 1; Length 28;
Best Local Similarity 95.5%; Pred. No. 5.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels
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                                                                               Sequence 28 BP; 14 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
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                                                                                                                                                                                                                        Claim 8; Page 9; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratain MJ;
                                                                                                                                                                                                                                                                                                                                      BP.
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                                                                                                                                                                                                                                                                                                                                      AAL50672 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ARCH-) ARCH DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rienzo AD, Iyer L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-FEB-1999;
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Best Loca Matches

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AAL50672;

RESULT 31 AAL50672/

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Homo

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Gaps

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The present invention relates to identifying a rice variety as amplification genetic marker and identifying whether test rice variety is any one of the 32 rice varieties e.g., Kasalath, breath which came or Hayamasari, Italica Livorno, Dunghan Shali, Arroz Da Terra, Fany, USR22, Nihonbare. The method is useful for identifying rice variety and identifies excellent rice variety. The present sequence represents a base - containing SSR sequence of the invention.
                                                                                                            Identifying rice variety using base sequence containing SSR sequence and
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28 BP; 14 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
(HOKU-) HOKUREN NOGYO KYODO KUMIAI.
(HOKK-) HOKKAIDO GREEN BIO KENKYUSHO KK
                                                                                                                                                                             Claim 50; SEQ ID NO 13; 30pp; Japanese.
                                                                                                                                 amplifying genetic marker
                                                               WPI; 2004-003560/01
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1; Indels 0.5%; Score 20.4; DB 1; 95.5%; Pred. No. 5.8e+02; 0; Mismatches 2823 TATATACATATATATATA 2844 28 TATATATATATATATATATA 7 21; Conservative Sest Local Similarity Query Match Matches ઠે

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ACIS8589 standard; DNA; 25 13-OCT-2003 (first entry) ACI58589;

BP.

Human microarray DNA oligonucleotide SEQ ID NO 58580.

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison

Homo sapiens.

US2003104410-A1

05-JUN-2003.

15-MAR-2002; 2002US-00098263

16-MAR-2001; 2001US-0276759P

(AFFY-) AFFYMETRIX INC

Mittmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 58580; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises

hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attended to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the cucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific nutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html

Sequence 25 BP; 5 A; 3 C; 7 G; 10 T; 0 U; 0 Other;

Gaps ö Length 25; 3; Indels Score 20.2; DB 1; Pred. No. 5.4e+02; 0; Mismatches 3; 0.5%; Query Match 0.5 Best Local Similarity 88.0 Matches 22; Conservative

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Gaps

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Length 28;

ACIS8588 standard; DNA; 25 RESULT 316 ACI58588/

ACI58588;

(first entry) 13-OCT-2003 Human microarray DNA oligonucleotide SEQ ID NO 58579.

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC

Mittmann MP;

WPI; 2003-567953/53

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 58579; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid

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8888888888888888888
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probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific blot hybridisation to identify or detect the sequence or specific brimatations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html

Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 U; 0 Other;

ö Gaps ; 0 Query Match

0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 98.0%; Pred. No. 5.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels

장. 쉽

RESULT 317

ADB38952 standard; DNA; 25 ADB38952

BP.

(first entry) 04-DEC-2003 ADB38952;

Human interleukin 1RNic single nucleotide polymorphism (SNP) region 21.

interleukin 1 gene cluster; IL-1 gene cluster; IL-1 like gene; IL-1 locus; single nucleotide polymorphisms; SNP; IL-1 haplotype; inflammatory disease; IL-1 associated inflammatory phenotype; primary inflammatory cytokine; IL-1 alpha; IL-1 beta; ILIA; IILB; ILIRN; anti-inflammatory; chromosome 2q13; anti-inflammatory; chromosome 2q13; anti-inflammatory; antiarthritic; hepatotropic; osteopathic; gene therapy; arthritis; hepatic inflammation; chronic obstructive pulmonary disease; osteoporosis; ds; IL-IRNic.

Homo sapiens

Location/Qualifiers replace(11,T) /*tag= a variation

/standard_name= "Single nucleotide polymorphism"

WO2003064600-A2

07-AUG-2003

27-JAN-2003; 2003WO-US002232.

25-JAN-2002; 2002US-0351951P

(INTE-) INTERLEUKIN GENETICS INC.

Govindaraju R; Kornman K, Kolpin MR, Hsieh C, Nicklin M, Duff G, Aziz N;

WPI; 2003-618359/58.

Determining whether the subject has or is predisposed to developing a disease or condition that is associated with an IL-1 inflammatory haplotype, useful for treating inflammation, comprises detecting an IL-1 allele

Claim 18; Fig 10A; 96pp; English

cc information relates to the luterlication and use of yearerlication information from the human interleukin 1 (IL-1) gene cluster including the structure and organisation of novel IL-1 like genes found within the the structure and organisation of novel IL-1 like genes found within the the structure and ostenisates of the polymorphisms (single nucleotide polymorphisms).

CC SNPs) and associated haplotypes within these genes. The invention also crelates to the use of these polymorphisms and haplotypes for predicting relates to the use of these polymorphisms and haplotypes for predicting inflammatory disease) and for treating IL-1 associated inflammatory phanotypes. IL-1 is a primary inflammatory cytokine and has been conficiently functionally similar molecules, IL-1 alpha and IL-1 beta of implicated in mediating both acutes molecules, IL-1 alpha and IL-1 beta, are encoded by genes ILA and ILLB. A third gene of the family (ILIRN) are encoded by genes ILA competes for receptor binding with IL-1 alpha and IL-1 beta. The IL-1 gene cluster is on the long arm of chromosome configurable and inclusion and inclusion with inclusion and inclusion and inclusion or orteopathic activity. In addition, the sequences encoding the IL-1 corporating and electronic partorpoic or proteins may be useful for gene therapy. The methods and polymucleotide proteins may be useful for diagnosing and treating an inflammatory disease, for example arthritis, heapeatic inflammation, chronic obstructive in the new arrangement of inclusion and including a single nucleotide polymorphism of the inclusion, in the harmonic polymorphism of the inclusion in the back in the polymorphism of the inclusion in the back in the polymorphism of the inclusion in This invention relates to the identification and use of genetic invention in the human ILIRN gene.

Sequence 25 BP; 0 A; 1 C; 11 G; 13 T; 0 U; 0 Other;

Gaps ö Score 20.2; DB 1; Length 25; 3; Indels 5.46+02 0; Mismatches Pred. No. 0.5%; 88.0%; Query Match Best Local Similarity 88.0°

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RESULT 318

ВР AAX34894 standard; DNA; 20 AAX34894/

AAX34894;

(first entry) 28-JUN-1999

PCR primer used to amplify FGFR3.

Immortalized human hair papila cell; HPC; screening; hair growth; SV40 viral Large T-antigen gene; deleted replication initiation point; hair growth stimulating agent; PCR primer; ss.

Synthetic.

JP11089565-A.

06-APR-1999

19-SEP-1997;

97JP-00271927. 19-SEP-1997;

(SHIS) SHISEIDO CO LTD.

WPI; 1999-281045/24.

Immortalised human hair papila cells used for evaluation of hair growth agent - are prepared by transformation of human hair papila cells with gene with deleted replication initiation point.

Example 2; Page 7; 23pp; Japanese.

The specification describes the preparation of immortalized human hair papila cells (HPC). The method comprises transformation of HPC with an SV40 viral Large T-antigen gene with deleted replication initiation

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The identification of fibroblast growth factor receptor 3 (FGFR3) mutations in a biological sample such as tissue, bone marrow or body fluid e.g. urine, from a warm-blooded animal, preferably human is useful for diagnosing carcinomas such as human bladder and cervix carcinomas, or cancers associated with lung, breast, colon and skin. The pharmaceutical preparations comprising agents which inhibit the synthesis and expression of FGFR3 and so have an anti-proliferation effect on carcinomas can be used to treat cancer. Two primers (AAA54426, AAA54838) were used in PCR reactions on urine samples to detect the S249C mutation in FGFR3
point. The immortalized HPC can be used in a screening method for a hair growth agent, by culture of immortalized HPC in the presence of a substance to be tested and observation of the growth of the immortalized HPC. HPC is also used in development of hair growth stimulating agents. The present sequence represents a PCR primer, which is used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing carcinoma e.g. bladder or cervix carcinomas in a biological sample such as tissue, bone marrow or body fluid, preferably from animal or human, by identifying fibroblast growth factor receptor 3 mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fibroblast growth factor 3 receptor; FGFR3; mutant; detection; cancer;
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer used for detecting mutant fibroblast growth factor receptor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carcinoma; lung cancer; breast cancer; colon cancer; skin cancer; bladder; cervix; human; primer; ss.
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                                                                                                                                                                     Query Match 0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thiery J;
                                                                                                                                      Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                     1297 AAGATGCTGAAAGACGATGC 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Page 13; 41pp; English.
                                                                                                                                                                                                                                                                        20 AAGATGCTGAAAGACGATGC 1
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                                                                                                                                                                                                                                                                                                                                                                                   AAA54426 standard; DNA; 20 BP
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, UTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
                                                                                                                                                                                                                                                                                                                     /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
                                                                                                                                                        Human, antisense, fibroblast growth factor receptor 3, prophylaxis,
developmental disorder, hyperproliferative disorder, antisense therapy;
FGFR-3, ACH, JTK4, CEK2, cancer, phosphorothioate, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
                                                                                                                                                                                                                                                                                                                                                                                                       /mod_base= OTHER
/note=_"2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                                                                             Human FGFR-3 antisense oligonucleotide, ISIS #125165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antisense oligonucleotide targetted to human FGFR-3
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                               BP.
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                               AAD55461 standard; DNA; 20
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/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-313244/30.
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modified_base
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                                                                                             07-AUG-2003
                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder.
                                                               AAD55461;
RESULT 320
                  AAD55461
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Length 20;

0.5%; Score 20; DB 1; Lord 100.0%; Pred. No. 4.4e+02;

Query Match Best Local Similarity

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Gaps

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0; Indels

0.5%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 4.4e+02;

100.0%; Prec. ...

20; Conservative

Local Similarity

Query Match Best Local & Matches 20 557 CCAACCAGACGGCGGTGCTG 576

Gaps

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Indels

Matches

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, UTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, hyperproliferative disorders or skin. They are useful as research reagents, therapeuties, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER
/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                            Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOB) nucleotides"
16. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                       Score 20; DB 1; Length 20;
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                           Human FGFR-3 antisense oligonucleotide, ISIS #125118.
Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
                                0.5%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                         127 CTGTGCCACTTCAGTGTGCG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER
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/mod_base=
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                                                                                    Conservative
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                                                               Local Similarity
ses 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                 Query Match
                                                                                                                                                                                                                             RESULT 322
                                                                                        Matches
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/mod base OTHER
/nore= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder, hyperproliferative disorder, antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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                Gaps
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                Indels
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                  Mismatches
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                      Conservative
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modified base
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AAD55428;

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AAD55449 standard; DNA; 20
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modified_base
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Synthetic.
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Matches
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                                                                                                                                                                                                                                                     Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                Gaps
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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                                                            Length 20;
                                                                              0; Indels
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                                        Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
                                                                     4.46+02;
                                                         0.5%; Score 20; DB 1;
100.0%; Pred. No. 4.4e+03
ive 0; Mismatches (
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/mod base= OTHER
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modified_base
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AAD55440/c
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/noce= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human PGFR-3
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/*tag= c
//mcd= c OTHER
/mote= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, UTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; 88.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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16. .20
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Pred. No. 4.4e+02;
                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                    antisense oligonucleotide targetted to human PGFR-3
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100.0%; Pred. No...
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Synthetic.
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, VIK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breach or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/noce= "2'-methoxyethyl (2'-MOE) nucleotides"
116. .20
/*tag= c
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100.0%; Pred. No. 4.40+02;
tive 0; Mismatches 0; Indels
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/*tag= a
/mod_base= OTHER
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      Claim 3; Page 79; 120pp; English.
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/note= "2
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Best Local Similarity 100.
Matches 20; Conservative
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Wyatt JR;
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   Monia BP,
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                                                                         The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or conditions hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mod_base= OTHER
/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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                                                                                                                                                                                                                                        0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human FGFR-3 antisense oligonucleotide, ISIS #125194.
                                                                                                                                                                                                                        Sequence 20 BP; 1 A; 5 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                          CACCACCGACAAGGAGCTAG 739
                                                       Claim 3; Page 79; 120pp; English
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AAD55488 standard; DNA; 20
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                                                                                                                                                                                                                                                       Local Similarity
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/*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH, JTK4; CEK2; cancer; phosphorothloate; ss.
                                                               Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. 20
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/note= "2 -methoxyethyl (2'-MOB) nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
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ID AAD55432 standard; DNA; 20
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Best Local Similarity 100.
Matches 20; Conservative
WPI; 2003-313244/30.
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20-MAR-2003.
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                                                                                                                                                      The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRP-3) ACH, JTK4 and CBK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGRP-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, broagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGPR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; antisense; fibroblast growth factor receptor 3; prophylaxis; developmental disorder; hyperproliferative disorder; antisense therapy; FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                  Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotiģes"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides'
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100.0%; Pred. No. 4.4e+02;
cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                          230 ACTGGACACGGCCCGAGCGG 249
20 ACTGGACACGGCCCGAGCGG 1
                                                                                                                                         Claim 3; Page 78; 120pp; English.
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     10-SEP-2001; 2001US-00953047.
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/*tag= b
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Matches 20; Conservative
                         (ISIS-) ISIS PHARM INC.
                                               Monia BP, Wyatt JR;
                                                                  WPI; 2003-313244/30.
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, hoper least to skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                   Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
/mod_base= OTHER
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1. .20
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06-SEP-2002; 2002WO-US028549.
                                                   10-SEP-2001; 2001US-00953047.
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                                                                                                               (ISIS-) ISIS PHARM INC
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRF-3, ACH, TYK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression
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/note= "Phosphorothioate backbone; All cytidine residues
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                                                                        note = "2 - methoxyethyl (2'-MOE) nucleotides"
"2'-methoxyethyl (2'-MOE) nucleotides'
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                                                        /mod base= OTHER
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nes 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRF-3, ACH, TVR4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophlaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                 06-SEP-2002; 2002WO-US028549
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                                                                           20-MAR-2003
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGPR-3. ACH, JTK4 and CEK2) to inhibit the expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, hyperproliferative disorders, especially cancer of colorectal, bladder, broagents, therapeutics, prophylaxis, kits and disgnostics, and as tools in differential and/or combinatorial analyses to elucidate expression in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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developmental disorder, hyperproliferative disorder; antisense therapy,
PGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; se.
                                              /note= "Phosphorothioate backbone; All cytidine residues
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/mod= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                                                                         are 5-methylcytidines"
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AAD55443/c
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 0; Indels
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             are 5-methylcytidines"
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostiss, and as tools in differential and/or combinatorial mantyes to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
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/not== "Phosphorothioate backbone; All cytidine residues
Human, antisense, fibroblast growth factor receptor 3, prophylaxis,
developmental disorder, hyperproliferative disorder, antisense therapy;
FGFR-3, ACH, JTK4, CEK2, cancer, phosphorothloate, ss.
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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Pred. No. 4.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGP) receptor 3 (also known as FGRP-3, ACH, TVK4 and CBK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or conditions hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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                                                                                                                                      /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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0
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/note= "2'-methoxyethyl (2'-MOE) nucleotides'
16. .20
                                                                                                                                                                                                                                                                                                                         -methoxyethyl (2'-MOE) nucleotides'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human FGFR-3 antisense oligonucleotide, ISIS #125189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
                                                            Location/Qualifiers
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                                                                                                    /*tag= a
/mod base= OTHER
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/note= "2 -metho
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Best Local Similarity 100.0
Matches 20; Conservative
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                                                                                    .20
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                                                            Key
modified base
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    Homo sapiens
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                     Synthetic.
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Gaps

AAD55483;

AADSS483/ ID AADS XX AAC AC AADS XX OT 07-A XX XX

RESULT 335

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AAD55503 standard; DNA; 20

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, WITK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, hopen, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to calucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence, is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                     /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
                                                    Human; antisense; fibroblast growth factor receptor 3; prophylaxis; developmental disorder; hyperproliferative disorder; antisense therapy; FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/mod base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
                         Human FGFR-3 antisense oligonucleotide, ISIS #125193.
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                                                                                                                                                                         Location/Qualifiers
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07-AUG-2003 (first entry)
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Best Local Similarity 100.
Matches 20; Conservative
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Synthetic.
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                                                                                                                                                                                                                                                                                              /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
                                                                                                                 Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; 88.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
/*tag= C OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                    Human FGFR-3 antisense oligonucleotide, ISIS #125209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
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                                                            (first entry)
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*tag=
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modified_base
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                                                          07-AUG-2003
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RESULT 337 AAD55503/c

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, TKY4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues.
                                                                                                                                                                                                                                                                                                         /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                  Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel compound targeted to a nucleic acid molecule encoding fibroblast
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "2 -methoxyethyl (2'-MOE) nucleotides'
                                                                                                                       Human FGFR-3 antisense oligonucleotide, ISIS #125146.
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base= OTHER
                           AAD55445 standard; DNA; 20 BP.
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/*tag= b
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                                                                                                                                                                                                                                                               Key
modified_base
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                                                                                        07-AUG-2003
                                                                                                                                                                                                                                   Synthetic.
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                                                          AAD55445;
RESULT 338
                AAD55445,
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, UTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperporliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial naalyses to calucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/mod_base= OTHER
/mote= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                         Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothloate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. 20
/*tag= c
/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                             Human FGFR-3 antisense oligonucleotide, ISIS #125164.
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1. .20
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2534 CTGGGCCCGACATGGCTCGG 2553
                20 CTGGGCCCGACATGGCTCGG 1
                                                                                                              ВР
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                                                                                                             AAD55460 standard; DNA; 20
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/*tag= b
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                                                                                RESULT 339
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0; Indels

0.5%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 4.4e+02;

100.0%; Pred. M. Tive 0; Mismatches

20; Conservative

Best Local Similarity Matches 20; Conserva

Query Match

Sequence 20 BP; 3 A; 8 C; 7 G; 2 T; 0 U; 0 Other;

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WO2003023004-A2.
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                                                                                                                                    RESULT 341
AAD55490/c
                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
                                                                                                                                                                                              Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; 88.
                               Gaps .
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                                                                                                                                                                                                                                                                                                                                                         nucleotides
     Score 20; DB 1; Lengtn 20;
Pred. No. 4.4e+02;
O: Lindels
                                                                                                                                                                             Human FGFR-3 antisense oligonucleotide, ISIS #125166.
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                   100.0%; Pred. N.C.
                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                    3652 TTGCTTGCCTGCAGGGCCAT 3671
                                                                                                                                                                                                                                                                                                                                                  mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                         mod_base= OTHER
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                                                                      20 TrgcrrcccrccAcccar 1
                                                                                                                         BP.
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                0.5%;
                                                                                                                         AADSS462 standard; DNA; 20
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                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wyatt JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-313244/30.
                         Similarity
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                                                                                                                                                                                                                                                                                modified base
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                                                                                                                                                               07-AUG-2003
                                    20;
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                                                                                                                                             AAD55462;
                 Query Match
                           Best Local
                                    Matches
                                                                                                      RESULT 34
AAD55462/
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder,
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/mote "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothloate; ss.
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They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16.20
/ttag= 0
/mod_base= OTHER
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                                                                                                                                                   Length 20;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human FGFR-3 antisense oligonucleotide, ISIS #125196.
                                                                                       Sequence 20 BP; 3 A; 2 C; 5 G; 10 T; 0 U; 0 Other;
                                                                                                                                                0.5%; Score 20; DB 1; L. 100.0%; Pred. No. 4.4e+02; iive 0; Mismatches 0;
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1. 20
/*tag= a
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                                                                                                                                                                                                                                                                      3767 TCCGAAAATAAAGACACCT 3786
                                                                                                                                                                                                                                                                                                                         20 rccgaaaaaraaagacaccr
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                                                                                                                                                               Query Match
Best Local Similarity
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Gaps

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as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or conditions hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
1...5
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, antisense, fibroblast growth factor receptor 3, prophylaxis;
developmental disorder, hyperproliferative disorder; antisense therapy;
FGFR-3; ACH, JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. 20
/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                 DB 1; Length 20; 4.4e+02;
                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human FGFR-3 antisense oligonucleotide, ISIS #125148.
                                                                                                                                       antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                     Sequence 20 BP; 6 A; 9 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                               Query Match 0.5%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 4.4 Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                             2457 CGAGGGCCTTTGTTCTGGG 2476
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AAD55447/c
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                                                                                                                                                                                                                                                                                                                                                                                                                          Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tool in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                     0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                 Human FGFR-3 antisense oligonucleotide, ISIS #125145.
                                                                                                         Sequence 20 BP; 7 A; 8 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                               100.0%; Preq. ....
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Synthetic.
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Monia BP, Wyatt JR;
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AAD55479/c
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                  The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRF-3). ACH, JTK4 and CEKZ) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGRF-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                        Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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                                                                                                                                                                           Score 20; DB 1; Length 20;
Pred. No. 4.4e+02;
                                                                                                                                                                                                0; Indels
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                                                                                                                                                        Sequence 20 BP; 7 A; 4 C; 2 G; 7 T; 0 U; 0 Other;
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Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                      2798 CTATAAATAGATGCTGTGTA 2817
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'mod_base= OTHER
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     Claim 3; Page 79; 120pp; English.
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                                                                                                                                                                                                                                                                           RESULT 344
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially caner of colorectal, bladder, hyperproliferative disorders, especially caner of colorectal, bladder, horse, unique, cervical, breaptorial, kits and diagnostics, and as tools in differential and/or combinatorial analyses to chucidate expression in differential and/or combinatorial analyses to chucidate expression in differential and/or combinatorial analyses to chucidate expression. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
1...5
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; 88.
growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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/*tag= c
/mod_bag= OTHER
/mod_bag= n2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides
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                                                                                                                             Claim 3; Page 79; 120pp; English.
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Best Local Similarity
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07-AUG-2003
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                                                             Monia BP,
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                                                                                                                                                                                                           The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorated. bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; antisense; fibroblast growth factor receptor 3; prophylaxis; developmental disorder; hyperproliferative disorder; antisense therapy; FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                    Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides
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                                                                                                                                                                       Claim 3; Page 79; 120pp; English
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                  WPI; 2003-313244/30
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/mod_bage= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                              Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/*tag= b
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1.0cte= "2'-methoxyethyl (2'-MOE) nucleotides"
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Pred. No. 4.4e+02;
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Matches 20; Conservative
(ISIS-) ISIS PHARM INC.
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                                                          Wyatt JR;
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                                                                                                                                                                                                                               The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRP-3) ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGRP-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, hyperproliferative disorders, especially cancer of colorectal, bladder, beagents, they are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "Phosphorothicate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                              Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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'note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 4.4e+02;
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/mod_base= OTHER
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AAD55452 standard; DNA; 20 BP.
                   06-SEP-2002; 2002WO-US028549.
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                                                                     (ISIS-) ISIS PHARM INC
                                                                                                Monia BP, Wyatt JR;
                                                                                                                      WPI; 2003-313244/30.
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nes 20;
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                  Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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10-SEP-2001; 2001US-00953047
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AAD55500 standard; DNA; 20 BP
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Matches 20; Conservative
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/*tag=
                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC.
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/mod_base= OTHER
/mod="Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                      Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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                     /mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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            /*tag= c
/mod_base= OTHER
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                                                                                                     06-SEP-2002; 2002WO-US028549.
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 16. .20
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Best Local Similarity
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Synthetic.
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, brasst or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/*tag= c
//mod bas = OTHER
//note= "2 -methoxyethyl (2'-MOE) nucleotides"
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
                                                                              /mod_base= OTHER
/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
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                                                                                                                                                                                                          nucleotides
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100.0%; Pred. No. 4.40+02;
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/note= "2'-methoxyethyl (2'-MOE)
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/mod base= OTHER
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Matches 20; Conservative
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developmental disorder, hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                           /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
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                                                                                                               /note=="2'-methoxyethyl (2'-MOE) nucleotides"
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                                                                 are 5-methylcytidines"
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                                                                                                           /*tag= b
/mod_base= OTHER
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AAD55438 standard; DNA; 20
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Best Local Similarity 100.
Matches 20, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wyatt JR;
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Gaps

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ò 셤 RESULT 352 AAD55438/

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/*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                Human, antisense, fibroblast growth factor receptor 3, prophylaxis,
developmental disorder, hyperproliferative disorder, antisense therapy,
FGFR-3, ACH, JTK4, CEK2, cancer, phosphorothioate, ss.
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                                                                                                                                                                                                                                                                         /mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                     /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
developmental disorder; hyperproliferative disorder; antisense therapy; FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                                                                           are 5-methylcytidines'
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                                                                                                     Location/Qualifiers
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Matches 20; Conservative
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modified base
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                                                      Homo sapiens
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                                                                      Synthetic.
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                                                       The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or byperporliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
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100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense oligonucleotide targetted to human FGFR-3
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Example 15; Page 79; 120pp; English.
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Best Local Similarity 100.
Matches 20, Conservative
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AAD55454/c
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20 CCAACAATGTGAGGGGTCCC 1

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AAD55451 standard; DNA; 20 BP

RESULT 354 AAD55451/c

07-AUG-2003 (first entry)

AAD55451;

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RESULT 356

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGP) receptor 3 (also known as FGRR-3) ACH, TWT4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or conditions hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
                                                                                                                                                                                                                                                                      /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                     Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothicate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/mod bass= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16 .20
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                        Human FGFR-3 antisense oligonucleotide, ISIS #125156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antisense oligonucleotide targetted to human FGFR-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 15; Page 79; 120pp; English.
                                                                                                                                                                                                                        Location/Qualifiers
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                                             (first entry)
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Best Local Simi
Matches 20;
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                                           07-AUG-2003
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               AAD55454;
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The invention relates to antiense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, UTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to chucidate expression in differential and/or combinatorial analyses to chucidate expression
                                                                                                                                                                                                                                                                                                                /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                     Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/mod_base= OTHER
/force= "2'-methoxyethyl (2'-MOB) nucleotides"
/force= 12'-methoxyethyl (2'-MOB) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -methoxyethyl (2'-MOE) nucleotides"
                                                                                                         Human FGFR-3 antisense oligonucleotide, ISIS #125191.
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                                                                                                                                                                                                                                                                 Location/Qualifiers
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/mod_base= OTHER
              BP.
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              AAD55485 standard; DNA; 20
                                                                              (first entry)
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AAD55485,
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Gaps

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Query Match

0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels

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Gaps ; 0

Score 20; DB 1; Length 20; Pred. No. 4.4e+02; 0; Mismatches 0; Indels

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Conservative

Similarity

Length 20;

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0.5%; Score 20;

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Query Match
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are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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GTGGGCCCGGACGCACACC 686
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Synthetic.
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antisense oligonucleotide targetted to human FGFR-3 Sequence 20 BP; 6 A; 9 C; 5 G; 0 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                          /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
                                                                                                                                                                                                                                                                               Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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                Gaps
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/*tag= b
/mod_bage= OTHER
10cte= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
              Indels
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 4.4e+02;
ilarity 100.0%; Pred. No. 4.4
Conservative 0; Mismatches
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                                               825 CTCTGCGTGCTGGTGC 844
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 Best Local Similarity
Matches 20; Conserv
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modified_base
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AAD55431;

Matches

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothloate; 88.
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reagents, therapeutics, prophylaxis, kits and diagnostics, and as tool in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human FGFR-3 antisense oligonucleotide, ISIS #125116.
                                                                                                              Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                           197 CTGAGGACACAGGTGTGGAC 216
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/*tag= a
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Best Local Similarity 100.
Matches 20; Conservative
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are 5-methylcytidines"
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2'-methoxyethyl (2'-MOB) nucleotides"
16. .20
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                                                                                             Length 20;
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                      antisense oligonucleotide targetted to human FGFR-3
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                                                                                          0.5%; Score 20; DB 1; Le
100.0%; Pred. No. 4.4e+02;
Live 0; Mismatches 0;
                                                          Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                       1434 GCTGGTGGAGTACGCGGCCA 1453
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/mod_base= OTHER
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Best Local Similarity
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RESULT 35
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compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                                                                                                                                  ch 0.5%; Score 20; DB 1; Length 20; 1 Similarity 100.0%; Pred. No. 4.4e+02; 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                      antisense oligonucleotide targetted to human FGFR-3
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/mod_base= OTHER
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Synthetic.
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR.3, ACH, JTH4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to eluvidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/*tag= b
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%; Score 20; DB 1; Length 20; 00.0%; Pred. No. 4.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
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/note= "2'-methoxyethyl
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/note= "2 -
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Best Local Similarity 100.
Matches 20, Conservative
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/*tag=
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AAD55482/c
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WPI; 2003-313244/30.
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                                                 The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRF-3) ACH, WIX4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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   receptor and for treating an animal having cancer or developmental
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/note= "2 -methoxyethyl (2'-MOE) nucleotides'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotides
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                                                                                                                                                                                        Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                           ch 0.5%; Score 20; DB 1; Le 1 Similarity 100.0%; Pred. No. 4.4e+02; 20; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                       396 GCATCAGCAGTGGAGCCTGG 415
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/mod_base= OTHER
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                                  Claim 3; Page 79; 120pp; English.
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modified_base
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                 disorder
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                                                                                                                                                                                                                                                                                                           RESULT 363
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                                                                                                                                                                                                                                                                                                                                                           hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; 88.
Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/mod_base= OTHER
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/note= "2 -methov
                                                                                                                                                             Claim 3; Page 79; 120pp; English.
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ID AAD55480 standard; DNA; 20 BP.
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/*tag= b
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                                                                                                           disorder
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (RGP) receptor 3 (also known as FGRR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGRR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
1. .5
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                                                                                                                                                                                                                Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human FGFR-3 antisense oligonucleotide, ISIS #125110.
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1. .20
/*tag≈ a
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06-SEP-2002; 2002WO-US028549.
                                           10-SEP-2001; 2001US-00953047.
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                                                                                      (ISIS-) ISIS PHARM INC
                                                                                                                            Monia BP, Wyatt JR;
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                                                                                                                                                                                                                                                                           The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, TVR4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                               Novel compound targeted to a nucleic acid molecule encoding fibroblast
                                                                                                                               growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/mod base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
/fo. 20
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100.0%; Pred. No. 4.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                         Claim 3; Page 79; 120pp; English
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(ISIS-) ISIS PHARM INC.
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Matches 20, Conserva
                                             Wyatt JR;
                                                                                   WPI; 2003-313244/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003023004-A2
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                                           Monia BP,
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AAD55497;

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RESULT 365

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AAD55497

Query Match

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Gaps

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06-SEP-2002; 2002WO-US028549.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
168 20; Conservative
                                                                                                                            (ISIS-) ISIS PHARM INC
                                                                                                                                                 Monia BP, Wyatt JR;
                                                                                                                                                                    WPI; 2003-313244/30.
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                                                              20-MAR-2003.
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Matches
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                                                                                                                                                                                                                        The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRE-3) ACH, TYR4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, antisense, fibroblast growth factor receptor 3, prophylaxis;
developmental disorder, hyperproliferative disorder, antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                        Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.
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/mod_base= OTHER
/mote= "2'-methoxyethyl (2'-MOE) nucleotides"
16. 20
                                                                                                                                                                                                                                                                                                                                                                                        Score 20; DB 1; Length 20;
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                   162 ATCCTCGGGAGATGACGAAG 181
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                                                                                                                                                                                                        Claim 3; Page 78; 120pp; English.
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                                           06-SEP-2002; 2002WO-US028549.
                                                               10-SEP-2001; 2001US-00953047.
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                                                                                     (ISIS-) ISIS PHARM INC
                                                                                                           Monia BP, Wyatt JR;
                                                                                                                                WPI; 2003-313244/30.
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modified_base
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Synthetic.
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                       20-MAR-2003
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRFA.3 ACH, TYK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breach or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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/*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
1. .5
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 78; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccrccarcrccrccrcaad 1
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRF-3) ACH, TYK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeuties, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
      /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, antisense, fibroblast growth factor receptor 3, prophylaxis, developmental disorder, hyperproliferative disorder; antisense therapy; FGFR-3; ACH, JTK4, CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/*tag= b
/mod_base= OTHER
/mod_base= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/mod_base= OTHER
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                                                               modified base
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AADS5502/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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                  /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
/*tag= //mod base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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                                                                 modified base
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FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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AAD55441/c
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                                  /*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone, All cytidine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; antisense; fibroblast growth factor receptor 3; prophylaxis; developmental disorder; hyperproliferative disorder; antisense therapy;
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                                                                                                 /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                         'note= "2 -methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human FGFR-3 antisense oligonucleotide, ISIS #125109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 3 A; 9 C; 6 G; 2 T; 0 U; 0 Other;
                                                                  are 5-methylcytidines"
             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3626 GGGCCCTGAGTCTGGGCAGC 3645
                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 79; 120pp; English.
                                                                                                                                                /mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 GGGCCCTGAGTCTGGGCAGC 1
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               Key
modified base
                                                                               modified_base
                                                                                                                        modified_base
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, TYK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or
                                                                                                                                                                                          /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
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/mod_base= OTHER
/notE= "2'-methoxyethyl (2'-MOE) nucleotides"
16..20
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 4.4e+02;
iive 0; Mismatches 0; Indels
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                                                                                    Location/Qualifiers
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                                                                                                                                                                              OTHER
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*tag=
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                                                                                          Key
modified_base
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Homo sapiens
Synthetic.
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3) ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperporliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
                                                                                                                                                                                                                                                                                                                                /mod_base= OTHBR
/mod= Phosphorothioate backbone; All cytidine residues
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                        Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH, JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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/*tea b
/*mod base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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                                                                                  Human FGFR-3 antisense oligonucleotide, ISIS #125150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antisense oligonucleotide targetted to human FGFR-3
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                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2853 GGAAGAGGAAAAGGCTGGTA 2872
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                                          (first entry)
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Matches 20; Conservative
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                                                                                                                                                                                                                                         Synthetic.
  AAD55448;
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                                                                                                                                                                                                                                                                            /note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                     Human, antisense, fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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100.0%; Pred. No. 4.4e+02;
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Human FGFR-3 antisense oligonucleotide, ISIS #125142.
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/mod base= OTHER
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                                                                                                                            Homo sapiens
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                                                                                                                                                  Synthetic.
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Gaps

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AAD55448 standard; DNA; 20 BP

RESULT 373 AAD55448/c ID AAD554 XX

Best Loca Matches

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRF-3.) AGH, JUX4 and CEX2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or conditions byperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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are 5-methylcytidines"
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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AADSSS01 standard; DNA; 20
                                                                                                                              (first entry)
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGRPA.3 ACH, JUTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGRPA.3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, bready or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to clucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                             /note= "phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
                                                                                                                                                   Human, antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
                                                                                                                       Human FGFR-3 antisense oligonucleotide, ISIS #125200.
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/mod base=
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                             AAD55494 standard; DNA;
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*tag=
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modified base
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                                                               AAD55494;
RESULT 375
                  AAD55494/
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DB 1; Length 20;

Score 20;

0.5%;

Query Match

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Gaps ö

0.5%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 4.4e+02; cive 0; Mismatches 0; Indels

U.Dr Best Local Similarity 100.0 Matches 20, Conservative

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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                        Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/note= "2 -methoxyethyl (2'-MOE) nucleotides"
                Indels
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 Pred. No. 4.4e+02;
 nilarity 100.0%; Pred. No. 4.4
Conservative 0; Mismatches
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                                            2031 TACCGTGACGTCCACCGACG 2050
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/mod_base= OTHER
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Best Local Similarity
Matches 20; Conserv
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                      Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                             Query Match 0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 20; Conservative 0; Mismatches 0; Indels
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BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
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                                                                                             3565 GCTACCTTTCAAAGCTTGGA 3584
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AAD55491 standard; DNA; 20 BP
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
 in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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                                                                  0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                    Human FGFR-3 antisense oligonucleotide, ISIS #125199.
                                                 Sequence 20 BP; 0 A; 7 C; 8 G; 5 T; 0 U; 0 Other;
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                                                                                                          1260 CAAGGACCGGGCCGCCAAGC 1279
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                                                                        Query Match
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AAD55493/
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associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothloate; ss.
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/mod_base= OTHER
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
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16. .20
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0.5%; Score 20; DB 1; L
Best Local Similarity 100.0%; Pred. No. 4.46+02;
Matches 20; Conservative 0; Mismatches 0;
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/mod_base=
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RESULT 381
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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and disgnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences which can be used to detect single nucleotide polymorphisms (SNPB). The DNA sequences of the invention are useful for detecting SNPs existing in human genes and for the diagnosis of human disease. The present DNA sequence represents a human gene PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide for detecting single nucleotide polymorphisms existing in human gene, contains isolated human gene having specified sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises isolated human gene sequences and PCR primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; gene sequence; single nucleotide polymorphism; SNP; disease diagnosis; 88; PCR; primer.
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                                                                                                                                                                                                                                                                         Score 20; DB 1; Length 20;
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                         Sequence 20 BP; 4 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                              0.5%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                   2557 CTGCCTTTGCACCACGGGAC 2576
                                                                                                                                                                                                                                                                                                                                                                      20 CTGCCTTTGCACCACGGGAC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH93220 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-DEC-2001; 2001JP-00377637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-DEC-2001; 2001JP-00377637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene PCR primer #65.
                                                                                                                                                                                                                                                                                                             20; Conservative
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                                                                                                                                                                                                                                                                                            Local Similarity
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Best Local S
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Matches
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The invention comprises isolated human gene sequences and PCR primer sequences which can be used to detect single nucleotide polymorphisms (SNPs). The DNA sequences of the invention are useful for detecting SNPs existing in human genes and for the diagnosis of human disease. The present DNA sequence represents a human gene PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide for detecting single nucleotide polymorphisms existing in human gene, contains isolated human gene having specified sequence.
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                                                                                                                        human; gene sequence; single nucleotide polymorphism; SNP; disease diagnosis; ss; PCR; primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 1049; 529pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                                                                                                                                                                                                                                                                          (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1824 GCTCTGGGAGATCTTCACGC 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCTCTGGGAGATCTTCACGC 20
              BP.
                                                                                                                                                                                                                                                                                11-DEC-2001; 2001JP-00377637.
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                                                                                                                                                                                                                                                      11-DEC-2001; 2001JP-00377637
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              ADH93212 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH93215/c
ID ADH93215 standard; DNA; 20
                                                                                                Human gene PCR primer #57.
                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene PCR primer #60.
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                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                          24-JUN-2003.
                                                                     22-APR-2004
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                                          ADH93212;
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ADH93212
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The present invention describes a method for the inspection of flat
c epithelial cells in which it is judged that flat epithelial cells
c eparated from an organism can proceed to flat epithelial cancer when the
c 2128th base in fibroblast growth factor receptor (FGFR) gene of the cells
c is mutated from guanine to thymine. Also described is a method for
c screening treating or preventive agents for flat epithelial cancers in
which a candidate subtenace of treating agent for flat epithelial cancer
c is applied to flat epithelial cancer cells producing FGFR protein in
which the 2128th (exon 17) amino acid in FGFR3 gene is mutated from
c guanine to thymine or the 697th amino acid is mutated from glycine to
c guenine to candidate substance is selected by using the facts that
the 2128th base in the flat epithelial cell FGFR3 gene after the
c the 2128th base in the flat epithelial cell FGFR3 gene after the
c protein produced returned to glycine as the indices. The method is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inspection of flat epithelial cell, screening of treating or preventive agents for flat epithelial cancers, the treating or preventive agents for flat epithelial cancer.
                                                                                                                                       The invention comprises isolated human gene sequences and PCR primer sequences which can be used to detect single nucleotide polymorphisms (SNPs). The DNA sequences of the invention are useful for detecting SNPs existing in human genes and for the diagnosis of human disease. The present DNA sequence represents a human gene PCR primer of the invention.
                                          Polynucleotide for detecting single nucleotide polymorphisms existing in human gene, contains isolated human gene having specified sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; fibroblast growth factor 3; FGF3; flat epithelial cell; cancer; flat epithelial cell cancer; PCR primer; 88.
                                                                                                                                                                                                                                                                                          0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human fibroblast growth factor 3 exon 19 PCR primer #2.
                                                                                                                                                                                                                                                          Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                           Claim 2; SEQ ID NO 1052; 529pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                               462 CGTGGAGAACAAGTTTGGCA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 6; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZERI ) ZERIA SHINYAKU KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                         20 CGTGGAGAACAAGTTTGGCA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC79688 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                         20; Conservative
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity
              WPI; 2003-819215/77.
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Synthetic.
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for the inspection of flat epithelial cells. The present sequence represents a PCR primer for human FGFR3, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                              cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer; chromosome mapping; human; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NOVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of a PCR primer which was used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Furtak K;
Spytek KA;
M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or
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                                                                                                                           Gaps
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                                                                                          0.5%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 4.4e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
                                                               Sequence 20 BP; 2 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                     Human NOVX protein-related PCR primer SeqID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example C; SEQ ID NO 140; 433pp; English.
                                                                                                                                                          2188 CGGACGTGAAGGGCCACTGG 2207
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2002US-0370349P.
2002US-0370969P.
2002US-0372019P.
                                                                                                                                                                                                                                                                 BP
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2002US-00160619.
2002US-0403748P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002US-0374379P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-NOV-2002; 2002US-00287226.
31-MAR-2003; 2003US-00403161.
                                                                                                                                                                                                                                                                 ADK51119 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                 Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003083046-AZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-2002;
30-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-2002;
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04-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2002;
08-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                          17-JUN-2004
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                                                                                                      Query Match
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Gaps ö

DNA preparation; 5' mRNA; linker synthesis; primer synthesis; gene regulation; gene expression; ss; tag. mRNA DNA preparation method related tag DNA sequence #8.

1 CCTACGTTACCGTGCTCAAG 20

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ADK70840 standard; DNA; 20

06-MAY-2004

ADK70840;

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                                                                                                                                                                                                                                                                                                     cytostatic; NOVX-agonist; NOVX-antagonist; vaccine; gene therapy; cancer; chromosome mapping; human; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NOVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of a PCR primer which was used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g. cancer or for chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson DW, Bento P, Boldog FL, Burgess CE, Casman SJ, Furtak K; Gorman L, Gould-Rochberg BE, Gunther E, Heyes MP, Li L, Spytek KA; Stone DJ, Zhong M, Malyankar UM, Edinger SR, Patturajan M; Rothenberg ME, Smithson G;
                                 Gaps
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 Length 20;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
0.5%; Score 20; DB 1; Le
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                        Human NOVX protein-related PCR primer SegID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example C; SEQ ID NO 143; 433pp; English.
                                                             02-APR-2002; 2002US-00115479.
08-APR-2002; 2002US-0370349P.
08-APR-2002; 2002US-0370969P.
12-APR-2002; 2002US-0374379P.
30-MAY-2002; 2002US-0374379P.
30-MAY-2002; 2002US-0384543P.
03-JUN-2002; 2002US-0160619.
15-AUG-2002; 2002US-0160619.
04-NOV-2002; 2002US-0160619.
                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-2003; 2003WO-US010142
                                                                                                                                                                           70
                                                                                                                                                                                                                                          (first entry)
                                 Conservative
                                                                                                                                                                         ADK51122 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
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                Best Local Similarity
Matches 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                    WO2003083046-A2
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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   Query Match
                                                                                                                                            RESULT 385
                                                                                                                                                            ADK51122
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Harbers MT

Carninci P,

Hayashizaki Y,

(RIKE) RIKEN KK. (DNAF-) DNAFORM KK.

12-JUN-2003; 2003WO-JP007514. 12-JUN-2002; 2002JP-00171851. 12-AUG-2002; 2002JP-00235294.

WO2003106672-A2

24-DEC-2003.

Unidentified

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises a method for preparing a DNA fragment corresponding to a nucleotide sequence of a 5' end of an mRNA. The method is useful for synthesising a nucleotide sequence to be used as a linker or primer and selectively collecting multiple nucleic acid fragments containing information on the nucleotide sequences at the 5' end of multiple mRNA in a sample. The method is also useful for identifying regions in the genome, which are required for gene regulation and gene expression. The present DNA sequence was used in an example of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer #6, used for amplification of pear plant microsatellite DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                          Preparing DNA fragment corresponding to nucleotide sequence of 5' end region of mRNA, by preparing nucleic acid corresponding to nucleotide sequence of 5' end of mRNA, cleaving nucleic acid with restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; SEQ ID NO 40; 121pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK50766 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-082194/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK50766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK50766/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #X#X#X#X#
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686 CCTACGTTACCGTGCTCAAG 705

20; Conservative

Matches

Local Similarity

Query Match

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Gaps

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The present invention relates to a new microsatellite DNA comprising a fully defined sequence of 389 base pairs as given in the specification. The microsatellite DNA can be used as a DNA marker effective for discriminating the species and grades, selecting useful species and isolating useful species and areas and isolating useful genes. The present nucleic acid sequence represents one of a collection (ABKS0761-ABKS0766) of PCR primers used in the methods of the invention for amplification of pear plant microsatellite DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obtaining unknown DNA sequence flanking a single known sequence for use as PCR templates, involves single site amplification with polymerase having strand displacement capability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simple sequence repeat; SSR; single site amplification; SSA; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microsatellite DNA of Pyrus, useful as DNA marker for discriminating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20; DB 1; Length 27; Pred. No. 6.2e+02;
grade discrimination; species selection; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSA primer 2 for amplifying A. thaliana and Z. mays DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                        (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2332 TGCGTGTGTGTGTGTGTGCACA 2355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 36; Page 27; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00915609
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                                                                                                                                                                                                                                                    21-JUL-2000; 2000JP-00220340
                                                                                                                                                                                                                                                                                                                 21-JUL-2000; 2000JP-00220340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 0.5%;
Local Similarity 79.2%;
Les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ89470 standard; DNA; 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-328353/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-366818/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   species and grades.
                                                                                                                             JP2002034562-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUN-2000
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                                                                                                                                                                                          05-FEB-2002
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                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Gaps

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This invention describes a novel method for obtaining DNA of unknown sequence flanking a single site of known sequence involves single site and sequence that can be application of circular DNA template flanking a target DNA of known sequence using a polymerase having strand displacement capability. The method is used for obtaining a particular target DNA sequence that can be useful as templates that contain entire simple sequence repeat (SSR) alleles for amplification (SSA) procedures e.g. PCR or can be employed as unarkers, e.g. in distinguishing between species, strains or variety and ecotype identification, marker condition. It also provides a marker for use in areas such as import and export regulation, variety and ecotype identification, marker condition. It also provides a marker for use in areas such as import and ecotype identification, marker conditions in the same of a single stranded DNA template and flanking treed to generate a linear DNA molecule containing two target sequences. It can also be used for e.g. for cloning cDNA or genomic DNA which flanks any known short target sequence. Conding cDNA or genomic DNA which flanks any known short target sequence. Conding cDNA or genomic DNA which flanks any known short target sequence. Conding cDNA or genomic DNA which flanks any known short target sequence. Conding cDNA or genomic DNA which flanks any known short target sequence. Conding cDNA or genomic DNA which flanks any known short target sequence. Conding cDNA or genomic DNA which flanks accelerated development of high resolution DNA markers that may be used for fingerprinting, mapping etc., using small amounts of tissue than 1 mug). It also allows the production of a PCR template and scenarion of target DNA sequence, the size of which is regulated only by the primer design. The present method also eliminates consuming steps, typically requiring no less than three months, with consuming steps, typically requiring no less than three months, with consuming steps, typically requiring between the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28 BP; 2 A; 1 C; 13 G; 12 T; 0 U; 0 Other;
                         Example 1; Col 9-10; 11pp; English
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Gaps ö Query Match 0.5%; Score 20; DB 1; Length 28; Best Local Similarity 82.1%; Pred. No. 6.5e+02; Matches 23; Conservative 0; Mismatches 5; Indels 2314 GGTCTGTGTGTGTGTGTGTGTGTG 2341 SNP specific upper PCR primer SEQ ID 1801. 1 GGAATTCGTGTGTGTGTGTGTGTG 28 AAH39005 standard; DNA; 23 BP 14-AUG-2001 (first entry) 셤 ઠે

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Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPB; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfects; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss. WO200129262-A2. Homo sapiens 26-APR-2001.

99US-0160096P.

15-OCT-1999;

13-OCT-2000; 2000WO-US028436.

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liver growth, hepatocyte proliferation, pathological liver condition, liver damage; vascular endothelial growth factor receptor modulator; VEGFR modulator; hepatchropic; antiinflammatory; liver growth promoter; liver failure; hepatitis; liver cirrhosis; toxic liver damage; medicamentary liver damage;
                                                                                                                                                                                                                                                                                                                    Sequence 23 BP; 0 A; 0 C; 10 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                  for a human SNP containing DNA sequence
                                                                                                                                                                                                                                                                                                                                                                       2311 TITGGTCTGTGTGTGTGTGTG 2333
                                                                                                                                                                                                                                                                                                                                                                                hepatic necrosis; PCR primer; ss.
                                                                                     Claim 1; Page 59; 83pp; English.
(ORCH-) ORCHID BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG82642 standard; DNA; 23 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIGF gene reverse PCR primer.
                                                                                                                                                                                                                                                                                                                                      0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2002; 2002US-0386637P
                  Pohl M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                      21; Conservative
                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                  WPI; 2001-290930/30
                 Picoult-Newburg L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003103581-A2.
                                                                    acid sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG82642;
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 390
8
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Gaps

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liver growth; hepatocyte proliferation; pathological liver condition; liver damage; vascular endothelial growth factor receptor modulator; VEGFR modulator; hepatotropic; antiinflammatory; liver growth promoter; liver failure; hepatitis; liver cirrhosis; toxic liver damage; medicamentary liver damage; hepatic encephalopathy; hepatic coma;

hepatic necrosis; probe; ss

Synthetic

BP.

ADG82637 standard; DNA; 23

ADG82637/c

ADG82637;

(first entry)

bFGF gene probe. 11-MAR-2004

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The present invention describes a method for promoting (M1) liver growth or promoting (M2) hepatocyte proliferation in the liver of a subject, or protecting CCC treating (M3) a pathological liver condition in a subject, or protecting CCC (M4) liver from damage in the subject due to exposure to a hepatotoxic agent, which involves administering to the subject a vascular endothelial growth factor receptor (VEGFR) modulating agent (I). Also described: (I) an article of manufacture comprising a container, composition contained within the container and a label on the container instructing uses of the composition for promoting liver growth, where the composition comprising a first container, a LABEL on the first container, and a composition comprising a first container, a LABEL on the first container, and a composition comprising a first container, a label on the container, where the composition comprision contained within the first container, and a composition contained within the first container, where the composition comprising a profer modulating agent in the amount comprising a buffer and an instruction for using the kit for promoting liver growth. (I) has negligate to promote liver growth promoter. (I) can be used for promoting container, and a liver growth promoter. (I) can be used for promoting container, and a liver growth promoter. (I) can be used for promoting container, hepatics, liver firm damage in a subject due to exposure to conform the protecting liver firm damage in a subject due to exposure to chapatotoxic agent. The VEGFR modulator create a local cascade of signaling events originating in sinusoidal endothelial cells following composition, which is much more potent and beneficial in growth more potent and beneficial in the receptor activation liver growth were potent and beneficial in further amount and beneficial in the receptor activation in the exemplification of the present conformation in the liver growth factor (HGP).
                                                                                                                                                                                                                            Promoting liver growth or promoting hepatocyte proliferation in liver of subject, treating pathological liver condition e.g. cirrhosis in subject, by administering vascular endothelial growth factor receptor modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23 BP; 4 A; 9 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19.8; DB 1;
Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O.5%; Score 19.8; L
Local Similarity 91.3%; Pred. No. 5.5e
es 21; Conservative O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002 CAGCTGGTGGAGGACCTGGACCG 2024
                                                                                                     Le Couter J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 CAGTTGGTGGAAGACCTGGACCG 1
                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 44; 64pp; English.
                                                                                                 Ferrara N, Hillan KJ,
                                  (GETH ) GENENTECH INC.
                                                                                                                                                                WPI; 2004-071254/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide continues of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the includes kits for determining the presence or absence of a SNP, using the coligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPs primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The coligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, costeogenesis imperfects and acute intermittent porphyria. Phenotypic traits also include symptoms of or useceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune conference intermitations, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and contents and patents and presents a PCR primer specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                            New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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The present invention describes a method for promoting (MI) liver growth or promoting (M2) hepatocyte proliferation in the liver of a subject, treating (M3) a pathological liver condition in a subject, or protecting (M4) liver from damage in the subject due to exposure to a hepatotoxic agent, which involves administering to the subject a vascular endothelial growth factor receptor (VEGFR) modulating agent (I). Also described: (I) an article of manufacture comprising a container, composition contained within the container and a label on the container instructing uses of the composition for promoting liver growth, where the composition comprises a VEGFR modulating agent in the amount effective to promote liver growth, and (2) a kit comprising a lirst container, a LABEL on the first container, and a composition container of a LABEL on the first container, and an instruction for using the kit for promoting liver growth. (I) has hepatotropic and antinflammatory activities, and can be used as a VEGFR modulator, and a liver growth promoter. (I) can be used for promoting modulacor, and a liver growth promoter. (I) can be used for promoting treating a pathological liver conflictation in the liver of a subject, treating a pathological liver confliction in a subject such as liver contains. Inver cirrhosis, toxic liver damage, medicamentary callure, hepatitis, liver cirrhosis, toxic liver damage, medicamentary
                                                                                                                                                                                                                                                                                                                                                  Promoting liver growth or promoting hepatocyte proliferation in liver of subject, treating pathological liver condition e.g. cirrhosis in subject, by administering vascular endothelial growth factor receptor modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the principal liver mitogen, hepatocyte growth factor (HGF). sequence is mand in the community.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or for protecting liver from damage in a subject due to exposure to hepatotoxic agent. The VEGFR modulator create a local cascade of signaling events originating in sinusoidal endothelial cells following VEGF receptor activation, which is much more potent and beneficial in promoting hepatocyte proliferation and liver growth than systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      liver damage, hepatic encephalopathy, hepatic coma or hepatic necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 43; 64pp; English.
                                                                                                   05-JUN-2003; 2003WO-US017591
                                                                                                                                                   05-JUN-2002; 2002US-0386637P
                                                                                                                                                                                                                                                      Hillan KJ,
                                                                                                                                                                                                  (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                      WPI; 2004-071254/07.
WO2003103581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĕ
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                                                 18-DEC-2003
                                                                                                                                                                                                                                                      Ferrara N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         delivery
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Gaps ö Length 23; 2; Indels Sequence 23 BP; 4 A; 9 C; 5 G; 5 T; 0 U; 0 Other; Score 19.8; DB 1; Pred. No. 5.5e+02; 0; Mismatches 0.5%; 21; Conservative Query Match Best Local Similarity Matches

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2002 CAGCTGGTGGAGGACCTGGACCG 2024 23 CAGTTGGTGGAAGACCTGGACCG 1 ð ద

ADH70580/c

human; T-cell associated disease; Vbeta; autoimmune disease; degenerative nervous system disease; graft versus host disease; Human Vbeta gene repeat sequence #370. ADH70580 standard; DNA; 23 25-MAR-2004 (first entry) ADH70580; ***********

Addison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; type I hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; doodpasture's syndrome; type IV hypersensitivity; leprosy; infectious disease; viral infection; HIV; fungal infection; Candida; parasitic infection; eschistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer; hypersensitivity disease; infectious disease; neoplastic disease; 94US-00309335. 95US-00531241. 99US-00263959 WPI; 2004-059052/06. breast cancer; ds. Hood LE, Rowen L; L E (HOOD/) HOOD L E (ROWE/) ROWEN L. US2002150891-A1. Homo sapiens. 19-SEP-1994; 19-SEP-1995; 05-MAR-1999; 17-OCT-2002.

Le Couter J;

Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a Vbeta gene

Disclosure; SEQ ID NO 774; 164pp; English.

The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers pecifically priming and allowing amplification of each Vbeta gene, vbetaRNA or cDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, or including autoimmune diseases, hypersensitivity diseases, infectious diseases, and neoplastic diseases. Autoimmune diseases include Addison's disease, and neoplastic disease. Autoimmune diseases include Addison's disease, atrophic gastritis. Degenerative nervous system diseases include multiple sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type of Inpersensitivities such as contact with allargens that lead to allergies, Type II hypersensitivities such as those coused by viruses such as HIV, fungal infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by such as lukamental infections such as those caused by such as lukamental and pacterial infections such as those caused by such as lukamental and pacterial infections such as those caused by such as lukamental and pacterial infections such as those caused by such as lukamental and pacterial infections such as those caused by such as lukamental and pacterial infections such as those caused by such as lukamental and cancers such as cancer of the brain, and and and cancers such as cancer of the brain, and pacterial and cancers such as cancer of the brain, and and and cancers such as cancer of the brain, and and and cancers such as cancer of the brain, and and and cancers such as cancer of the brain, and and and cancers and and and cancers and and and cancers and and cancers and and cancer of the brain, and and cancers and and cancers and and cancers and and breast. The present sequence represents a Vbeta gene repeat sequence.

Gaps ; 0 0.5%; Score 19.8; DB 1; Length 23; 91.3%; Pred. No. 5.5e+02; ive 0; Mismatches 2; Indels Sequence 23 BP; 12 A; 10 C; 0 G; 1 T; 0 U; 0 Other; 2318 TGTGTGTGTGTGTGTGTGT 2340 21, Conservative Similarity Query Match Local Matches ò . B

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AAZ98498 standard; DNA; 24 BP AAZ98498;

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The invention relates to producing a sub-population of labeled nucleic acides (NAs) comprising contacting a NA sample from a physiological source, with a pool of 50 distinct gene specific primers under suitable conditions to enzymatically generate sub-population of NAs, where each gene specific primer has a sequence complementary to a distinct mRNA, and each labeled NA is generated using a single gene specific primer. The method is useful for producing a sub-population of labeled NAs which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing sub-population of labeled nucleic acids, useful for analyzing differences in RNA profiles between several different physiological sources, using set of distinct gene specific primers.
                                                                                                                                                                                                                                              The present invention relates to protein 9.90, which contains characteristic histone and hexokinase sequences (see ABP59132). The protein can be used for treating various diseases (e.g. malignant tumours, haemopathy, HIV infection, immunological diseases and various inflammations. The present sequence is a PCR primer, which was used in example from the invention. Note: The present sequence is the SEQ ID 3 shown in the sequence listing. This sequence differs from the SEQ ID 3 shown in the disclosure (see ABZ70123)
                                                                                                                                               Characteristic sequence protein 9.90 containing histone and hexokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer; 88; DNA microarray; differential expression analysis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19.8; DB 1; Length 24; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 24 BP; 2 A; 2 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                 Example 3; Page 24 (Disclosure); 30pp; Chinese.
                                                                                                                                                                        and polynucleotides encoding this polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chenchik A, Jokhadze G, Bibilashvilli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; SEQ ID NO 1107; 11pp; English
                  CO LTD SHANGHAI
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                    (BODE-) BODE GENE DEV
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Best Local Similarity
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                                                             Mao Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AAZS94883-514 represent sequences from Haliotis discus, used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
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                                                                                             Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
Haliotis discus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                    (first entry)
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                                                                                                                                                                        Haliotis discus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein 9.90
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                  19-JUN-2000
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ABZ70117;

RESULT 394
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different physiological sources, where the method comprises producing different physiological sources, where the method comprises producing cubpopulation of labeled Mas for the different physiological sources, comprising the populations for each physiological sources, differences in the population, where the comparison is preferably performed by hybridising the labeled Mas for each of the distinct physiological sources to an array of probe NAs stably associated with the surface of a substrate to produce a hybridisation pattern for each of the sources, where sources, and comparing the patterns of the sources, where sources, and comparing the patterns a trial sed in differential expression assays are utilised in differential expression assays are utilised e.g. neoplastic a normal case, or different tissue or subtissue types. The present sequence is a the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed the pattern of the pattern of the printed the pattern of the pattern of the printed the pattern of the pattern of the pattern of the printed the pattern of the 
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                                                   859999999999999999988<del>8</del>8
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Sequence 26 BP; 2 A; 9 C; 6 G; 9 T; 0 U; 0 Other;

ö Match 0.5%; Score 19.8; DB 1; Length 26; Local Similarity 91.3%; Pred. No. 6.3e+02; Los 21; Conservative 0; Mismatches 2; Indels 2546 TGGCTCGGCCTCTGCCAC 2568 1 TGGGTCGGCCTCTACCTTTGCAC 23 Query Match Best Local S Matches g 8

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Gaps

AAZ89469 standard; DNA; 27 BP

AAZ89469;

(first entry) 16-JUN-2000 SSA primer 1 for amplifying A. thaliana and Z. mays DNA.

Simple sequence repeat; SSR; single site amplification; SSA; disease; primer; 88.

Arabidopsis thaliana

Zea mays.

US6054300-A.

25-APR-2000

97US-00915609. 21-AUG-1997; 97US-00915609. 21-AUG-1997;

(USDA) US SEC OF AGRIC.

Mckendree WL;

WPI; 2000-328353/28.

Obtaining unknown DNA sequence flanking a single known sequence for use as PCR templates, involves single site amplification with polymerase having strand displacement capability.

Example 1; Col 7-8; 11pp; English.

This invention describes a novel method for obtaining DNA of unknown sequence flanking a single site of known sequence involves single site amplification of circular DNA template flanking a target DNA of known sequence using a polymerase having strand displacement capability. The method is used for obtaining a particular target DNA sequence that can be useful as templates that contain entire simple sequence repeat (SSR) alleles for amplification (SSA) procedures e.g. PCR or can be employed as molecular markers, e.g. in disstinguishing between species, strains or varieties within species or identifying the presence of a disease

export regulation, trains provides a mearker to use in access access as imported and ecotype identification, marker development, forensic DNA fingerprinting, etc. The method can also be used to generate a linear DNA molecule containing two target sequences from one sequence within a single stranded DNA template and flanking regions for these target sequences. It can also be used for e.g. for cloning cDNA or genomic DNA which flanks any known short target sequence. The present method can also be used to obtain entire coding regions of genes based upon a known nucleic acid sequence or by using a degenerate nucleic acid sequence derived from amino acid sequence back translation using a polymerase having strand displacement capability which can synthesize up to 10 kb fragments. This is especially useful for obtaining plant genes which are usually less than 10 kb in length. The method allows accelerated development of high resolution DNA markers that may be used for ingerprinting, mapping etc., using small amounts of tissue to used for ingerprinting, mapping etc., using small amounts of tissue to used for ingerprinting, mapping etc., using small amounts of tissue to required only by the primer design. The present method also eliminates genomic DNA library preparation and screening which are the most time consuming steps, typically requiring no less than three months, with the consuming steps, typically requiring no less than three months, with the present method of the invention consuming steps. ö condition. It also provides a marker for use in areas such as import and 289474 represent primers used to illustrate the method of the invention Gaps ö 0.5%; Score 19.8; DB 1; Length 27; 91.3%; Pred. No. 6.5e+02; ive 0; Mismatches 2; Indels Sequence 27 BP; 12 A; 11 C; 2 G; 2 T; 0 U; 0 Other; Local Similarity 91.3 hes 21; Conservative Query Match Matches %\$GGGGGGGGGGGGGGGGGGGG

2331 GIGCGIGIGIGIGIGIGIGCA 2353

27 Grererererererereas 5

ઠે 셤 RESULT 397 AD039594,

ADO39594 standard; DNA; 27

29-JUL-2004 (first entry) AD039594;

PCR primer #4 used to construct heterologous 3'-termination DNA.

Heterologous gene; expression cassette; gene expression; PCR; primer; ss.

Unidentified.

US2004092020-A1.

13-MAY-2004.

20-JUN-2003; 2003US-00600230.

20-JUN-2002; 2002US-0390529P.

(WILK/) WILKINSON J Q. (MCBR/) MCBRIDE K. (BERT/) BERTAIN S.

Wilkinson JQ, Mcbride K,

Bertain S;

WPI; 2004-374960/35.

New recombinant expression cassette comprising a promoter that is functional in plants, operably linked with a coding sequence and a non-plant 3' termination sequence, useful for gene expression in plant cells.

Claim 5; SEQ ID NO 15; 74pp; English

The present invention relates to heterologous genes comprising non-plant 3'-termination sequences and plant expression cassettes incorporating the heterologus genes. The invention is useful for gene expression in plant

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polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a polymorphic site described in the exemplification of the invention
                                                                                       Human, inflammatory bowel disease, Crohn's disease, ulcerative colitis single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forenaic test; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Testing for the presence of polymorphisms associated with inflammatory bowel disease, using a hybridization assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for detecting the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer; 88; DNA microarray; differential expression analysis; human.
                                                     Human inflammatory bowel disease associated polymorphic site #452
                                                                                                                                                                                                                                        /*tag= a
/note= "SNP, optionally T or A at this position"
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Pred. No. 6.9e+02;
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Best Local Similarity 81.5%;
Matches 22; Conservative (
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New set of inter-Bimple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and animal systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties.
is a PCR primer used to construct DNA. This sequence is used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                         inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant; animal; Basmati rice; 88.
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Pred. No. 6.5e+02;
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                                                   Sequence 27 BP; 14 A; 10 C; 1 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from evolved Basmati rice varieties. The curren 5' anchored (ISSR)-PCR primer of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 17; 60pp; English
                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                       (ISSR) - PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39-JAN-2003; 2003WO-IB000041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-APR-2002; 2002IN-CH000260
                                                                                       ch 0.5%;
1 Similarity 91.3%;
21; Conservative
cells. The present sequence heterologous 3'-termination
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                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                            ADD69512 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                         5' anchored
                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2004
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Gaps

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AAH91377

RESULT 399
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The invention relates to producing a sub-population of labeled mucleic acids (NAs) comprising contacting a NA sample from a physiological acids (NAs) comprising contacting a NA sample from a physiological conditions to enzymatically generate sub-population of NAs, where each cent labeled NA is generated using a single gene specific primer. The each labeled NA is generated using a single gene specific primer. The cach labeled NA is generated using a single gene specific primer. The method is useful for producing a sub-population of labeled NAs which is useful for analysing the differences in the RNA profiles between several difference in the populations for the different physiological sources, where the comprises producing comprising the population, where the comparison is preferably differences in the population, where the comparison is preferably configurated by Nybridising the labeled NAs for bed is the distinct physiological sources to an array of probe NAs stably associated with the surface of a substrate to produce a hybridisation pattern for each of the sources, and comparing the patterns for each of the sources, where confiferential gene expression assays are utilised in differential expression analysis of diseased a normal tissue e.g. neoplastic a normal crissue, or different tissue or subtissue types. The present sequence is a human gene specific PCR primer used in the method of the invention. Note: the confidency of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                    Producing sub-population of labeled nucleic acids, useful for analyzing differences in RNA profiles between several different physiological sources, using set of distinct gene specific primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 0.5%; Score 19.6; DB 1; Length 28; ilarity 84.6%; Pred. No. 7.2e+02; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28 BP; 7 A; 6 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA307.
                                                                                                                                                                                 Bibilashvilli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1765 GAGGCCTTGTTTGACCGAGTCTACAC 1790
                                                                                                                                                                                                                                                                                                                                                                      Example 3; SEQ ID NO 350; 11pp; English
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                                         99US-00225928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                    Chenchik A, Jokhadze G,
                                                                                                                                      (CLON-) CLONTECH LAB INC
                                                                                                                                                                                                                                  WPI; 2002-314699/35
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                                           05-JAN-1999;
                                                                                            21-MAY-1997;
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02-FEB-1993
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05-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
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AAQ33891
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Matches
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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine Mbol DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequence information
commercem of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
microsatellity individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits sep. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                 Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 5.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microsatellite sequence from clone TGLA419.
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                                                                                                                                                                                                      Table 7; Page 286; 517pp; English
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92WO-US000340.
                               91US-00642342.
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                                                                                            Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-284684/34.
                                                                                                                        WPI; 1992-284684/34.
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Matches 20; Conserv
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                                                             (GENM-) GENMARK.
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 15-JAN-1992;
                                 15-JAN-1991;
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02-FEB-1993
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                                                                 The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mool DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mool sites, the frequency of (T6)n .9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellites sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be missed to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective
                                                                                                                                                                                                                                                                             breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                 Score 19.4; DB 1; Length 21; Pred. No. 5.5e+02; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microsatellite sequence from clone TGLA301.
                                                                                                                                                                                                                                                                                                                                                                                                               2319 GTGTGTGTGTGTGTGTG 2339
                                          Table 7; Page 336; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ33879 standard; DNA; 21 BP.
                                                                                                                                                                                                                                                                                                                                                     0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                    20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ33879;
                                                                                                                                                                                                                                                                                                                                                     Query Match
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 ollgonuclectide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites

Polymorphic bovine DNA markers - used in genetic identification, gene

Table 7; Page 281; 517pp; English.

mapping, and selective breeding.

WPI; 1992-284684/34.

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in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligo:nucleotide which reduces CD28 gene expression in T cells - for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
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                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD28, inhibition, antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
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                                                                                                                                                                                                                                        0.5%; Score 19.4; DB 1; Length 21; larity 95.2%; Pred. No. 5.5e+02; Conservative 0; Mismatches 1; Indels
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Pred. No. 5.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide RTC05 used in an Example from US5932556.
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                                                                                                                                                                                                             Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
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1 Similarity 95.2%;
20; Conservative
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Les 20; Conserv
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Best Local Similarity
Matches 20; Conserv
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RESULT 40 AAT65738/

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The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple crepeats of dinucleotides such as GT, TG, etc., according to specific crepeats of dinucleotides such as GT, TG, etc., according to specific cormula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of activation of activation of apoptosis or production of cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TMF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis cidependent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4), drug resistance, caspase 3, transforming growth factor (TGP)-beta 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer by inducing cell cycle arrest, inhibiting proliferation, activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
                                                                                                     Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis; cell cycle arrest; cell proliferation; caspase; cytokine; interleukin; tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 5.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2318 TGTGTGTGTGTGTGCGTGT 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 17; 77pp; English.
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                                                                Synthetic oligonucleotide 13.
                                                                                                                                                                                                                                                                                                                                                                               12-DEC-2000; 2000WO-CA001467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-2000; 2000US-0228925P.
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                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Filion MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-398150/42.
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                                                                                                                                                                                                                                                                                 WO200144465-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-1999;
                                                                                                                                                                                       lymphoma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phillips NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-2001
                   12-SEP-2001
                                                                                                                                                                                                                                                                                                                                21-JUN-2001.
                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH46014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caspases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly (dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers AAT65798-T66047. Those clones where the repeat sequence has been determined are shown in AAT65704-977. This repeat sequence has the marker clone Mdf37 which contains the repeat sequence is from the marker clone Mdf37 which contains the repeat sequence and formula: (AC)10A. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                               Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                     Repeat sequence from polymorphic marker clone Mfd37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 21 BP; 11 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 9-10; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2318 TGTGTGTGTGTGTGTGTGT 2338
  GTGTGTGTGTGTGCGTGTG 2339
                             rererererererererer
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91US-00754351.
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                                                                                                                                                                   AAT65738 standard; DNA; 21
                                                                                                                                                                                                                                                                  (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1989;
05-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                  25-MAR-2003
17-JUN-1997
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Gaps ö

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RESULT 406

AAH46013

AAH46013 ID AAH4 XX AC AAH4

Query Match

Matches

vivlemore401-10.rng

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Vaccine, cytostatic, virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infections disease; allergy; immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunostimulatory nucleic acid #818.
                                                                                                                                                                                                                                                                                                                                                            2319 GTGTGTGTGTGTGCGTGTG 2339
                                                                                                                                                                                                                                                                                                                                                                         crerererererererere 21
                                                                                                                                                                                                                                                                                                                                                                                                            AAF99702 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                               0.5%;
                                                               12-DEC-2000; 2000WO-CA001467
                                                                             13-DEC-1999; 99US-0170325P.
                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                              20; Conservative
                                                                                                                Filion MC;
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                              WPI; 2001-398150/42.
                                  WO200144465-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200122972-A2
        lymphoma; ss
                                                                                                               Phillips NC,
                                                21-JUN-2001.
                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAF99702;
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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae, and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 101; Page 56; 338pp; English.
                                                                                                                                                                                                                                                                                                                              Krieg AM, Schetter C, Vollmer J;
                                                     25-SEP-2000; 2000WO-US026383.
                                                                                                                                                 27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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(COLE-) COLEY PHARM GMBH
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                                                                                                                       25-SEP-1999;
05-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a synthetic oligonucleotide useful to the invention. The invention relates to a composition, comprising a 2 to 20 base 3.049. $1.049 synthetic oligonucleotide which comprises multiple repeats of dinucleotides such as GT. TG, etc., according to specific formula and having cytostatic activity. The oligonucleotide compositions are useful for inducing cell cycle arrest, inhibition of proliferation, activation of caspases and induction of apoptosis or production of cytokines such as interleukin (IL)-1.beta, IL-6, IL-10, IL-12 and tumour necrosis factor (INF)-alpha by immune system cells, in an animal having cancer such as primary carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or bone cancer. The compositions induce apoptosis resistance, caspase 3, transforming growth factor (IGF)-beta 1 receptor and hormone dependence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition comprising synthetic oligonucleotides which comprise multiple repeats of dinucleotides such as GT, TG useful for treating cancer·by inducing cell cycle arrest, inhibiting proliferation, activating
tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.4; DB 1; Length 21;
Pred. No. 5.5e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 17; 77pp; English.
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                                 Gaps
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Score 19.4; DB 1; Length 21; Pred. No. 5.5e+02;
                               1; Indels
                                                                                                                                                                                                                                                                             Angiogenesis inhibitory oligonucleotide #907.
                                 0; Mismatches
                                                                 2318 TGTGTGTGTGTGTGCGTGT 2338
                                                                                               1 rerererererererer 21
                                                                                                                                                                                ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-DEC-2001; 2001WO-US048458.
 Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                              ABS78423 standard; DNA; 21
                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                              13-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                ABS78423;
                                                                                                                                                  RESULT 409
                                                                                                                                                                   ABS78423
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Gaps

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Human, ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; Cytochrome P450 02B; CYP45002B1; LTF;

Cytochrome P450 A2; CYP4501A2; Cytochrome P450 02B; CYP45002B1; LTF;

Cytochrome P450 A2; CYP4501A2; Cytochrome P450 02B; CYP45002B1; LTF;

Cytochrome Cytochrom receptor nuclear translocator; ARNT; Cathepsin S; CTSS;

Cyclooxgenase 2; CXX2; diazepam binding inhibitor; DBI; haematological;

Cyclooxgenase 2; CXX2; diazepam binding inhibitor; DBI; haematological;

Cyclooxgenase 2; CXX2; diazepam binding inhibitor; DBI; haematological;

Cyclooxgenase 2; CXX2; diazepam binding inhibitor;

Cyclooxgenase 2; CXX2; diazepam binding inhibitor;

Cyclooxgenase 2; CXX2; diazepam binding inhibitor;

Cyclooxgenase 2; CXX2; diazepam binding protein; FLAP;

Cyclooxgenase 2; CXX2; diazepam binding protein; FLAP;

Cyclooxgenase 2; CXX2; diazepam binding protein; FLAP;

CYCLOOXGENASE 2; CXX2; diazepam binding protein; CAPNT;

CYCLOOXGENASE 2; CXX2; diazepam binding protein; CAPNT;

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                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, macular glaucoms, retrolental fibroplasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                         Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     нимал NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.5%; Score 19.4; DB 1; Length 21; Best Local Similarity 95.2%; Pred. No. 5.5e+02; Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2318 TGTGTGTGTGTGTGCGTGT 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 35; 276pp; English
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                                                            (COLE-) COLEY PHARM GROUP INC.
14-DEC-2000; 2000US-025534P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid of the invention
                                                                                                                                                                                      WPI; 2002-566690/60.
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                                                                                                                            Bratzler RL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 410
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This invention relates to the sequence of an isolated mucleic acid

molecule comprising at least one base variation from that of a known

molecule comprising at least one base variation from that of a known

muman cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),

cytochrome P450 O2E1 (CYP4501B1), adrenergic receptor beta1 (ADBE1),

cytochrome P450 O2E1 (CYP4501B1), adrenergic receptor (ARNY), cathepsin S (CYP41), adrenerming CC

cytochrome P450 O2E1 (CYP4501B1), adrenergic receptor (ANDE2), intermine-N-methyl

craneferase (HNWY), NADPH quinone S-transferase 12 (GYC12), by Edmournoopyl

culfocransferase (HNWY), NADPH quinone SATORYMORYMORY LYANGER EAST (UGT2B4), upp-glucuronosyl transferase 2B4

(UGT2B4), upp-glucuronosyl transferase 2B7 (UGT2B7), upp-glucuronosyl

cytochrome P450 O2E1 (CYPM), multidrug resistance associated protein 3

(WRP3), lactocransferain (LTP), multidrug resistance acceptor 1, 2, 3, 4, or 5 (CHMM2), changes condition are useful as a result of their e.g., overexpression, constitutive candor underexpression, which may be used in diagnosing and/or tracting and associated or versening individuals for altered cardiovascial and proposition or underexpression, which may be used in diagnosing and/or tracting when and over underexpression, multidrug or order for alter Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for nervous system function. The present sequence represents a Gaps .. 0 0.5%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 5.5e+02; tive 0; Mismatches 1; Indels Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other; polymorphic DNA sequence of the invention Example 16; Page 130; 714pp; English 2324 TGTGTGTGTGCGTGTGTGT 2344 21 TATGTGTGCGTGTGTGTGT 1 28-NOV-2001; 2001WO-US044838. 28-NOV-2000; 2000US-00724389. 0.5 Best Local Similarity 95.2 Matches 20, Conservative disorder-related traits. (DNAS-) DNA SCI LAB INC. VPI; 2002-698522/75 Guida M, Hall J; peripheral RESULT 411 용 8

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ABS97832/c ID ABS97832 standard; DNA; 21

23-DEC-2002 (first entry)

ABS97832;

Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #40

Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NRIL1;

Adrenergic receptor nuclear translocator; DRNT; cathepsin S; CTSS;

Cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

Mycyclooxgenase 2; EPHK2; S-lipoxygenase activating protein; FLAP;

Mycyclooxgenase 2; NGO2; sulfotransferase thermolabile; STM;

Wycyclooxgenase 2; NGO2; sulfotransferase thermolabile; STM;

Wycyclooxgenase 2; NGO2; sulfotransferase 2BT;

Wultidrug resistance 1; lactotransferrin; orphan nuclear receptor;

Multidrug resistance associated protein 3; cancer; prostate;

multidrug resistance associated protein 3; cancer; prostate;

altered drug metabolism; cardiovascular function; colorectal tumour;

multidrug resistance associated protein 5NP;

altered drug metabolism; cardiovascular function; colorectal tumour;

central nervous system; pulmonary; immunological; SNP; single nucleotide polymorphism

Homo sapiens.

WO200257410-A2.

25-JUL-2002.

28-NOV-2001; 2001WO-US044838

28-NOV-2000; 2000US-00724389

(DNAS-) DNA SCI LAB INC

Guida M, Hall J;

WPI; 2002-698522/75

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 16; Page 131; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid
molecule comprising at least one base variation from that of a known
cc molecule comprising at least one base variation from that of a known
cc human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
cytochrome P450 02E1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
cytochrome P450 02E1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
cytochrome P450 02E1 (CYP4500E1), adrenator translocator
corporation (CARWT), MARPH quincowabase 2 (COX2), diazepam binding
inhibitor (DEI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
cransferase (HNWT), MADPH quincowabase 2 (MCOZ),
cransferase (HNWT), (kallikrein 2) KLK2, nicotinamide -N-methyl
cc transferase (HOWT), lamph quincome oxidoreductase 2 (MCOZ),
culfortansferase thermolabile (GYM), UDP-glucuronosyl
culfortansferase (UGT2B1S), urokinase receptor (UPA), multidrug resistance 1
culfortansferase (UGT2B1S), urokinase receptor (UPA), multidrug resistance 1
cmpR1), lactotransferrin (LTF), multidrug resistance associated protein 3
creceptor 1, 2, 3, 4, or 5 (CHWA1, CHWR2, CHWR3, CHWR4) or CHWR5) sequence.
creceptor 1, 2, 3, 4, or 5 (CHWA1, CHWR2, CHWR4), CHWR5) sequence.
creceptor 1, 2, 3, 4, or 5 (CHWA1, CHWR2, CHWR4), chromion are useful as
creceptor 1, 2, 3, 4, or 5 (CHWA1, CHWR2, CHWR4), chromion are useful as
creceptor 1, 2, 3, 4, or 5 (CHWA1, CHWR2, CHWR4), chromion and eventually
creceptor 1, 2, 3, 4, or 5 (CHWA1, CHWR2, CHWR4), chromion and eventually
creceptor 1, 2, 3, 4, or 5 (CHWA1, CHWR2, CHWR5), constitutive
creceptor 1, 2, 3, 4, or 5 (CHWA1, CHWR2, CHWR5), constitutive
creceptor 1, 2, 3, 4, or 5 (CHWA1, CHWR2, CHWR4), chromion and eventually
creceptoring the genes responsible for a variety of disorder-related
craits as a result of their e.g., overexpression, constitutive
craceptoring the disorders. The nucleic acid molecules comprising the
creaptoring the disorders. The nucleic acid molecules
contained in CYP4501A2, CYP4501A2, CYP4501A2,
chrifty and/or mura may also be used t

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Gaps

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Score 19.4; DB 1; Length 21; Pred. No. 5.5e+02; 0; Mismatches 1; Indels

Query Match 0.5%; Best Local Similarity 95.2%; Matches 20; Conservative

Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;

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used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DBI or CHMR1 for altered central immunological or haematological and HNMT for altered pulmonary.

protease activity in the prostate, in LTF for altered serine protease activity in the prostate, in LTF for altered immunological or heamatological tunction, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic context dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therspy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating non-allergic inflammatory diseases, such as psoriasis, ecze allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
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                                                                                                                                                                                                           Score 19.4; DB 1; Length 21;
Pred. No. 5.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                        Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunostimulatory nucleic acid #876.
                                                                                                                                                                                                                                                                                        2344
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                                                                                                                                                                                                                                                                                        2324 TGTGTGTGTGCGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                        ACH03241 standard; DNA; 21 BP
                                                                                                                                                                                                              0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-2003 (first entry)
                                                                                                                                                                                                           Query Match 0.5
Best Local Similarity 95.2
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KRIE/) KRIEG A M.
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                                                                                                                                                                                                                                                                                                                                                                                 RESULT 412
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Pluripotent embryonic-like stem cells derived from dental fuseful e.g. for engineering teeth or dental tissue, and for transplantation.
                                                                                                                                               Schierholz J, Brenner N, Zeilhofer F, Hoffmann KH,
gene therapy; PCR primer; ss.
                                                                                  05-FEB-2003; 2003WO-EP001131.
                                                                                                       06-FEB-2002; 2002US-0354152P.
                                                                                                                           CAES-) STIFTUNG CAESAR
                                                                                                                                                                    WPI; 2003-663591/62.
                                         WO2003066840-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                             14-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosling and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                  Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stem cell; dental follicle; tooth; membrane structure; periodontal ligament; pluripotent mesenchymal stem cell; osteopathic; antiinflammatory; stem cell therapy; tissue replacement; tissue repaitransplantation; periodontal tissue; periodontitis; dental cementum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                           ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibroblast growth factor receptor 3-IIIC reverse PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19.4; DB 1;
Pred. No. 5.5e+02;
                                                                                                                                                                      hypo-responsive subject; immunostimulatory.
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                                                                                                                                                                                                                                                                                                                                          Fouron Y;
                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 17; 221pp; English.
                                                                                                                                        Immunostimulatory nucleic acid #818.
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 TGTGTGTGTGTGTGCGTGT 2338
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                                                                                                                                                                                                                                                                            03-FEB-2000; 2000US-0179991P
                                                                                                                                                                                                                                                                                                                                          Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC64706 standard; DNA; 21
                                                                        ADB37204 standard; DNA; 21
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                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                (BRAT/) BRATZLER R L.
(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-657977/62.
                                                                                                                                                                                                              US2003087848-A1
                                                                                                                   04-DEC-2003
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                                                                                                                                                                                                                                   08-MAY-2003.
                                                                                                                                                                                           Synthetic.
                                                                                              ADB37204;
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  2318
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The present invention describes a stem cell (A) that is obtained from non-embryonic tissue isolated from the dental follicle of a (wisdom) tooth which can differentiate in vitro into a membrane structure that resembles periodontal ligament. Also described: (1) a stem cell (A1), derived from con-embryonic or post-natal animal cells or tissue, that is capable of self-remewal and differentiation to cells of endo-, ecto- or meso-dermal lineages, and (2) pluripotent mesenchymal stem cells (A2) obtained from (A). (A) has osteopathic and antiniflammatory activities, and can be used con stem cell therapy, and in tissue replacement. (A), and cells can stem cell therapy, and in tissue replacement. (A), and cells can stem cell therapy, and in tissue replacement. (A), and cells catensplantation. They can be used to prevent or treat cellular defects, dysfunction and/or disease, e.g. tissue repair or transplantation. They can especially be used to rebuild periodontal clissue (in cases of periodontitis) or dental cementum, and to improve the challing of tooth extraction or skin lesions. They can also be used in associated bone) or association with a scaffold, for growing teeth (or associated bone) or arterial/venous vessels in the mouth or as gene therapy carriers. The present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; ss; short interfering RNA; siRNA; angiogenesis; vascular endothelial growth factor; VEGF; VEGF receptor; Flt-1; Flk-1/KDR; kinase domain region; diabetic retinopathy; age-related macular degeneration; inflammatory disease; psoriasis; rheunatoid arthritis; cancer; breast; retinoblastoma; Wilm's tumour; lymphoma; cytostatic; antidiabetic; ophthalmological; antiinflammatory; antipsoriatic; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Flk-1/KDR DNA sequence, a target for siRNA inhibition SeqID 774
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Example; Page 23; 68pp; English.
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interfering RNA (SIRNA) molecules, which can be used to inhibit
angiogenesis. Specifically, it refers to siRNAs that target and cause
KNA1-induced degradation of mRNA from human vascular endothelial growth
factor (VEGF), the VEGF receptor (FIL-1) and the FIR-1/KDR (kinase domain
region) genes, as well as mutants derived thereof. The present invention
condition of the target mRNA, such that expression is inhibited and the target
condition of the target mRNA, such that expression is inhibited and the target
condition of the target mRNA, which include diabetic retinopathy, age-
concerspression of VEGF, which include diabetic retinopathy, age-
crelated macular degeneration, inflammatory disease, psoriasis and
crheumatoid arthritis. Furthermore, it can be used to treat various
cancers including breast, retinoblastoma, wilm's tumour and lymphoma.
CC Accordingly, these compositions exhibit cytostatic, anticiabetic, ophthalmological, antiinflammatory, antipsoriatic, anticiabetmatic and
antiarthritic activities. This oligonucleotide is a human FIk-1/KDR DNA
coligo, a target for siRNA inhibition of the invention.
                                                                                                                                                                                                                                                                                                             Novel short interfering RNA (siRNA) comprises sense and antisense RNA strands, useful for inhibiting expression of human vascular endothelial growth factor mRNA, for treating angiogenic disease, e.g. diabetic retinopathy and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porcine; pig; wild boar; quantitative trait locus; QTL; chromosome 2; mapping; 2pl.7; select breeding; genotype; phenotype; muscle mass; fat deposition; IGF2; insulin-like growth factor 2; microsatellite; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to novel compositions that comprise short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 0.5%; Score 19.4; DB 1; Length 21; Best Local Similarity 95.2%; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porcine microsatellite PIGQTL1 oligonucleotide #29.
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                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 774; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1609 AAGTGCATCCACAGGGACCTG 1629
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                                                                                             18-JUL-2003; 2003WO-US022444
                                                                                                                                24-JUL-2002; 2002US-0398417P.
14-NOV-2002; 2002US-00294228.
                                                                                                                                                                                             (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
                                                                                                                                                                                                                                    Tolentino MJ, Reich SJ;
                                                                                                                                                                                                                                                                          WPI; 2004-203472/19.
                    WO2004009769-A2
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                                                           29-JAN-2004.
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The present invention describes a method (M1) for selecting a domestic animal for having desired genotypic properties. The method comprises cresting the animal for the presence of a parentally imprinted quantitative trait locus (QTL). The pig QTL is located at chromosome 2, mapping at around position 2pl.7. Also described are: (1) an isolated and/or recombinant nucleic acid (M1) comprising a parentally imprinted QTL or its functional fragment; (2) an isolated and/or recombinant nucleic acid (M2) comprising a synthetic parentally imprinted QTL derived trom at least one chromosome or its functional fragment; (3) an animal cuch is spig selected for having desired genotypic or potential phenotypic properties; (4) a transgenic animal comprising N1 or N2; and (5) sperm or an embryo derived from the animal of (3) or (4). N1 or its fragment is an embryo desired genotypic or potenties or a breeding animal having desired genotypic or potenties. The properties are related to muscle mass and/or fat deposition. The sperm or an embryo are useful in breeding animals destined for slaughter. The present sequence represents a microsatellite oligonucleotide, which is given in an example from the present invention for the identification of but any sequence polymorphisms in the IGF2 (insulin-like growth factor 2) and
                                                                                                                                                                                                                                  Selecting a domestic animal for having desired genotypic properties comprises testing the animal for the presence of a parentally imprinted quantitative trait locus which is related to muscle mass and/or fat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22 BP; 11 A; 0 C; 0 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porcine microsatellite PIGQTL1 oligonucleotide #29.
                                                                                                                                                       Andersson L, Georges M, Spincemaille G;
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                                                                                                                                                                                                                                                                                                                                        Example 4; Fig 10; 107pp; English.
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99WO-EP010209.
                                     98EP-00204291
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                                                                                                                  (SEGH-) SEGHERSGENTEC NV
                                                                                                                                                                                               WPI; 2000-431612/37.
                                                                            (UYLI-) UNIV LIEGE.
                                                                                                 MELICA
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16-DEC-1999;
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                                     16-DEC-1998;
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                                                                                                                                                                                                                                                                                                deposition.
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Matches
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RESULT 419
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                                                                                                                                                                                                                       The present invention describes a method (M1) for selecting a domestic animal for having desired genotypic properties. The method comprises testing the animal for the presence of a parentally imprinted quantitative trait locus (QTL). The pig QTL is located at chromosome 2, mapping at around position 291.7. Also described are: (1) an isolated and/or recombinant nucleic acid (M1) comprising a parentally imprinted QTL or its functional fragment; (2) an isolated and/or recombinant nucleic acid (M2) comprising a synthetic parentally imprinted QTL cutleic acid (M2) comprising a synthetic parentally imprinted QTL cutleic acid (M2) comprising a synthetic parentally imprinted QTL derived from at least one chromosome or its functional fragment; (3) an animal cutleic acid (M2) comprising desired genotypic or potential phenotypic properties; (4) a transgenic animal comprising N1 or N2; and (5) sperm or an embryo derived from the animal of (3) or (4). N1 or its fragment is animal having desired genotypic or potential phenotypic properties. The properties are related to muscle mass and/or fat deposition. The sperm or an embryo are useful in breeding animals destined for slaughter. The present sequence represents a microaatellite oligonucleotide, which is given in an example from the present invention for the identification of farming land in the lGF2 (insulin-like growth factor 2) and
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                                                                                                                                Selecting a domestic animal for having desired genotypic properties comprises testing the animal for the presence of a parentally imprinted quantitative trait locus which is related to muscle mass and/or fat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 0.5%; Score 19.4; DB 1; Length 22; 1 Similarity 95.2%; Pred. No. 5.8e+02; 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22 BP; 11 A; 0 C; 0 G; 11 T; 0 U; 0 Other;
                                                                              Spincemaille G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunostimulatory nucleic acid #821.
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98EP-00204291
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                          (UYLI-) UNIV LIEGE.
(MELI-) MELICA HB.
(SEGH-) SEGHERSGENTEC NV.
                                                                                Georges M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                           WPI; 2000-431612/37.
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  16-DEC-1998;
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                                                                                 Andersson L,
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                                                                                                                                                                              deposition.
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                                                                                                                                                                                                                                                                                                              Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.
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                                                                                                                                                                                          Vollmer J;
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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23-AUG-2000; 2000US-0227436P.
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                                                                               (IOWA.) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GMBH.
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Best Local Similarity 95.2
Matches 20, Conservative
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(COLE-) COLEY PHARM GMBH
                                                                                                                                                                                             Krieg AM, Schetter C,
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                                                            Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
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WPI; 2001-273485/28
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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; blaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
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                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 19.4; DB 1; Length 22; 95.2%; Pred. No. 5.8e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 11 A; 0 C; 0 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiogenesis inhibitory oligonucleotide #910.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 20; Conservative
                                                                                                                                                                                                                                                                                              acid of the invention
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ABS78426/c
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diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases. The method is psoriatis, eczema, allergic contect dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunostimulatory, antiinflammatory, dermatological, antipsoriatic, antiulcer, gene therapy, vaccine, non-allergic inflammatory disease, psoriasis, eczema, allergic contact dermatitis, latex dermatitis; inflammatory bowel disease; ulcerative colltis; Crohn's disease; ss.
                                                                                                                                                                                                                         Gaps
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0.5%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 5.8e+02;
Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                   Length 22;
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Pred. No. 5.8e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunostimulatory nucleic acid #879.
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                                                                                                                                                                                                            Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         ACH03244 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                    Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; s8.
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                                                                                             Immunostimulatory nucleic acid #879.
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BP.
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                                                                (first entry)
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 ACH03244 standard; DNA;
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Best Local Similarity
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Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention factored of single nucleotide polymorphisms SNPs. The present invention the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid, sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to
                                                                                                                       The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                     preventing allergy or asthma using an immunostimulatory one or in combination with an asthma/allergy medicament.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
                                                                                                                                                                                                                                                                                                                                Score 19.4; DB 1; Length 22;
Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                        Sequence 22 BP; 11 A; 0 C; 0 G; 11 T; 0 U; 0 Other;
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                                                                                      Disclosure; Page 17; 221pp; English
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Best Local Similarity 95.2%;
Matches 20; Conservative
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ID AAH39074 standard; DNA; 24
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                     gand/or pre
acid alone
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                  Treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22 BP; 11 A; 0 C; 0 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19.4; DB 1;
Pred. No. 5.8e+02;
hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fouron Y;
                                                                                                                                                                                                                                                                                                                                                            Fouron Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 17; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunostimulatory nucleic acid #821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2824 ATATATATATATATATA 2844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                               02-FEB-2001; 2001US-00776479
                                                                                                                                                                                                                            03-FEB-2000; 2000US-0179991P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-2001; 2001US-00776479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-2000; 2000US-0179991P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                                                                            Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB37207 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BRATZLER R L.
PETERSEN D M.
FOURON Y.
                                                                                                                                                                                                                                                                 (BRAT/) BRATZLER R L. (PETE/) PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-657977/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-657977/62
                                                                                                                                                                                                                                                                                           (PETE/) PETERSEN (FOUR/) FOURON Y.
                                                                                      US2003087848-A1
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08-MAY-2003

(BRAT/) I (PETE/) I (FOUR/) I

Synthetic

ADB37207

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assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterchaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune disease, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a PCR primer specific for a human SNP containing DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of the target sequence #8 which was used in an experiment to determine the in vitro cleavage of target duplexes to evaluate the lengths of purine and pyrimidine tracts which are useful in obtaining oligonucleotides capable of triple helix formation with target nucleic acids. The complementary strand overhangs the 3' end by the sequence CTAG and the sense strand overhangs the complementary strand by the sequence AATT. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New oligo:nucleotide(s) forming triple helix with target nucleic acid contain purine and pyrimidine tracts in specific orientations, useful therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purine; pyrimidine; tracts; therapeutic; diagnostic; control; gene expression; mRNA synthesis suppression; ds.
                                                                                                                                                                                                                                                                                                       Score 19.4; DB 1; Length 24;
Pred. No. 6.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26 BP; 2 A; 1 C; 11 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                    Sequence 24 BP; 12 A; 11 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                  2318 IGIGIGIGIGIGIGCGIGT 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Fig 14a; 101pp; English.
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92US-00826934.
                                                                                                                                                                                                                                                                                                         0.5%;
ilarity 95.2%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92WO-US010792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ44016 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-214172/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Target sequence #8.
                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (STRI ) SRI INT.
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21-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9312230-A1
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28-OCT-1993
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 427
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0.5%; Score 19.4; DB 1; Length 26;

Query Match

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer pairs KITDEL1-FOR (AAT84432) and KITDEL1-REV (AAT84433), and KITDEL2-FOR (AAT84434) and KITDEL2-REV (AAT84435), can be used in a claimed method for identifying the presence or absence of a deletion of the KIT gene sequence in pig genomic DNA. Other claimed primers (see AAT84420-27) are used to detect a duplication of the KIT gene. The 3 alleles for coar colour (I, inhibition, of coat colour; I(p), patch; and i, development of colour) can be differentiated on the basis of duplication/deletion in the KIT gene. This allows breeding of pigs with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determn, of coat colour genotype in pigs by analysis of the KIT gene for duplication or deletions, or analysis of KIT protein, used to establish breeding programmes for pigs of selected colour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
           Gaps
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           ö
                                                                                                                                                                                                                           KIT gene primer KITDEL2-FOR for pig coat colour determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plastow GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Score 19.4; DB 1; Length 26; ilarity 80.0%; Pred. No. 7e+02; Conservative 2; Mismatches 3; Indels
             Indels
                                                                                                                                                                                                                                                     coat colour; pigmentation; primer; PCR;
             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26 BP; 6 A; 3 C; 8 G; 7 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Siggens KW,
95.2%; Pred. No. 7e+02;
           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the desired, usually white, coat colour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1796 AGAGTGACGTCTGGTCTTTGGGGT 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGTGAYGTCTGGTCCTATSGGAT 26
                                         2319 GTGTGTGTGTGTGTGCGTGG 2339
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                                                                  e crerererererererere 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 39; Page 43; 49pp; English.
                                                                                                                                                                                                                                                        KIT gene; pig; coat colour; pi
polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                    96WO-GB001794.
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95GB-00025364.
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                                                                                                                                          AAT84434 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                  (first entry)
             20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andersson L, Moller MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-145712/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DALG-) DALGETY PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
ses 20; Conserv
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      34-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                               27-JUL-1995;
12-DEC-1995;
                                                                                                                                                                                                  13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-1999
                                                                                                                                                                                                                                                                                                                                                          13-FEB-1997.
                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV80712;
                                                                                                                                                                      AAT84434;
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Matches
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                                                                                                               RESULT 428
              Matches
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ID AAV8
XX
AC AAV8
XX
DT 26-M
                                                                                                                              AAT84434
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products according to breed origin; (b) determining or testing the breed origin; (c) validating an animal product. The method corigin of a product or (c) validating an animal product. The method continuo of a product; or (c) validating an animal product. The method comprises analysing a sample of the product for the allele(s) of at least one breed-determinant (BD) gene. The present invention also describes: (1) methods for determining the coat colour genotype of a pig by determining; (i) the allele(s) of the alpha melanocyte-stimulating correspond to a protein at positions associated with coat colour, or the size of the alpha-MSHR protein; (ii) the amino acid sequence of an alpha-MSHR protein; (iii) detecting which microsatellites (or other linked marker alleles), linked to the alpha-MSHR gene, or particular alleles of it, are present; and (iv) analysing nucleic acid to determine if the KIT gene carries a polymorphism associated with the Belt genotype. The main method of the invention is applied to samples from fish, birds and nammals, especially pigs. Particular applications are confirming stated origin of meats; in quality control; for maintaining stock purity, and in the present sequence conly very small samples and many samples can be screened quickly and inverpensively. The process can be made quantitative. The present sequence in perpensively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Differentiating products from different animal breeds - by the analysis of alleles of breed-determinant genes, at the nucleic acid or protein
                                       Porcine, wild boar, meishan, pietrain, large white; hampshire, duroc; differentiation; breed origin; alpha-MSHR; coat colour; stock purity; alpha melanocyte-stimulating hormone receptor; KIT; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26 BP; 6 A; 3 C; 8 G; 7 T; 0 U; 2 Other;
KIT gene PCR forward primer KITDEL2-FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 14; Page 53; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                       Giuffra E,
                                                                                                                                                                                                                                                                                                                                                                             (PIGI-) PIG IMPROVEMENT CO UK LID.
                                                                                                                                                                                                                                                                                                          97GB-00011214.
98GB-00001990.
                                                                                                                                                                                                                                                                98WO-GB001531
                                                                                                                                                                                                                                                                                                                                                                                                                         Andersson L, Kijas J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-070222/06.
                                                                                                                                                                        WO9854360-A1
                                                                                                                                                                                                                                                                27-MAY-1998;
                                                                                                                                                                                                                                                                                                            30-MAY-1997;
                                                                                                                                                                                                                                                                                                                                 31-JAN-1998;
                                                                                                                                                                                                                       03-DEC-1998.
                                                                                                                                 Synthetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               level
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Plastow GS;

Wales R,

Evans GJ,

ö Gaps ö 0.5%; Score 19.4; DB 1; Length 26; 80.0%; Pred. No. 7e+02; 3; Indels 2; Mismatches 1796 AGAGTGACGTCTGGTCCTTTGGGGT 1820 20; Conservative Local Similarity Query Match Matches 8

2 AAAGTGAYGTCTGGTCCTAISGGAI 26 g

FGFR-3 PCR antisense primer. AAX00036 standard; DNA; 24 16-MAR-1999 (first entry) AAX00036,

Neuroepithelial stem cell; lineage restricted intermediate precursor; oligodendrocyte; astrocyte; self-renewal; neuron; differentiation;

Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;

H. discus derived sequence #23.

19-JUN-2000 (first entry)

AAZ98505 standard; DNA; 24

AAZ98505,

AAZ98505;

recognithelial stem cells, which are capable of self-remewal in adherent feeder-cell-independent (AFCI) culture medium and differentiation to central nervous system (CNS) neuronal or glial cells and to neuronal cerest stem cells. Also described is an isolated population of mammalian crest stem cells. Also described is an isolated population of mammalian CNS glial-restricted precursor (GRP) cells which can self-renew in the CNS plial-restricted precursor (GRP) cells which can self-renew in the CNS neuronal cells. The stem cells can be used to generate a population of mammalian motor neurons by incubating the stem cells in a medium comprises laminin-coated plates and NBP medium lacking chick embryo extract. The stem cells conditions and neuronal differentiation. The medium comprises laminin-coated plates and NBP medium lacking chick embryo extract. The stem cells or differentiate in vitro. The inducing step comprises replating the cells on a laminin-coated substrate and preferably creplating a mitogen (preferably fibroblast growth factor; FGP) and chick embryo extract. Inducing can also comprise adding a dorsalizing agent to the cells preferably a bone morphogenetic protein (BMP) such as BMP-2, -4 or -7. The stem cells can be used to produce cells of the cells or a laminin-coated bush can be used to produce cells of the course cells on a laminin-coated substrate and preferably such as gent to neural crest stem cells, and inducing these cells to differentiate in the present invention to amplify different FGF and contral creat stem cells, represent propertion to amplify different FGF and ö The present invention describes an isolated, pure population of mammalian Mammalian neuroepithelial stem cells and glial restricted precursor - car self renew and differentiate into central nervous system cells, used for generating various types of cells. neural crest cell; fibroblast growth factor; FGF; FGFR; receptor; CNS; central nervous system; glial cell; PCR primer; amplification; ss. Gaps .. 0 Score 19.2; DB 1; Length 24; Pred. No. 6.7e+02; 0; Mismatches 3; Indels Sequence 24 BP; 4 A; 9 C; 8 G; 3 T; 0 U; 0 Other; Rao MS, Mayer-Proschel M, Mujtaba T; 984 GAAAGGCCTGGGCTCCCCCACCGT 1007 Example 26; Page 58; 78pp; English. 24 GAAGGCTTGGGCTCGCCCACCGT 98WO-US009630. 97US-00852744. 98US-00073881. Match 0.5%; Local Similarity 87.5%; Les 21; Conservative ((UTAH) UNIV UTAH RES FOUND WPI; 1999-070093/06 Homo sapiens WO9850526-A1 07-MAY-1998; 06-MAY-1998; 12-NOV-1998. FGFR genes Synthetic. Query Match Best Loca Matches RESULT 431 ઠે g

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The invention provides a novel method for isolation of satellite sequences from genomic DNA that comprises fragmentation of the DNA by a method which is not dependent on base sequences, then selection of the satellite sequences from the obtained genomic library of high homogeneity. The method is useful for the isolation of microsatellite DNA sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AAX29483-514 represent sequences from Haliotis discus, used in the method
                                                                                                                                                                                                                                                                                                      Isolation of satellite sequences from genomic DNA for use as DNA markers comprises isolating a library with high homogeneity by DNA fragmentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24 BP; 10 A; 10 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                      (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
                                                                                                                                                                                                                                                                                                                                                            Example 5; Page 14; 35pp; Japanese.
                                                                                                                                  99WO-JP003551
                                                                                                                                                                      98JP-00232153
                                                                                                                                                                                                                                        Sekino M;
                                                                                                                                                                                                                                                                          WPI; 2000-224692/19.
 88
Haliotis discus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention
                                Haliotis discus
                                                                   WO200011156-A1
                                                                                                                                                                                                                                        Takahashi H,
                                                                                                                                      01-JUL-1999;
                                                                                                                                                                      18-AUG-1998;
                                                                                                    02-MAR-2000.
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Gaps
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ch 0.5%; Score 19.2; DB 1; Length 24; l Similarity 87.5%; Pred. No. 6.7e+02; 21; Conservative 0; Mismatches 3; Indels
                                                                         2328 TGTGTGCGTGTGTGTGTGTGTG 2351
                                                                                             24 TGCATGCATGTGTGTGTGTGTG 1
                       Best Local Similarity
       Query Match
                                         Matches
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alpha-2 macroglobulin-like polypeptide variant;
antileukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1;
transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
                                                                                                                                                                            antiarteriosclerotic; anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozocatde; notropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antijarlamatory; dermatological; antiathmatic; antilipaemic; gene therapy; fibroblast growth factor receptor 4; FGFR4; complement factor I precursor; matrix metalloproteinase-15 precursor; fibroblast growth factorical; FGF-21; metalloproteinase-15 precursor; fibroblast growth factor-21; FGF-21;
                                                                                                                                              Human NOV1 TET/TAMRA labelled probe SEQ ID NO:147.
                                   ADL57202 standard; DNA; 24 BP
                                                                                                           (first entry)
                                                                                                           03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                      ADL57202;
RESULT 43
ADL57202
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The invention relates to a novel isolated polypeptide (NOVX) comprising a mature form of any of the 37 amino acid sequences fully defined in the specification. A polypeptide of the invention has antidiabetic.

anorectic, cardiant, Apolypeptide of the invention has antidiabetic, anorectic, and anorectic, and man disease, preferably a NOVX-associated disorder.

The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases (viral, bacterial, fungal, end anorectic, anorectic, anorectic, anorectic, disorders, obsenty, infectious diseases (viral, bacterial, fungal, end (by protocollered), anorectic, anorectic, and protocolles, anorectic, anorectic, and protocolles, and protocolles, anorectic, anorectic, and polypeptides (osteomrhitic), hemanorepoietic disorders, inflammatory skin disorders, and various dyslipidaemias. The mucleic acids and polypeptides of that modulate or inhibit e.g. neurogenesis, inflammatory skin deneration, heematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunosperifically to NoVX substances for use in therapeutic or diagnostic methods. The nucleic cides of the invention show homology to certain known human part of instable growth factor receptor (FGFR4); NOV2a shows homology to fibroblast growth factor-1 precursor; NOV4a shows to marriat; NOV to nuclear hormone receptor NOR-1; NOV11a-11; show homology to transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin dynorphin precursor. The present sequence represents a probe used in the New isolated NOVX polypeptides and polynucleotides, useful for preventing, disquosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections Zhong M, Guo X, Anderson DW, Ort T, Padigaru M, Rieger DK; Example 12; SEQ ID NO 147; 214pp; English. exemplification of the invention. 23-SEP-2002; 2002US-0412766P. 23-SEP-2002; 2002US-0412825P. 24-SEP-2002; 2002US-0412767P. 25-SEP-2002; 2002US-0413342P. 09-SEP-2003; 2003WO-US028141. 2002US-0409544P. 2002US-0410320P. 2002US-0411060P. 2002US-0409145P 2002US-0414832P (CURA-) CURAGEN CORP. WPI; 2004-315567/29. 30-SEP-2002; 10-SEP-2002; 12-SEP-2002; 16-SEP-2002;

Gaps ; 0 tch 0.5%; Score 19.2; DB 1; Length 24; al Similarity 87.5%; Pred. No. 6.7e+02; 21; Conservative 0; Mismatches 3; Indels Sequence 24 BP; 5 A; 9 C; 6 G; 4 T; 0 U; 0 Other; Best Local Similarity Query Match Matches

1317 CACTGACAAGGACCTGTCGGACCT 1340

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MO2004022723-A2

18-MAR-2004.

RESULT 434

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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST; 88; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                   Human microarray DNA oligonucleotide SEQ ID NO 80269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 80269; 9pp; English.
ACI80278 standard; DNA; 25 BP
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                                                                                                                                                                                                                                                                                                                                         14-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-567953/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mittmann MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-2003
                                                                                                                                                                                                                                                                        ACI80278;
                                                                                                                                  RESULT 43:
10 ACI8 10278, XX
XX ACI8 14-0
XXX WW 12-0
XXX Green CC ACI8 15-M
XXX Green CC ACI8 15-M
XXX WR 16-M
XXX CC ACI8 16-C
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring of many members of a gene and a cross-species comparison. Each of the cucleic acids further comprises a tag sequence. The array of nucleic acid brobes is useful in in situ hybridiaation, in Southern, Northern or dotbot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termin of many had been been and a cross-species comparises by primer extensions or in screening conducting the primer extensions or in screening conducting the primer extensions or subclones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from USPTO at segdata.uspto.goc/sequence.html
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                                                       Gaps
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0
                         Score 19.2; DB 1; Length 25; Pred. No. 7e+02;
                                                       3; Indels
Sequence 25 BP; 3 A; 8 C; 9 G; 5 T; 0 U; 0 Other;
                                                      0; Mismatches
                                                                                    2569 CACGGGACATCACAGGGTGCGCTC 2592
                         0.5%;
                                                         21; Conservative
                         Query Match
Best Local Similarity
                                           Best Loca
Matches
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24 caccedacacacacacerecere 1

RESULT 435 AAD40532/c

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The invention relates to a method for stimulating a population of stem cells to differentiate into osteoblast cells by contacting the population with an agent which increases fibroblast growth factor receptor 3 (FGFR3) expression or activity, where increase in FGFR3 protein expression or activity, where increase in FGFR3 protein expression or activity results in differentiation of the stem cells into osteoblast cells. The method is useful for stimulating the population of stem cells increases bone density. The method is useful for accening the agent increases bone density, or ameliorates the effects of osteoporosis. The method is useful for diagnosing a condition characterised by abnormal stem cell differentiation, bone density or rate of osteoblast formation and treating a patient with a condition characterised by an abnormal rate of osteoblast formation of seteblast formation conference is a RT-PCR primer used for human FGFR3 expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stimulating a population of stem cells to differentiate into osteoblast cells useful for treating osteoporosis, by contacting the cells with agent which increases fibroblast growth receptor 3 expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                         Human; stem cell; fibroblast growth factor receptor 3; FGFR3;
osteoblast cell; bone density; osteoporosis; osteopathic; receptor;
RT-PCR; primer; ss.
                                                                                                                       Forward RT-PCR primer used for FGFR3 expression in human tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cook JS, Axelrod DW;
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100.0%; Pred. No. 5.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 3 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ji D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mertz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 58; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3706 TGGTGGCCAGAGGTGTCAC 3724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGGTGGCCAGAGGTGTCAC 19
              ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                         24-APR-2001; 2001US-0285691P.
23-JUL-2001; 2001US-0306879P.
10-SEP-2001; 2001US-0317974P.
                                                                                                                                                                                                                                                                                                                                         18-DEC-2001; 2001WO-US048270.
                                                                                                                                                                                                                                                                                                                                                                            L8-DEC-2000; 2000US-0255882P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENE LOGIC INC.
(PROC ) PROCTER & GAMBLE CO.
              AAD40531 standard; DNA; 19
                                                                                   (first entry)
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jaiswal N, Houghton A,
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                                                                                                                                                                                                                                                                  WO200250246-A2.
                                                                                     30-0CT-2002
                                                                                                                                                                                                                                                                                                     27-JUN-2002
                                                  AAD40531,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity
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AAD40531
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19-NOV-2002 (first entry)

vivlemore401-10.rng

AAD40532 standard; DNA; 19

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The invention relates to a method for stimulating a population of stem cells to differentiate into osteoblast cells by contacting the population with an agent which increases fibroblast growth factor receptor 3 (FGFR3) carpression or activity, where increase in FGFR3 protein expression or activity results in differentiation of the stem cells into osteoblast cells. The method is useful for stimulating the population of stem cells to differentiate into osteoblast cells. The method is useful for screening the agent increases bone density. The method is useful for screening the agent increases bone density, or ameliorates the effects of osteoplast cells, increases bone density, or ameliorates the effects of osteoplast in the method is useful for diagnosing a condition characterised by abnormal stem cell differentiation, bone density or state of osteoblast formation of osteoblast formation in a condition characterised by an abnormal rate of osteoblast formation, bone density or osteoplosis. The present of osteoblast formation, bone density or osteoplosis. The present of osteoblast formation, bone density or osteoplosis. The present of osteoblast formation, bone density or osteoplosis. The present of osteoblast formation, bone density or osteoporosis. The present of osteoblast formation, bone density or osteoporosis. The present of osteoblast formation, bone density or osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stimulating a population of stem cells to differentiate into osteoblast cells useful for treating osteoporosis, by contacting the cells with agent which increases fibroblast growth receptor 3 expression or
                                                                                                                                                Human, stem cell, fibroblast growth factor receptor 3; FGFR3;
osteoblast cell, bone density; osteoporosis; osteopathic, receptor;
RT-PCR; primer; ss.
                                                                                                                    Reverse RT-PCR primer used for FGFR3 expression in human tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cook JS, Axelrod DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.5%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 5.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ji D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jaiswal N, Houghton A, Mertz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 58; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3751 ACCCAGCGACGAACTITCC 3769
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24-APR-2001, 2001US-0289591P.
2001, 2001US-0388691P.
10-SEB-2001, 2001US-0317974P.
                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2001; 2001WO-US048270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENE LOGIC INC.
(PROC ) PROCTER & GAMBLE CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ81991 standard; DNA; 19
                                                                               (first entry)
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                        WO200250246-A2.
                                                                                                                                                                                                                                                 Homo sapiens.
                                                                               30-OCT-2002
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                                        AAD40532
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ABQ81991
ID ABQ81995
XX
AC ABQ81995
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The present invention describes a method for determining if an individual has a tumour cell or site of anglogenesis, or if a treatment is effective in changing anglogenesis or changing a status of a set of target cells, comprising determining if a sample of the subject has an expression product of at least one marker gene. Also described is a compound capable of altering the expression or activity of Keratin 14, TIE 1, Salloadhesin or Siglec in a cell. Pertipheral blodd monouclear cell (PBMC)-expressed Keratin 14, TIE 1, Salloadhesin or Siglec, and kits containing them from the present invention can be used in a diagnostic method, particularly as an indicator of anglogenesis or to determine presence of a tumour cell. The method of the invention is suitable to determine within a few days if a certain treatment against Kaposi's Sarcoma is successful. ABQ81851 to ABQ82006 represent nucleotide sequence used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         marker gene; tumour; Kaposi's Sarcoma; peripheral blood mononuclear cell; PBMC; expressed keratin 14; TIE 1; Salioadhesin; Siglec 1; anglogenesis; drug target; tag; SAGE library; KS3; KS4; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                            Determining presence of a tumor cell or angiogenesis, and the effectiveness of treatment, by detecting the presence of marker genes is useful to detect and monitor treatment of Karposi's Sarcoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                   88.
                                                                Human; Kaposi's sarcoma; tumour; angiogenesis; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 5.4e+02; rive 0; Mismatches 0; Indels
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                                Kaposi's Sarcoma TAG PCR primer SEQ ID NO:141.
                                                                                                                                                                                                                                                                                                                      (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 10; Page 24; 38pp; English
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                                                                                                                                                                                                                                             23-JAN-2001; 2001EP-00200228.
28-SEP-2001; 2001EP-00203703.
28-SEP-2001; 2001US-0325722P.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention
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                                                                                                         Homo sapiens
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EP1298221-A1

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Gaps

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The present invention describes a method for the inspection of flat
epithelial cells in which it is judged that flat epithelial cells
separated from an organism can proceed to flat epithelial cancer when the
2128th base in fibroblast growth factor receptor (FGFR) gene of the cells
is mutated from guanine to thymine. Also described is a method for
cs escreening treating or preventive agents for flat epithelial cancers in
which a candidate substance of treating agent for flat epithelial cancers
is applied to flat epithelial cancer cells producing FGFR protein in
which the 2128th (exon 17) amino acid is mutated from glycine to
cysteine and said candidate substance is selected by using the facts that
the 2128th base in the flat epithelial cell FGFR3 gene after the
cysteine and said candidate substance is selected by using the facts that
the 2128th base in the flat epithelial cell FGFR3 gene after the
gpplication returned to guanine and that the 697th amino acid of FGFR3
protein produced returned to glycine as the indices. The method is used
for the inspection of flat epithelial cells. The present sequence
                                                                Inspection of flat epithelial cell, screening of treating or preventive agents for flat epithelial cancers, the treating or preventive agents for flat epithelial cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inspection of flat epithelial cell, screening of treating or preventive agents for flat epithelial cancers, the treating or preventive agents for flat epithelial cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represents a PCR primer for human FGFR3, which is used in an example from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, fibroblast growth factor 3; FGF3; flat epithelial cell; cancer; flat epithelial cell cancer; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.5%; Score 19; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 5.4e+02; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human fibroblast growth factor 3 exon 17 PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 4 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2048 ACGAGTACCTGGACCTGTC 2066
                                                                                                                                                      Example; Page 6; 18pp; Japanese.
(ZERI ) ZERIA SHINYAKU KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Page 6; 18pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZERI ) ZERIA SHINYAKU KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 ACGAGTACCTGGACCTGTC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAR-2001; 2001JP-00083352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-2001; 2001JP-00083352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention
                                      WPI; 2003-345602/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-345602/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACC79683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel method for determining whether a treatment is effective in changing a status of a certain set of target cells in an individual. The method comprises obtaining a sample from an individual after initiation of the treatment; and determining whether the sample comprises an expression product of at least one marker gene. The marker gene and a proteinaceous molecule (which can bind to the protein derived from the marker gene of the invention) are useful for determining whether a treatment is effective in counteracting a tumour in an individual, especially Kaposi's Sarcoma. Peripheral blood mononuclear cell impact of a fully defined sequence given in the specification, their analogues are useful as indicators for angiogenesis and for their analogues are useful as indicators for angiogenesis and for their analogues. The compound is useful for product of a gene comprising a marker gene of the invention is useful as a drug target. The compound is useful for preparing a medicament. This polymucleotide sequence represents a PCR primer of a Kaposi's Sarcoma tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                 Determining whether a treatment is effective in changing a status of a certain set of target cells in an individual comprises determining whether the sample comprises an expression product of at least one marker
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flat epithelial cell cancer; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human fibroblast growth factor 3 exon 17 PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 7 A; 8 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 143; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1702 CACAACCTCGACTACTACA 1720
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                                                                                                                                                                         Cornelissen
                                                        28-SEP-2001; 2001EP-00203703
                                                                                              28-SEP-2001; 2001EP-00203703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAR-2001; 2001JP-00083352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-2001; 2001JP-00083352
                                                                                                                                (PRIM-) PRIMAGEN HOLDING BV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of the invention.
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                                                                                                                                                                       Van Der Kuyl AC,
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                      02-APR-2003.
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Gaps

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Gaps

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0.5%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 5.4e+02; ive 0; Mismatches 0; Indels

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WO2003083046-A2
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                                                                                                                   15-AUG-2002;
                                                                                                    02-APR-2002;
05-APR-2002;
                                                                                    Ното варіеля
                                                                      17-JUN-2004
                                                                                            09-OCT-2003
                                                                  ADK51125;
                                        Query Match
                                                          RESULT 440
                                                             ADK51125
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This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NOVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromosome mapping. The present sequence is that of a PCR primer which was used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 5 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
Example C; SEQ ID NO 146; 433pp; English.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   invention.
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      The present invention describes a method for the inspection of flat
c epithelial cells in which it is judged that flat epithelial cells
separated from an organism can proceed to flat epithelial cancer when the
separated from an organism can proceed to flat epithelial cancer when the
cc 122th base in fibroblast growth factor receptor (FGFR) gene of the cells
is mutated from guanine to thymine. Also described is a method for
cs screening treating or preventive agents for flat epithelial cancers in
cs applied to flat epithelial cancer cells producing FGFR protein in
which the 2128th (exon 17) amino acid is mutated from glycine to
cysteine and said candidate substance is selected by using the facts that
cc quanine to thymine or the 697th amino acid is mutated from glycine to
cysteine and said candidate substance is selected by using the facts that
cthe 2128th base in the flat epithelial cell FGFR3 gene after the
cthe 2128th base in the flat epithelial cell FGFR3 gene after the
cyptication returned to guanine and that the 697th amino acid of FGFR3
cprotein produced returned to glycine as the indices. The method is used
cfor the inspection of flat epithelial cells. The present sequence
c for the inspection of flat epithelial cells. The present sequence
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MP, Li L, Spytek
Patturajan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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100.0%; Pred. No. 5.4e+02;
vative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 5 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NOVX protein-related PCR primer SeqID.
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08-APR-2002; 2002US-0370969P.
12-APR-2002; 2002US-03729P.
22-APR-2002; 2002US-037473P.
30-MAX-2002; 2002US-0384543P.
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31-MAR-2003; 2003US-00403161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Matches 19; Conservative
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The invention relates to a method of detecting the base sequence for RNA interference by detecting the regions in the DNA sequence fulfilling the following requirements such as: (i) the base at 3' terminal is adenine, thymine or uracil; (ii) the base at 5' terminal is quanine or cytosine; (iii) the seven base sequence at 3' terminal is rich in adenine, thymine and uracil, and; (iv) there are bases in a such a number that it causes RNA interference without showing cytotoxicity. The method is used for designing and synthesizing siRNA causing RNA interference. This sequence corresponds to an RNA interference target sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting sequence of RNA interference useful for synthesizing siRNA, by detecting regions in sequence fulfilling specific criteria such as base at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
                                                                                                                                                                                                    detection; RNA interference; siRNA; gene silencing; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 7 A; 8 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 61; 325pp; Japanese.
                                                                                                                                                                         RNA interference target sequence #47.
BP.
                                                                                                                                                                                                                                                                                                                                              21-NOV-2003; 2003WO-JP014893.
                                                                                                                                                                                                                                                                                                                                                                           22-NOV-2002; 2002JP-00340053
                                                                                    ADQ27139 Standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Naito Y;
                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             guanine or cytosine.
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                                                                                                                                                                                                                                                                                                                                                                                                        (NATO/) NATORI Y.
(SAIG/) SAIGO K.
(TEIK/) TEI K.
(NAIT/) NAITO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tei K,
                                                                                                                                                                                                                                                                                      WO2004048566-A1.
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                            cytotoxicity
                                                                                                                                                 26-AUG-2004
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                                                                                                                    ADQ27139;
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The invention relates to a method of detecting the base sequence for RNA interference by detecting the regions in the DNA sequence fulfilling the following requirements such as: (i) the base at 3 terminal is adenine, thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine; (iii) the seven base sequence at 3' terminal is guanine or cytosine; (iii) the seven base sequence at 3' terminal is rich in adenine, thymine and uracil, and; (iv) there are bases in a such a number that it causes RNA interference without showing cytotoxicity. The method is used for designing and synthesizing siRNA causing RNA interference. This sequence corresponds to an RNA interference target sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting sequence of RNA interference useful for synthesizing siRNA, by detecting regions in sequence fulfilling specific criteria such as base at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
                                                                                                       ss; detection; RNA interference; siRNA; gene silencing; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss; detection; RNA interference; siRNA; gene silencing; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 0; Indels
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                                                                         RNA interference target sequence #48.
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                                                                                                                                                                                                                                              21-NOV-2003; 2003WO-JP014893.
                                                                                                                                                                                                                                                                            22-NOV-2002; 2002JP-00340053.
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                                            26-AUG-2004 (first entry)
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               guanine or cytosine.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-487423/46
                                                                                                                                                                                                                                                                                                       (NATO/) NATORI Y.
(SAIG/) SAIGO K.
(TEIK/) TEI K.
(NAIT/) NAITO Y.
                                                                                                                                                                                  WO2004048566-A1
                                                                                                                                                      Homo sapiens.
                                                                                                                       cytotoxicity
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                                                                                                                                                                                                                                                                                                                                                                                  Saigo K,
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               ADQ27140;
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N X S X X X X S X S X S X S X S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of detecting the base sequence for RNA interference by detecting the regions in the DNA sequence fulfilling the following requirements such as: (i) the base at 3 'terminal is adenine, thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine; (iii) the seven base sequence at 3' terminal is rich in adenine, thymine and uracil, and; (iv) there are bases in a such a number that it causes RNA interference without showing cytotoxicity. The method is used for designing and synchesizing siRNA causing RNA interference. This sequence corresponds to an RNA interference target sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting sequence of RNA interference useful for synthesizing siRNA, by detecting regions in sequence fulfilling specific criteria such as base at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
                                                                                                                                                                                                                                                                                                          expression;
                                            Gaps
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                                                                                                                                                                                                                                                                                                          detection; RNA interference; siRNA; gene silencing; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 19; OB 1; Length 19; 100.0%; Pred. No. 5.4e+02; ive 0; Mismatches 0; Indels
               Length 19;
                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 4 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
              DB 1; Le 5.4e+02;
    0.5%; Scor.
100.0%; Pred. No. 5...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 65; 325pp; Japanese.
                                                                                                                                                                                                                                                                            RNA interference target sequence #51.
                                                                           1702 CACAACCTCGACTACTACA 1720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGTICCACTGCAAGGTGT 607
                                                                                                   1 CACAACCTCGACTACTACA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                21-NOV-2003; 2003WO-JP014893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-NOV-2002; 2002JP-00340053
                                                                                                                                                                                 ADQ27143 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tei K, Naito Y;
                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-487423/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                guanine or cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NATO/) NATORI Y.
(SAIG/) SAIGO K.
(TEIK/) TEI K.
(NAIT/) NAITO Y.
                                                                                                                                                                                                                                                                                                                                                                                     WO2004048566-A1.
                                                                                                                                                                                                                                                                                                                          cytotoxicity
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                              26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                    .0-JUN-2004.
                                                                                                                                                                                                                 ADQ27143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
               Query Match
                                                                                                                                                      442
                                            Matches
                                                                                                                                                                 RESULT
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Gaps

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WO2004048566-A1

ADQ27140 standard; DNA; 19 BP

RESULT 443

ADQ27140 ID ADQ2

Homo sapiens.

cytotoxicity

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Saigo K,
                                                                                                                                                                                                                                                                                                                       ADQ27142;
                                                                                                                                                                                                   Query Match
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Matches
                                                                                                                                                                                                                                                                                    RESULT 446
                                                                                                                                                                                                                                                                                              ADQ27142
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                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                           The invention relates to a method of detecting the base sequence for RNA interference by detecting the regions in the DNA sequence fulfilling the following requirements such as: (i) the base at 3' terminal is adenine, thymine or uracil, (ii) the base at 5' terminal is guanine or cytosine; (iii) the seven base sequence at 3' terminal is rich in adenine, thymine and uracil, and; (iv) there are bases in a such a number that it causes MNA interference without showing cytocoxicity. The method is used for designing and synthesizing siRNA causing RNA interference. This sequence corresponds to an RNA interference target sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; detection; RNA interference; siRNA; gene silencing; gene expression;
                                                                                                                                               Detecting sequence of RNA interference useful for synthesizing siRNA, by detecting regions in sequence fulfilling specific criteria such as base at 3' terminal is adenine, thymine or uracil, base at 5' terminal is guanine or cytosine.
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                        0.5%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 5.48+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                         Sequence 19 BP; 5 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                             Disclosure; SEQ ID NO 63; 325pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA interference target sequence #46.
                                                                                                                                                                                                                                                                                                                                                                 455 CCTGCGTCGTGGAGAACAA 473
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                                21-NOV-2003; 2003WO-JP014893
                                                22-NOV-2002; 2002JP-00340053
                                                                                                                                                                                                                                                                                                                                                                                                                               ADQ27138 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Naito Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                Tei K, Naito Y;
                                                                                                                                                                                                                                                                                                                                               19; Conservative
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                  WPI; 2004-487423/46.
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SAIGO K.
TEI K.
NAITO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tei K,
                                                                    (NATO/) NATORI Y.
(SAIG/) SAIGO K.
(TEIK/) TEI K.
(NAIT/) NAITO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004048566-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytotoxicity
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               10-JUN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NATO/) N
(SAIG/) (TEIK/) (NAIT/)
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                                                                                                                Saigo K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting sequence of RNA interference useful for synthesizing siRNA, by detecting regions in sequence fulfilling specific criteria such as base at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
                                                                                                                                                                                                                                                 The invention relates to a method of detecting the base sequence for RNA interference by detecting the regions in the DNA sequence fulfilling the following requirements such as: (i) the base at 3' terminal is adenine, thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine; (iii) the seven base sequence at 3' terminal is rich in adenine, thymine and uracil, and; (iv) there are bases in a such a number that it causes MNA interference without showing cytotoxicity. The method is used for designing and synthesiaing siRNA causing RNA interference. This sequence corresponds to an RNA interference target sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss; detection; RNA interference; siRNA; gene silencing; gene expression;
                                         Detecting sequence of RNA interference useful for synthesizing siRNA, by detecting regions in sequence fulfilling specific criteria such as base at 3' terminal is adenine, thymine or uracil, base at 5' terminal is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19; DB 1; Length 19;
Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 5 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                           Disclosure; SEQ ID NO 60; 325pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA interference target sequence #50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        676 GACGGCACACCCTACGTTA 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GACGGCACACCCTACGTTA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
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                                                                                                                                                     guanine or cytosine.
WPI; 2004-487423/46.
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(SAIG/) SAIGO K.
(TEIK/) TEI K.
(NAIT/) NAITO Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-2004.
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thymine or uracil; (ii) the base at 5' terminal is guanine or cytosine; (iii) the seven base sequence at 3' terminal is rich in adenine, thymine and uracil, and; (iv) there are bases in a such a number that it causes RNA interference without showing cytotoxicity. The method is used for designing and synthesizing siRNA causing RNA interference. This sequence corresponds to an RNA interference target sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of the nucleotide sequences that are complementary to a stretch of nucleotides
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                       siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
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                                                                                              Score 19; DB 1; Length 19;
Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stephen S;
                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                 Anti-FGFR3 siRNA related DNA sequence SEQ ID NO:722.
                                                                         Sequence 19 BP; 6 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            William M,
                                                                                                       100.0%; Pred. No. 5.3
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Devin L,
                                                                                                                                         1934 CACACGACCTGTACATGAT 1952
                                                                                                                                                      1 CACACGACCTGTACATGAT 19
                                                                                                                                                                                                                   BP
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                                                                                              0.5%;
                                                                                                                                                                                                                  ADQ61020 standard; RNA; 19
                                                                                                                                                                                                                                                           09-SEP-2004 (first entry)
                                                                                                                    19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-420527/39.
                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                 RNA interference.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the target
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                                                                                                                                                                                                                                                                                                                                                                               03-JUN-2004
                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                       ADQ61020;
                                                                                              Query Match
                                                                                                                                                                                             447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGAUAGUGAAGUAC; and GAAGACUCUGCUCAGUUUG. The siRNA molecule comprises a sense strand and an anti-sense strand. The siRNA molecule comprises a hairpin. The siRNA molecule comprises between 18 and 30 base pairs. The kit comprises at least two siRNA, comprising a first optimised siRNA and a second optimised siRNA. The method is useful in selecting siRNA for generating a gene silencing reagent. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of the nucleotide sequences that are complementary to a stretch of nucleotides
siRNA and a second optimised siRNA. The method is useful in selecting siRNA for generating a gene silencing reagent. The present sequence is used in the exemplification of the invention. The sequence is shown in
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene silencing; Bcl-2; optimised; short interfering RNA;
                                                                                                                                                                      .
0
                                                                                                                                 Length 19;
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                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-FGFR3 siRNA related DNA sequence SEQ ID NO:724.
                                                          the specification as DNA, but described as siRNA.
                                                                                           Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                 Score 19; DB 1; L. Pred. No. 5.4e+02;
                                                                                                                                          100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Devin L,
                                                                                                                                                                                                           383 GCATCAAGCTGCGGCATCA 401
                                                                                                                                                                                                                                            1 GCATCAAGCTGCGCCATCA 19
                                                                                                                                                                                                                                                                                                                                            ВЪ
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10-SEP-2003; 2003US-0502050P.
                                                                                                                                 0.5%;
                                                                                                                                                                                                                                                                                                                                          ADQ61022 standard; RNA; 19
                                                                                                                                                  Local Similarity 100.
Les 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the target sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss; siRNA; gene s
RNA interference.
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                                                                                                                                 Query Match
Best Local Si
Matches 19,
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Sequence 19 BP; 2 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
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interfering RNA) comprising selecting an siRNA molecule of 19-25

nucleoside bases by selecting a trarget gene and measuring the
functionality of sequences of 19-25 mucleotides in length that are
tunctionality complementary to a stretch of nucleotides of the target
cequence, where the functionality is dependent upon non-target specific
criteria. Also claimed are methods for gene-silencing, developing an
criteria. Also claimed are methods for gene-silencing, developing an
criteria algorithm for selecting siRNA, selecting, developing an
ceffective at silencing Bcl-2, and a kit for gene silencing comprising the
ceffective at silencing Bcl-2, and a kit for gene silencing comprising the
siRNA. The siRNA molecule comprises a sequence substantially similar to a
sequence consisting of GGGAGADAUGAGAGA, GAAGUACACCACUAUAAG,
GGAGAUAGUGAGACAACGGGAGAAA, AGAUAGUGAAAGAGACAACGGGGAGAAA,
CGGCCCUCGGUUGAGUU; GAAGACCUGGUCAGUUU;
CGGAGAUAGUGAAGUAC, and GAAGACUGGUCAGUUG, The siRNA molecule
comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
comprises a hairpin a gene silencing reagent. The present sequence is
siRNA and a second optimised siRNA. The method is useful in selecting
circulation of the invention. The sequence is shown in
the seneptical or man and a second optimised siRNA. The method is useful in selecting
cused in the examplification of the invention. The sequence is shown in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of the nucleotide sequences that are complementary to a stretch of nucleotides
 used in the exemplification of the invention. The sequence is shown in
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                   gene silencing; Bcl-2; optimised; short interfering RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to a novel method for selecting siRNA (short
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stephen S;
                                                                       Length 19;
                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                         Anti-FGFR3 siRNA related DNA sequence SEQ ID NO:721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the specification as DNA, but described as siRNA.
             the specification as DNA, but described as siRNA.
                                         Sequence 19 BP; 6 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
                                                                         Score 19; DB 1; Le
Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        William M,
                                                                0.5%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 12; SEQ ID NO 721; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Devin L,
                                                                                                                                1700 TGCACAACCTCGACTACTA 1718
                                                                                                                                                             1 TGCACAACCTCGACTACTA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-NOV-2002; 2002US-0426137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-2003; 2003WO-US036787
                                                                                                                                                                                                                                      ADQ61019 standard; RNA; 19
                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Angela R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the target sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DHAR-) DHARMACON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-420527/39.
                                                                                     Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                          ss; siRNA; gene s
RNA interference.
                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004045543-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anastasia K,
                                                                                                                                                                                                                                                                                               09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                       siRNA;
                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                     ADQ61019;
                                                                             Query Match
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The invention relates to a novel method for selecting siRNA (short interfering RNA) comprising selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of sequences of 19-25 nucleotides in length that are substantially complementary to a stretch of nucleotides of the target sequence. Where the functionality is dependent upon non-target specific sequence, where the functionality is dependent upon non-target specific sequence; where the functionality is dependent upon non-target specific criteria. Also claimed are methods for gene-silencing, developing an siRNA algorithm for selecting siRNA, selecting an siRNA with improved functionality, selecting hyperfunctional siRNA, an siRNA with improved siRNA. The siRNA molecule comprises a sequence substantially similar to a siRNA. The siRNA molecule comprises a sequence substantially similar to a candence and sire and season strand and an anti-sense strand. The siRNA molecule comprises a hairpin. The siRNA molecule comprises between 18 and 30 base pairs. The kit comprises at least two siRNA, comprising a first optimised siRNA and a second optimised siRNA. The siRNA molecule comprises the present sequence is used in the exemplification of the invention. The sequence is shown in
                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases by selecting a target gene and measuring the functionality of the nucleotide sequences that are complementary to a stretch of nucleotides
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene silencing; Bcl-2; optimised; short interfering RNA;
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stephen S;
Score 19; DB 1; Length 19;
Pred. No. 5.4e+02;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-FGFR3 siRNA related DNA sequence SEQ ID NO:723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 described as siRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 4 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Devin L, William M,
                                 ilarity 100.0%; Pred. No. 5.4
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 12; SEQ ID NO 723; 199pp; English
                                                                                                                                               1331 TGTCGGACCTGGTGTCTGA 1349
                                                                                                                                                                                                                 1 rereceacerecrereren 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the specification as DNA, but
                                                                                                                                                                                                                                                                                                                                                                                             ADQ61021 standard; RNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-2003; 2003WO-US036787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-NOV-2002; 2002US-0426137P.
10-SEP-2003; 2003US-0502050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anastasia K, Angela R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the target sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DHAR-) DHARMACON INC
       Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-420527/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88; siRNA; gene s:
RNA interference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004045543-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ61021;
                                                                                                                                                                                                                                                                                                                               RESULT 450
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Gaps

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The present invention describes using a leukotriene synthesis inhibitor

(I) for the manufacture of a medicament for the treatment of myocardial

infarction in an individual comparison of acute coronary

Also described is a method (MI) for the treatment of acute coronary

Syndrome (ACS) in an individual comprising administering (I). (I) has

antiatheroselerotic, cardiant and antianginal activities, and can be used

as a leukotriene biosynthesis inhibitor, and a leukotriene receptor

antiatheroselerotic, cardiant inhibitor, and a leukotriene receptor

cantagonist. (I) can be use for the manufacture of a medicament for the

treatment of myocardial infarction or susceptibility to myocardial

confarction in an individual Much has at least one risk factor chosen from

an at-risk haplotype for myocardial infarction, an at-risk haplotype in

the 5-lipoxygenase activating protein (FLAP) gene, a polymorphism in a

cc the 5-lipoxygenase (5-

CLO) gene promoter; in an individual who has at least one risk factor

chosen from diabetes, hypertension, hypercholesterolaemia, elevated

cc lp(a), obesity, past or current smoker; in an individual having elevated

cinflammatory marker chosen from C-reactive protein (CRP), serum amyloid

A, fibrinogen, leukotriene metabolite, interleukin-6, tissue

necrosis factor-alpha, soluble vascular cell adhesion molecule (sVCAM),
                                                                                                                                                                                                                                                                                                                                                                                                       leukotriene synthesis inhibitor; myocardial infarction; antianginal; acute coronary syndrome; antiatherosclerotic; cardiant; antianginal; leukotriene biosynthesis inhibitor; leukotriene receptor antagonist; 5-lipoxygenase activating protein; FiAP; human; chromosome 13; chromosome 134; polymorphism; 5-lipoxygenase gene promoter; 5-LO gene promoter; diabetes; hypertension; hyporrohisercholesterolaemia; obesity; inflammatory marker; low density lipoprotein; cholesterol; high density lipoprotein; angina; atherosclerosis; microsatellite marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of leukotriene synthesis inhibitor for manufacture of a medicament for treatment for myocardial infarction or susceptibility to myocardial infarction in individual.
  Length 19;
                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                     Human FLAP related microsatellite marker SEQ ID NO:394
  DB 1; Le
5.4e+02;
  0.5%; Score 19; DB
100.0%; Pred. No. 5.4
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 394; 306pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gulcher JR;
                                                                                    GGACGCCACACCCTACGTT 693
                                                                                                                             1 GGACGGCACACCCTACGTT 19
                                                                                                                                                                                                         17-OCT-2002; 2002US-0419433P.
21-FEB-2003; 2003US-0449331P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2003; 2003WO-US032556.
                                        19; Conservative
Query Match
Best Local Similarity
                                                                                       675
                                            Matches
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soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-1, matrix metalloprotease type-9, in an individual having increased low density lipoprotein (IDL) cholesterol and/or decreased high density lipoprotein (HDL) cholesterol; in an individual having increased leukotriene synthesis; in an individual having previous myocardial infarction or acute coronary syndrome (ACS) event, stable angina; or in an individual who has atherosclerosis or who requires treatment to restore blood flow in arteries. (MI) is useful for treating an individual suffering from acute coronary syndrome chosen from unstable angina, non-ST-elevation myocardial infarction (STEMI). The human FLAP gene is located on chromosome 13, more specifically to 13012. The present sequence represents a microsatellite marker used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a composition comprising a polypeptide having a first domain with carbohydrate binding activity and a second domain with kinase activity, a first domain with discoidin-type ligand binding characteristics and a second domain with tyrosine kinase activity. The invention is useful to diagnose, prognose and treat a patient having turnours of epithelial type cells which express the polypeptide on their surface. The present sequence represents a tyrosine kinase antisene oligonculeotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A new polypeptide has a discoidin-type ligand binding domain and a tyrosine kinase domain and is useful to diagnose and treat a patient having tumors of epithelial type cells which express the polypeptide on
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; antisense; tyrosine kinase; epithelial type cell tumour.
                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 19; DB 1; Length 20; 100.0%; Pred. No. 5:7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 9 A; 10 C; 1 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tyrosine kinase antisene oligonculeotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 3; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edman JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                 2318 TGTGTGTGTGTGCGT 2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 rererererererecer 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE79941 standard; cDNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00077254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00140378
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson JD, Rutter WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JOHN/) JOHNSON J D. (RUTT/) RUTTER W J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-009136/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDMAN J C.
                                                                                                                                                                                                                                                                              present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2003124133-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               their surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-1993;
16-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE79941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE79941/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8
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leogenic transgenic plant; line; T-DNA; transformation; cross-breeding; hybrid; plant; characterisation; amplification; PCR primer; ss.

28-JUL-1999; 99FR-0009990. 25-JUL-2000; 2000WO-FR002130.

(RHOB-) RHOBIO.

40200107632-A1.

Synthetic.

lantae

01-FEB-2001.

Isogenic transgenic plant line related GSPLB4 SEQ ID NO:8.

04-MAY-2001 (first entry)

AAF63628;

AAF63628 standard; DNA; 27 BP.

RESULT 454 AAF63628/

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The sequence is that of a bovine microsatellite sequence obtd. by

Conservating a library of bovine MboI DNA fragments of between 250 and 500

Conservation and (TC)15 and and (TC)15 oligomucleotide probe. One out of 50

Colones cross-hybridised. Assuming independent distribution of

Colones cross-hybridised. Assuming independent distribution of

microsatellites and MboI sites, the frequency of (TG)n >9 microsatellites

in the bovine genome is estimated at >100, 000. The sequence information

Concer 230 such bovine microsatellites is summarised in the

specification and indexed herein (see below). The sequences upstream and

constream of the microsatellite sequence waset to generate the

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellite (using the program OPTIPRIM). The microsatellites may be

microsatellity ingortant trait is espen in cattle, to allow selective

conomically important traits sep. in cattle, to allow selective

conomically important traits sep. in cattle, to allow selective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR, selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                             .;
0
                                                               Ouery Match
0.5%; Score 19; DB 1; Length 24;
Best Local Similarity 69.6%; Pred. No. 7.1e+02;
Matches 16; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26 BP; 2 A; 1 C; 12 G; 11 T; 0 U; 0 Other;
Seguence 24 BP; 1 A; 6 C; 7 G; 4 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of a microsatellite from clone TGLA70B.
                                                                                                                                                                                                                       1618 cacaggaccigcraccacaa 1640
                                                                                                                                                                                                                                                         24 CAYCGSGAYCTGGCYGCYCGSAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Table 7; Page 383; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US000340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ34131 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9213102-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ34131;
                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 453
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AAQ4131

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The present invention describes a method for the production of isogenic transgenic plant lines (A) by transforming cells of a hybrid with T-DNA transgene (I), the hybrid being derived by crossing a vector containing a transgene (I), the hybrid being derived by crossing a containing a transgene (I), the hybrid being derived by crossing a primary transformation (LT).

Colline of interest (LT) and a line suitable for transformation (LT).

Colline of interest (LT) and a line suitable for transformation (LT).

Colline of interest (LT) and a line suitable for transformation (LT).

Colline only, then back-crossed with LI and selection of products until collines cransgenic characteristics into a plant. (I) may express an antisense conformation or protein that confers resistance to disease or pathogens cand/or improves some agronomic or mutritional property. By selecting primary transformates, the method allows introduction of genes without additional fragments (representing a genetic burden) bound to the additional fragments (representing a genetic burden) bound to the cannessene, i.e. it makes possible production of truly isotransgenic lines which (I) can be transferred to a plant genome is increased, asince the which (I) can be transferred to a plant genome is increased, since the which (I) can be transferred to a plant genome is increased. The speed with sequence represents a gene specific PCR primer for amplifying a left sequence (LB) sequence (i.e. a GSPLB oligonucleotide) in an example from the paragraph.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production of transgenic plant lines, useful for producing elite hybrids with transgenic characteristics, includes selection for incorporation of transgene into particular parent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 0.5%; Score 19; DB 1; Length 27; Local Similarity 81.5%; Pred. No. 8e+02; conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27 BP; 5 A; 9 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3639 GGGCAGCTGTCCTTGCTTGCTGCAG 3665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 36; 44pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-168557/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perez P, Garcia D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
8 8
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GAGCAGCTGAAGCTTGCATGCCTGCAG 1

AAQ33888 standard; DNA; 22 BP.

RESULT 455

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0; Gaps

0; Indels

0.5%; Score 19; DB 1; Length 26; 00.0%; Pred. No. 7.7e+02;

Query Match 0.5%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 7.7 Matches 19; Conservative 0; Mismatches

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AAQ33888 ID: AAO3

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
by with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
comparteem of the microsatellite sequence waset to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
conomically important traits esp. in cattle, to allow selective
bredging. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuroepithelial stem cell; lineage restricted intermediate precursor; oligodendrocyte; satrocyte; self-renewal; neuron; differentiation; neural crest cell; fibroblast growth factor; FGF; FGFR; receptor; CNS; central nervous system; glial cell; PCR primer; amplification; 88.
                                                                                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.8; DB 1; Length 22;
Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22 BP; 1 A; 0 C; 11 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2316 rererererererecere 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 rerererererereres
                                                                                                                                                                                                                                                                                                                                                                                                                                              Table 7; Page 216; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                    92WO-US000340.
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                                                                                                                                                                                            91US-00642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX00035 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.5
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGFR-3 PCR sense primer.
                                                                                                                                                                                                                                                                                    Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                   WPI; 1992-284684/34.
                                                                                                                                                                                                                                           (GENM-) GENMARK
                                                            WO9213102-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9850526-A1.
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                                                                                                                                                    15-JAN-1992;
                                                                                                                                                                                              15-JAN-1991;
                                                                                                        16-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2-NOV-1998
                    Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX00035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 457
g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 by with an (ACL)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellite is summarised in the sequence information commerceam of the microsatellite sequence were used to generate the downstream of the microsatellite sequence were used to generate the microsatellite (using the program OFTIRMI). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gabs
                                                                                                                                                                     PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 0.5%; Score 18.8; DB 1; Length 22; 1 Similarity 90.9%; Pred. No. 6.7e+02; 20; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 1 A; 0 C; 11 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microsatellite sequence from clone TGLA135.
                                                                                                                             Microsatellite sequence from clone TGLA306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2330 TGTGCGTGTGTGTGTGTGTG 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reregarerererererere 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rable 7; Page 285; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                               92WO-US000340
                                                                                                                                                                                                                                                                                                                                                                                                                         91US-00642342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ33716 standard; DNA; 22
                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-284684/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENM-) GENMARK.
                                                            25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                                                                                                       WO9213102-A1
                                                                                                                                                                                                                                                                                                                                                                               15-JAN-1992;
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02-PEB-1993
                                                                                                                                                                                                                                                                                                                                   06-AUG-1992
                                                                                                                                                                                                                                           Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ33716;
                    AAQ33888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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RESULT 456
AAQ33716
XX
AC AAQ3371
DT 25-MAR.
DT 25-MAR.
DT 02-PEB.
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DE Micross
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XX
KW Genetic

Best Loca Matches

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Gaps

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Query Match 0.5%; Score 18.8; DB 1; Length 22; Best Local Similarity 90.9%; Pred. No. 6.7e+02; Matches 20; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans GRACE strain PCR primer SEQ ID NO 4135.
                                                                                                                                                                                                                                                                              Sequence 22 BP; 5 A; 2 C; 9 G; 6 T; 0 U; 0 Other;
                                       Mayer-Proschel M, Mujtaba T;
                                                                                                                                                                                                                                                                                                                        409 AGCCTGGTCATGGAAAGCGTGG 430
                                                                                                                                                                                                                                                                                                                                1 AGCTTGGTCATGGAAAGTGTGG 22
                                                                                              Example 26; Page 58; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-2001; 2001WO-US049486.
     97US-00852744.
                          (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                       ABZ29984 standard, DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                    WPI; 1999-070093/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida albicans
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     07-MAY-1997;
06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUL-2002.
                                                                                                                                                                                                                                                                   FGFR genes
                                                                                                                                                                                                                                                                                                                                                                                      ABZ29984;
                                        Rao MS,
                                                                                                                                                                                                                                                                                                                                                           RESULT 458
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8
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BP

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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by the construction of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells in which both alleles modified are useful for identifying a gene that cells having both alleles modified are useful for identifying a gene that contributes to the survival or growth of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a fungus to an antifungal agent that inhibits the growth of a mammalian disasse. (M1) is useful for identifying a compound which modulates the cativity of a gene product, preferably enzymatic activity, carbon compound catabolism, blosynthetic, transporter, transcriptional, cativity. The method is useful for identifying a compound having the cativity. The method is useful for identifying a compound having the cativity. The method is useful for identifying a compound having the cativity of a place in the method of the invention. Note: The sequence data for transity patent is not represented in the patent of the survent by the Buropean Patent Office on sequence information supplied to Derwent by the Buropean Patent Office
                                                                                                                                                                                                                                                                                                                                    Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASTH1 locus; ASTH11; ASTH1J; human; chromosome 11p; asthma; bronchial hyperreactivity; ets family; transcription factor; splice variant; genetic predisposition; polymorphism; antibody; drug screening; prophylaxis; therapy; diagnosis; single nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 18.8; DB 1; Length 22; 90.9%; Pred. No. 6.7e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 36; SEQ ID NO 4135; 167pp + Sequence Listing; English.
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                                                                                                                                                                                             Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22 BP; 9 A; 10 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                             Bussey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2322 TGTGTGTGTGTGCGTGTGTG 2343
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                                                                                                                                                                                                     Boone C,
                      20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.9
Matches 20, Conservative
                                                                                                                                  (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                     Roemer T, Jiang B,
                                                                                                                                                                                                                                                                        WPI; 2002-566694/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA80357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA80357
%X66666666666666666666666668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE XOX EXEX EXEX SX EX L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolater, pure pyperation. Of mammarian neurospithelial stem cells, which are capable of self-remewal in adherent feeder-cell-independent (ARCI) culture medium and differentiation to central nervous system (CNS) neuronal cells and to neuronal creet stem cells. Also described is an isolated population of mammalian creet stem cells. Also described is an isolated population of mammalian constitute medium and can differentiate to CNS glial cells but not to CNS neuronal cells. The stem cells can be used to generate a population of mammalian motor neurons by incubating the stem cells but not to CNS neuroning cells. The stem cells can be used to generate a population of mammalian motor neurons by incubating the stem cells in a medium comprises laminin-coated plates and NEP medium lacking chick embryo extract. The stem cells can also produce neural creet stem cells by inducing the cells on a laminin-coated substrate and preferably withdrawing a mitogen (preferably fibroblast growth factor; FGF) and colls withdrawing a mitogen (preferably fibroblast growth factor; FGF) and agent to the cells, preferably abone morphogenetic protein (BMP) such BMP-2, 4 or -7. The stem cells can be used to produce cells of differentiate in vitro to neural creet stem cells to inducing these cells to differentiate in vitro to neural creet stem cells and inducing these cells to differentiate in vitro comparing the cells of the proposet to produce cells of the 
                                                                                                                                                                                                                                                                                                                                           Mammalian neuroepithelial stem cells and glial restricted precursor - can self renew and differentiate into central nervous system cells, used for generating various types of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes an isolated, pure population of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fungus; yeast; tetracyclin; promoter; GRACB strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an example from the present invention to amplify different FGF and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Gaps

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Location/Qualifiers

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New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the 5' anchored (ISSR)-PCR primer of the invention.
                                                                                           inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant; animal; Basmati rice; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligodeoxyribonucleotide; intersubunit linkage;
phosphoramidate intersubunit; antisense activity; nuclease resistant;
in-vitro cell growth inhibition assay; infection;
smooth muscle cell proliferation disorder; inflammatory process;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18.8; DB 1; Length 23; Pred. No. 7.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23 BP; 1 A; 1 C; 10 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified DNA oligonucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                     (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                5' anchored (ISSR)-PCR primer - SEQ ID 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 5; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 crarcrerererererer 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2315 GTCTGTGTGTGTGTGTGCGT
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                                                                                                                                                                                                                                                                                                                       09-JAN-2003; 2003WO-IB000041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%;
                                                                                                                                                                                                                                                                                                                                                                     08-APR-2002; 2002IN-CH000260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic disorder; cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX59719 standard; DNA; 24
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.5
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-804317/75.
                                                                                                                                                                                                                   WO2003085133-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       animal systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09525814-A1
15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagaraju JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-1995
                                                                                                                                                                                                                                                                      16-OCT-2003
                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX59719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX59719/
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcripts has no effect on the open reading frame of ASTH1U as the exons involved are all 5' to the start codon in exon b. In contrast, alternative splicing of ASTH1I transcripts results in 3 different ASTH1I isoforms. The invention also encompasses mouse asth1j protein. The ASTH1I isoforms. The invention also encompasses mouse asth1j protein. The ASTH1I nucleic acids are useful as diagnostics to identify a hereditary predisposition to asthma, as probes for identifying ASTH1 related genes, correcting genetically modified non-human animals or site specific gene modifications in cell lines. The encoded ASTH1 proteins are useful as immunogens to raise specific antibodies; in drug screening for compositions that mimic or modulate activity or expression of ASTH1 and/or ASTH1 genes or fragments thereof, encoded proteins, ASTH1 genomic reginal or setting anti-ASTH1 and anti-ASTH1 and anti-ASTH1 and anti-ASTH1 and anti-ASTH1 and anti-ASTH1 of atthodies are useful in the identification of gene activity in vivo for prophylactic and therapeutic may have reaguents thereof may be used to modulate or reduce bronchial hyperreactivity. Sequences AAAGOSGO-ABOSGI and AAABOSG4-ABO416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the ASTH1 locus on the short arm of human chromosome (11p). This locus comprises the ASTH11 and ASTH1J genes, which are associated with a genetic predisposition to asthma and bronchial hyperreactivity. The ASTH1 locus, and have similar patterns of expression and common sequence metifs. They are both expressed in trachea, lung and several other tissues. ASTH1 and ASTH1J are novel members of the ets family of transcription factors, which have been implicated in the genes known to be important in the aetiology of asthma. Both ASTH1 and ASTH1J mand ASTH1J was a set in the activity of genes including the TCRs gene and cytokine genes known to be important in the aetiology of asthma. Both ASTH1I and ASTH1J mRNAR are alternatively spliced. Alternative splicing of
                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids other than naturally occurring chromosomes encoding ASTH1 protein. for e.g. screening compositions that modulate expression or function of ASTH1 proteins or as diagnostics for genetic predisposition to asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represent polymorphic sites within the ASTH1J or ASTH1I genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 18.8; DB 1; Length 23; 90.9%; Pred. No. 7.18+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                             Cardon L, Buckler A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 1 A; 2 C; 11 G; 9 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2318 TGTGTGTGTGTGTGCGTGTG 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Col 41-42; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 rererererarerececere 23
                                                                                                                                                                                                                                                                                             North M,
                                                                                                                                                                                                                                                                      Miller A, No.-.
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                                                                                                                     98US-00009913
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97US-0051432P
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                                                                                                                                                                                                                                               (AXYS-) AXYS PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-505109/45.
                                                                                                                                                                                                                                                                                             Galvin M, Miller
Brooks-Wilson AR,
                                                                                                                          21-JAN-1998;
                                                                                                                                                                        21-JAN-1997;
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                            US6087485-A
                                                                       11-JUL-2000
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Gaps ö

Indels

95WO-US003575 94US-00210505

20-MAR-1995; 18-MAR-1994;

ADD69447;

ADD69447
ID ADD6
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AC ADD6
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RESULT 460

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Query Match

Best Loca Matches

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                                                                                                                                                                    The specification describes oligodeoxyribonucleotides having contiguous nucleoside subunits joined by intersubunit linkages, where at least 3 contiguous subunits joined by phosphoramidate intersubunits. The contiguous subunits as a sequence of nucleoside subunits effective coligodeoxyribonucleotides has a sequence of nucleoside subunits effective to form a duplex with a target nucleic acid molecule. The coligodeoxyribonucleotides nucleic acid molecule. The have improved RNA and dsDNA hybridisation characteristics, relative to oligonucleotides not containing N3'-P5' phosphoramidate linkages. They also have excellent antisense activity against complementary mRNA targets in in-vitro cell growth inhibition assays. They also exhibit low cyccotoxicity. They may be used in diagnostic and therapeutic cyccotoxicity. They may be used in diagnostic and therapeutic cyccotoxicity. They may be used in diagnostic and therapeutic cyclosicity. They may be used in diagnostic and therapeutic cyclosic in treatment of smooth muscle cell proliferation diagnosters, inflammatory processes, certain genetic disorders, cancers, cetc. The present sequence represents an oligonucleotide of the invention
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                                                                                                 Oligo:nucleotide N3'-P5' phosphoramidate(8) - have improved resistance toward phosphodiesterase digestion, and form stable duplexes with DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "each base is linked by N3'-P5' phosphoramidate
linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag= a
note= "each base is linked by N3'-P5' phosphoramidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphoramidate intersubunit; antisense activity; nuclease resistant; in-vitro cell growth inhibition assay; infection; smooth muscle cell proliferation disorder; inflammatory process;
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified oligonucleotide containing N3'-P5' phosphoramidates
                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 18.8; DB 1; Length 24; ilarity 90.9%; Pred. No. 7.46+02; Conservative 0; Mismatches 2. T.A.'.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 10 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligodeoxyribonucleotide; intersubunit linkage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2823 TATATATATATATATATA 2844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                    Disclosure; Page 54; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 TATATATAAAATATATATA 1
                          (LYNX-) LYNX THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX59721 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic disorder; cancer; ss.
  94US-00214599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linkages"
                                                  Schultz RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                           WPI; 1995-344627/44.
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
Les 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified_base
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   18-MAR-1994;
                                                   Gryaznov SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1995.
                                                                                                                              RNA strands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX59721;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 462
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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The specification describes oligodeoxyribonucleotides having contiguous uncleoside subunits are joined by intersubunit linkages, where at least 3 contiguous subunits are joined by phosphoramidate intersubunits. The oligodeoxyribonucleotides has a sequence of nucleoside subunits effective consignation and the analysis of the angles where at least 3 coligodeoxyribonucleotides are more resistant to nuclease digestion and have improved RNA and dSDNA hybridisation characteristics, relative to oligonucleotides not containing N3'-P5' phosphoramidate linkages. They also have excellent antisense activity against complementary mRNA targets in in-vitro cell growth inhibition assays. They also exhibit low cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity. They may be used in diagnostic and therapeutic cytcoxicity in combatting infections agents such as bacteria, viruses, etc. or in treatment of smooth muscle cell proliferation disorders, inflammatory processes, certain genetic disorders, cancers, cetc. The present sequence represents an oligonucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                           Oligo:nucleotide N3'-P5' phosphoramidate(s) - have improved resistance toward phosphodiesterase digestion, and form stable duplexes with DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prostate cancer; human; marker; diagnosis; treatment; RT-PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 57; 101pp; English.
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                                                                                                                                                                                                                                     Chen J;
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                                                                                                                                                                    THERAPEUTICS INC
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95WO-US003575.
                                                                94US-00210505.
94US-00214599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                        Schultz RG,
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                                                                                                                                                                                                                                                                                                         WPI; 1995-344627/44.
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Matches 20; Conserv
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                                                                                                                                                                        (LYNX-) LYNX
20-MAR-1995;
                                                                                                                                                                                                                                        Gryaznov SM,
                                                                    18-MAR-1994;
                                                                                                       18-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA strands
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Veltri R, Ralph D, WPI; 1999-214055/18. Homo sapiens. 31-JUL-1996; US5882864-A. 16-MAR-1999 Synthetic AAX26085; Query Match RESULT 46, AAX26085, XX AAX26085, XX AAX2, XX DT 20-M ઠે g

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This primer is used in the relative quantitative RT-PCR to examine the expression of the genes which is used for the identification of markers of human prostate cancer. Isolated nucleic acid segments shown in AAV16881 to AAV16885, AAV16890 to AAV16903, AAV26351 and AAV26352 which can act as human prostate cancer markers are provided in the specification. The specification also provides methods for identifying markers for human prostate cancer and for detection of prostate cancer cells. The markers can be identified by amplifying human prostate RNA to provide nucleic acid amplification products, separating the products and identifying those RNA that are differentially expressed between human prostate cancers versus normal or benign human prostate. Prostate cancer cells in a sample can be detected by detecting a nucleic acid being a prostate cancer marker. Primers and probes derived from this marker can be used for the detection of prostate cancer cells in a sample. Antibodies against the protein encoded by the marker nucleic acid fragments, inhibitors of the protein and oligonucleotides antisense to the markers can be used for the diagnosis of
Human prostate cancer marker - useful for detection and treatment of
                                                                                                                                                                     Example 4; Page 121; 229pp; English.
                                                                 human prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human prostate cancer
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Gaps ö 0.5%; Score 18.8; DB 1; Length 24; 90.9%; Pred. No. 7.4e+02; 2; Indels Sequence 24 BP; 11 A; 10 C; 2 G; 1 T; 0 U; 0 Other; 0; Mismatches 2329 GTGTGCGTGTGTGTGTGTGT 2350 22 GTGTGCATGTGTGTCTGTGT 1 Best Local Similarity 90.9 Matches 20; Conservative

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AAX26085 standard; DNA; 24 BP.

20-MAY-1999 (first entry)

Prostate disease marker gene fragment amplifying RT-PCR primer.

Prostate cancer; benign prostatic hyperplasia; marker gene; tumour; differentiation; Reverse Transcription Polymerase Chain Reaction; diagnostic; progression; cancer; metastasis; RT-PCR; primer; ss.

96US-00692787.

95US-0001655P 31-JUL-1995;

(UROC-) UROCOR INC.

Diagnosing prostate cancer and benign prostatic hyperplasia cells - using oligonucleotide probes specific for marker genes associated with tumor differentiation and progression in Reverse Transcription Polymerase Chain Reaction analysis.

O'hara SM;

An G,

Example 4; Col 66; 74pp; English.

The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid analysis of prostate, bladder or breast biopsy samples. The probes and primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate till length gene sequences form various DNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate cancer. Ladder cancer or breast cancer. The encoded proteins may be used to immunodetection methods for detecting or quantifying the cancers, and for immunodetection methods for detecting or quantifying the cancers, and for The invention relates to methods for diagnosing prostate cancer or benign prostatic hyperplasia cells in a biological sample. The method uses oligomucleotides specific for marker genes associated with tumour differentiation and progression in Reverse Transcription Polymerase Chain Reaction (RT-PCR) analysis. The methods are diagnostic techniques useful for detecting and monitoring the progression of benign prostatic hyperplasia and human prostate cancer (the most prevalent form of cancer and a major cause of death in males) prior to the tumor undergoing metacasis, therefore allowing the optimal method of treatment to be determined before the condition becomes life threatening ö Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection; diagnosis; PCR primer; 88. Novel RNA biomarkers for diagnosis, prognosis and management of prostate, breast and bladder cancer. Gaps .; 0 Local Similarity 90.9%; Score 18.8; DB 1; Length 24; es 20; Conservative 0; Mismart. Sequence 24 BP; 11 A; 10 C; 2 G; 1 T; 0 U; 0 Other; Primer specific for cancer biomarker UC Band #210. An G, O'hara SM, Ralph D, Veltri RW; 2350 Example 2; Page 111; 191pp; English. 22 Grerecarerererererer 2329 GTGTGCGTGTGTGTGTGTGT BP 99WO-US013151. 98US-00097199. AAZ87571 standard; DNA; 24 (first entry) WPI; 2000-116557/10. (UROC-) UROCOR INC. 12-JUN-1998; WO9964631-A1 11-JUN-1999; 19-APR-2000 16-DEC-1999. AAZ87571; Query Match RESULT 465 Matches AAZ87571, *************

ss; probe; expressed sequence tag; microarray; gene expression; ic variation; biallelic marker; polymorphism; human;

cross-species comparison.

US2003104410-A1. sapiens

35-JUN-2003.

15-MAR-2002; 2002US-00098263. 16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC.

WPI; 2003-567953/53.

Mittmann MP;

Human microarray DNA oligonucleotide SEQ ID NO 77088.

(first entry)

14-OCT-2003

ACI77097;

22 GTGTGCATGTGTGTCTGTGT 1

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ACI77097 standard; DNA; 25 BP.

RESULT 46 ACI77097/

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The sequence represents nucleic acid biomarker UC band 210 primer #1, used in detection of prostate, breast and bladder cancer. Biomarker nucleic acid sequences can be used as hybridisation probes and primers that specifically hybridise to prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer markers. Proteins encoded by the nucleic acid markers can be used to produce antibodies for the detection of prostate, breast or bladder cancer. The nucleic acids can be used as targets for therapeutic intervention in these diseases, in the identification and isolation of full-length gene sequences, including regulatory elements for gene expression, from genomic human DNA libraries, as hybridisation probes for screening genomic human DNA libraries. The kits comprising the nucleic acid sequences are useful for detecting bladder, breast or prostate cancer cells in a biological sample
                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
clinical diagnosis of these cancers. The antibodies may also be used for radioimaging to quantify and localize the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                           Biomarker UC band 210 primer #1 used in diagnosis/prognosis of cancer.
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Prostate; breast, bladder; cancer; biomarker; probe; diagnostic;
benign prostatic hyperplasia; BPH; therapeutic; human; primer; ss.
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                                                                                       Length 24;
                                                                                                                            2; Indels
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                                                       Sequence 24 BP; 11 A; 10 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                       Score 18.8; DB 1;
Pred. No. 7.4e+02;
0; Mismatches 2;
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                                                                                                                                                               2329 GIGIGGGIGIGIGIGIGIGIGI 2350
                                                                                                                                                                                  22 GTGTGCATGTGTGTCTGTGT 1
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96US-0013611P.
96US-00692787.
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                                                                                         ουσιγ πατςη 0.5%;
Best Local Similarity 90.9%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-00097199
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                                                                                                                                                                                                                                                                                                                                                               29-AUG-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UROC-) UROCOR INC.
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11-JAN-1996;
31-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6218529-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUN-1998;
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                                                                                                                                                                                                                                                                                                                               AAS03988;
                                                                                                                                                                                                                                                          RESULT 466
AAS03988/c
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         SSXS
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

CC Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in monitoring gene expression levels by hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of hybridising at least one or more nucleic acids to at least two or more nucleic acids to at least two or more compounds. The nucleic acid stopes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Such of the cross-species comparison. Such of the cross-species comparison. The array of nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid for hybridisation, in Southern, Northern or doton hybridisation to identify or detect the sequence or specific comparisons of any gene, in mapping the 5' termini of mRNA molecules by crimer extensions of any gene, in mapping the 5' termini of mRNA molecules by crimer extensions or in screening solwh or genomic libraries or subclones containing segments of DNA that have been contained and preveiulally sequence. The sequence created for this patent can also be obtained in electronic format directly from USPTO at sequence them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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0.5%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 7.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25 BP; 4 A; 9 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 77088; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2569 CACGGGACATCACAGGGTGCGC 2590
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Gaps

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Query Match

Best Loca Matches

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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                             EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                               Human microarray DNA oligonucleotide SEQ ID NO 36641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 36641; 9pp; English.
                                                                 ACI36650 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-2001; 2001US-0276759P.
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     cross-species comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-567953/53.
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                                                                                                                                                                                                 13-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mittmann MP;
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                                                                                                                               ACI36650;
   468
RESULT 46

TO ACI3 6650

TO ACI3 6650

TO ACI3 6650

TO WE BELT;

WW BELT;
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises whybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are altached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acids further comprises a tag sequence. The array of nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises of the array of nucleic acids further comprises of the array of nucleic acids further comprises of the array of nucleic acids further comprises of the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html
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                               0.5%; Score 18.8; DB 1; Length 25; 90.9%; Pred. No. 7.8e+02; ive 0; Mismatches 2; Indels
Sequence 25 BP; 3 A; 5 C; 9 G; 8 T; 0 U; 0 Other;
                                                                                                     2334 CGTGTGTGTGTGTGCACA 2355
                                                                                                                        Best Local Similarity 90.9
Matches 20; Conservative
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Query Match

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The present invention describes the rat Nurrl coding and protein sequences. The Nurrl protein is involved in the induction of tyrosine hydroxylase expression in adult rat-derived hippocampal progenitor cells. The Nurrl gene and protein can be used in the treatment of catecholaminerelated diseases such as Parkinson's disease, manic depression and schizophrenia. They can also be used to induce tyrosine hydroxylase expression and identify tyrosine hydroxylase related deficiencies, which are linked to the same diseases. The present sequence is a PCR primer used in a method to differentiate adult neural progenitor cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams syndrome cognitive profile; WSCP; cognition; LIM-kinase 1; LIMK1 gene; supra-vascular aortic stenosis; protein kinase; human; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell comprising exogenous nucleic acid inducing tyrosine hydroxylase expression useful for treating catecholamine-related diseases such as Parkinson's disease, manic depression and schizophrenia.
                                                                                                                                         Rat; Nurr1; tyrosine hydroxylase; catecholamine-related disease;
Parkinson's disease; manic depression; schizophrenia; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 18.6; DB 1; Length 20; 90.0%; Pred. No. 6.4e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 6 A; 1 C; 7 G; 4 T; 0 U; 2 Other;
                                                                                                            Rat FGFR coding sequence PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                 (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1345 TCTGAGATGGAGATGAA 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 20; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCNGAGATGGAGRTGATGAA 20
                                                                                                                                                                                                                                                                                                                                                                                Gage FH;
                ВР.
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                                                                                                                                                                                                                                                                                    21-MAR-2000; 2000WO-US007544.
                                                                                                                                                                                                                                                                                                                    26-MAR-1999; 99US-00277078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinase domain 5' PCR primer.
                AAA95390 standard; DNA; 20
                                                                             12-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Sakurada K, Palmer T,
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-656165/63.
                                                                                                                                                                                         Rattus norvegicus.
                                                                                                                                                                                                                      WO200058451-A1.
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                                                                                                                                                                                                                                                    05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer; ss.
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                                               AAA95390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV05313;
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AAV05313
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27-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                         This oligonucleotide was designed to amplify the region of homology in the kinase domains of PDGF receptor, HER2, HER3, FGF-FIG, FGF-BEK, insulin receptor and IRK. It was used with another kinase homology domain -based primer (see AAV05314) in the amplification of human LIM-kinase 1 (LIMK1) sequences. The LIMK1 gene is composed of 16 exons (see AAV05315 and AAT99599-T99629) and is located 15.4 kb 3' of elastin in chromosome 7. It encodes a novel protein kinase (see AAW46576). Williams syndrome cognitive profile (WSCP) is detected by determining zygosity of the LIMK1 locus, with hemizygosity being indicative of impaired visuo-spatial constructive cognition. Chromosome 7 deletion analysis allows williams syndrome WSCP, SVAS (supra-vascular aortic stenosis) and Williams syndrome
                                                                                                                          Diagnosing Williams syndrome cognitive profile from hemi-zygosity of LIMX1 - gene on chromosome 7 encoding new kinase, allowing differentiation from classic Williams syndrome and supra-vascular aortic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZAP-70; Zeta chain-associated protein; treatment; prevention; disease; immunosuppressor; cancer; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                           ch 0.5%; Score 18.6; DB 1; Length 25; 1 Similarity 84.0%; Pred. No. 8.2e+02; 21; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 4 A; 6 C; 9 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                     1678 GACTTCGGGCTGGCCCGGGACGTGC 1702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV73860 standard; cDNA to mRNA; 25
                                                                                                                                                                             Example 3; Page 22; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalian ZAP-70 PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97JP-00130952.
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                               97WO-US011687
                                                  96US-00678039
                                                                    (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                       Keating MT, Morris CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
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                                                                                                           WPI; 1998-101185/09.
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP10313868-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAY-1997;
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26-FEB-1999
                               07-JUL-1997;
                                                   10-JUL-1996;
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            15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                             stenosis.
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                                                                                                                                                                                                                          AAV73860-V73865 are PCR primers used in the amplification of a mammalian zeta chain-associated protein, ZAP-70. This protein can be used for the prevention and the treatment of illnesses having an immunosuppressive component such as cancer and infectious diseases. (Updated on 27-AUG-2003
Immune activator comprising membrane-localised ZAP-70 - useful for the prevention and the treatment of conditions exhibiting immunosuppression such as cancers and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 18.6; DB 1; Length 25; 34.0%; Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25 BP; 3 A; 11 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PAPP-Ea associated 25-mer SEQ ID 1207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                        Example 1; Page 16; 18pp; Japanese.
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Best Local Similarity 84.05
warches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        to correct OS field.)
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Length 25;

Query Match

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Gaps

vivlemore401-10.rng

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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
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                                                          Length 25;
                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human microarray DNA oligonucleotide SEQ ID NO 44261
Sequence 25 BP; 2 A; 0 C; 10 G; 13 T; 0 U; 0 Other;
                                                          Score 18.6; DB 1;
Pred. No. 8.2e+02;
0; Mismatches 4;
                                                                                                                                                                                2321 GTGTGTGTGTGTGTGTGTGTGTGTG 2345
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                                                    0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                         ACI44270 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-2003 (first entry)
                                                                                                                     21; Conservative
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                                                       Query Match
Best Local Similarity
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AC144270/C
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AC144270/C
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BST; 8
KW GENET; 
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises which is a least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid concerned further comprises a tag sequence. The array of nucleic acid concerned further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific blot hybridisation to identify or detect the sequence or specific matations of any gene, in mapping the 5' terminio of matations of any gene, in mapping the 5' terminio of matations of any gene, in mapping the 5' terminio of matations of any gene, in mapping the 5' terminio of matations of any gene, in mapping the 5' terminio of matations of any gene, in mapping the 5' terminion of matations of any gene, in mapping the 5' terminion of matations of any gene, in mapping the 5' terminion of matations of any gene, in mapping the 5' terminion of matations of any gene, in mapping the 5' terminion of matations of any gene, in mapping the 5' terminion of matations of any gene, in mapping the 5' terminion of any capacity of the sequence or specific and the sequence of the primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at segdata.uspto.goc/seguence.html

Sequence 25 BP; 5 A; 9 C; 9 G; 2 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pp with an (AC)15 and a (TC)15 oligomuclectide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                Gaps

    used in genetic identification, gene

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                                                                                                                                                                                                                                                                                                                                PCR; selection; primers, OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                Indels
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0.5%; Score 18.6; DB 1;
84.0%; Pred. No. 8.2e+02;
ive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                   Sequence of a microsatellite from clone TGLA86.
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                                                                                                                                                                                  AAQ34170 standard; DNA; 20
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(first entry)
                                  Conservative
                                                                 1798 AGTGACGTCTGGTCC
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                 Best Local Similarity
Matches 21; Conserv
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02-FEB-1993
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GENM- ) GENMARK.
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modified base
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24-FEB-1998
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                                 Bos taurus.
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screening a library of bovine MboI DNA fragments of between 250 and 500
continuous and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100,000. The sequence information
continuous control of the microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
specification and indexed herein (see below). The sequences upstream and
consurream of the microsatellite sequence water used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program oPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
caption of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-WAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                         Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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                                                                                                            PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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                                                                                           Microsatellite sequence from clone TGLA22.
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               AAQ33816 standard; DNA; 20
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(first entry)
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(first entry)
                                                                                                                                                                                                                                                                                    Georges M, Massey JM;
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                                                                                                                                                                                                                                                              (GENM-) GENMARK
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02-FEB-1993
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                                                          25-MAR-2003
02-FEB-1993
                                                                                                                                                    Bos taurus.
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                                      AAQ33816;
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    AAQ3367
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The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (AC)15 and a (TC)15 oligomucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of clones repressibly and MboI sites, the frequency of (T6)n >9 microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites and the bovine genome is estimated at >100, 000. The sequence information constrain of the microsatellite sequence were used to generate the downstream of the microsatellite sequence were used to generate the correspondance of the microsatellite sequence were used to generate the correspondance of consistent in vitro amplification of the correspondance of microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of condition and the QTL trait of enhanced milk prodn. in Brown Swiss condition, the GTL trait of enhanced milk prodn. in Brown Swiss
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PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; 88.
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Best Local Similarity 95.0
Matches 19; Conservative
                                                     Rein A, Casas-Finet J,
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                                                                                     WPI; 1998-018230/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #O200023798-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA39091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agner E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA3909:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                        The present phosphodiesteric oligonucleotide is based on the generic formula, in the 3'-5' or 5'-3' direction: (GaTa')a'-(GbTb')b''-(Grafu')a''-(GaTa')a''-(Grafu')b''-(GaTa')a''-(Grafu')
                                                                                                                                                                                                                                                                                            New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and selective cytotoxic effect on tumour cells, for treating both solid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Retroviral nucleocapsid protein; NC; high affinity; viral replication; gene therapy; retroviral infection; HIV; transduced cell; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antitumour activity. (Updated on 25-MAR-2003 to correct PR field.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide which binds retroviral nucleocapsid protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 0.5%; Score 18.4; DB 1; Length 20; Local Similarity 95.0%; Pred. No. 6.7e+02; les 19; Conservative 0; Mismatches 1; Indels
                   /note= "phosphodiester oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 4; 38pp; English.
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                                                                                                                                                                                                                          Scaggiante B, Quadrifoglio F
                                                                                                                      96WO-EP005388
                                                                                                                                                      95IT-MI002539
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                                                                                                                                                                                        (SAIC-) SAICOM SRL.
                                                                                                                                                                                                                                                                                                                               liquid tumours.
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                                                                                                                      04-DEC-1996;
                                                                                                                                                      04-DEC-1995;
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                                                     WO9720924-A1
                                                                                     .2-JUN-1997.
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Matches
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This sequence represents an oligonucleotide which binds to a retroviral nucleocapsid (NC) protein with high affinity. The invention relates to a rargeted molecule which binds to a retroviral nucleocapsid protein with high affinity and comprises the oligonucleotide and a fusion partner. Retroviral nucleocapsid proteins, such as NC and the Gag precursors, bind cor specific nucleic acid sequences with high affinity. This binding is dependent upon the zinc fingers of the NC protein and has a strong hydrophobic component. The specific nucleic acid sequences which bind NC care useful as molecular decoys for retroviral NC proteins, for making fusion proteins which inactivate retroviral NC proteins, in screening assays for detecting molecules which inactivate retroviral NC proteins.

The inactivate and for purification of retroviral NC proteins. In particular, the targeted molecules, the transduced cells and gene therapy vectors based on the oligonucleotides can be used for treatment and prevention of retroviral infections such as those caused by HIV
                                                                                                                                                                                                       Oligo:nucleotide which binds to retroviral nucleocapsid protein with high affinity - used in targeted molecules, transduced cells and gene therapy vectors for treatment of retroviral infections such as those caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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Fisher R, Fivash M, Henderson LE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
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JP2000166563-A. chromatography Homo sapiens 04-DEC-1998; 04-DEC-1998; 24-NOV-2000 20-JUN-2000 application. AAA73096; Query Match RESULT 480 Matches $\overset{\alpha}{\times}\overset{\times}{\times}\overset{\circ}{\circ}{\circ}\overset{\circ}$ ठ 셤

Query Match RESULT 482 RESULT 481 AAA73096/ AAS13762 셤 ប្រក្រង់និ 8 엄 ò The present invention describes a method (I) for sample displacement chromatography separation. The method comprises applying a multicomponent sample along the bed by passing non-eluting mobile solvent phase over the bed, and recovering a desired component of the sample from at least portion of the bed by passing non-eluting mobile solvent phase over the bed, and recovering a desired component of the sample from at least portion of the bed. The sample components are applied in a non-homogeneous manner to bed. The sample components are applied in a non-homogeneous manner to and/or high affinity for the stationary phase material, respectively, and/or high affinity for the stationary phase material. The method sample components at significantly higher concentrations and recovery of sample components at significantly higher concentrations and recovery of sample components at significantly phase material. The method allows ten-fold greater loading than comparable gradient elution separation, it involves minimal use of costly HPC solvents and fraction analysis, avoids the use of displacer solution during actual separation analysis, avoids the use of displacer solution during actual separation of allognucleotide which is used in an example from the present invention contraction of the purification of an oligonucleotide by sample displacement ö from the human melanocortin-1 receptor (MCIR) gene upstream controlling sequence. Also described is a method for detecting a substance affecting synthesis of melanin in which a host transformed by an expression vector, comprising a control active polynucleotide derived from MCIR, is cultured in the presence of a sample to be tested and a signal formed by the expression of said reporter gene is detected. The control-active polynucleotide is used for the detection of a substance affecting The present invention describes a control-active polynucleotide derived Human; melanocortin-1 receptor; MC1R; promoter; regulation; detection; melanin; ds. Gaps Upstream controlling sequence of melanocortin1 receptor and its ; 0 Human MC1R gene related TATA box oligonucleotide SEQ ID NO:15. Score 18.4; DB 1; Length 20; Pred. No. 6.7e+02; 0; Mismatches 1; Indels Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other; Disclosure; Page 4; 21pp; Japanese. 2318 TGTGTGTGTGTGTGCGTG 2337 Example 2; Page 22; 37pp; English. 1 TGTGTGTGTGTGTGTG 20 98JP-00345881 98JP-00345881 95.0%; AAA73096 standard; DNA; 20 (first entry) Local Similarity 95.0 (SHIS) SHISEIDO CO LTD WPI; 2000-485552/43

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eguance represents a human melanocortin-1 receptor gene TATA box oligonucleotide, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; melanocortin-1 receptor; MC1R; promoter; regulation; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MCIR gene related TATA box oligonucleotide SEQ ID NO:15.
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                                                                                                                                                                                     0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; ive 0; Mismatches 1; Indels
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                                                                                                                                Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 4; 21pp; Japanese.
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-1998;
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AAS13705;

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New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                               Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
                                                                                                                                                                                                         UNIV SOUTHERN CROSS.
STATE VICTORIA DEPT NATURAL RES & ENVIRO.
UNIV ADELAIDE.
                                                                                                                                                                                                 STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
                                                                                                                                                                                                                                      ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
                                             Simple seguence repeat, SSR, #34
                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 6; 72pp; English.
                                                                                                                                                                     24-DEC-1999; 99AU-00004906.
04-MAY-2000; 2000AU-00007310.
                                                                                                                                                    03-JAN-2001; 2001NZ-00509193
                           08-MAY-2002 (first entry)
                                                                                                                                                                                                                                                           Forster JW, Jones ES;
                                                                                                                                                                                                                                                                             WPI; 2001-512563/56.
                                                                                           Lolium perenne.
                                                                                                                                 25-MAY-2001.
                                                                                                              NZ509193-A.
                                                                                                                                                                                                                                                                                                                             varieties
         AAS13762
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(VYAD-)
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The invention relates to a substantially purified or isolated nucleic acid (1) from ryegrass or fescue species including a simple sequence repeat (85R), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer 2 denicleotides in length. Also included are a nucleic acid primer 2 suitable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and included for SSRs and in selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties and testing the purity of grass or cereal cereal section of genes in grass or cereal breeding, for may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal section of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal section of genes in grass or cereal breeding, for grass or cereal sections, and for DNA profiling to establish the distinct identify, uniformity and/or stability of a cultivar. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence is a ryegrass or fescue SSR
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Gaps
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                             0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02;
                                                          1; Indels
Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                        95.0%; Pred. .v..
                                                            19; Conservative
                                              Best Local Similarity
                              Query Match
                                                          Matches
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erererererererer 20
                                                            AAS13705 standard; DNA; 20 BP
                                               AAS13705/c
ID AAS137
XX
                                    RESULT 483
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2319 GTGTGTGTGTGTGCGTGT 2338

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AAH75569;

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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence corect acid (SSR), having 2 or more tandemly repeated nucleotide core elements core uncleotides in length. Also included are a nucleic acid primer core included are a nucleic acid primer contains of preparase or fescue genomic DNA enriched for SRRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SRRs prepared by the MI, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are corected species will be breeding, a correct of the core of the purity of grass or cereal species varieties by assessing corected batches by assessing variation within seed batch of an SSR. The SSRs corected seed batches by assessing variation within seed batch of an SSR. The SSRs corected species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of grass or cereal species varieties, for testing the purity of sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species
                                                                                                                              Simple sequence repeat; plant, ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
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STATE VICTORIA DEPT NATURAL RES & ENVIRO.
UNIV ADELAIDE.
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                                                                                    Simple sequence repeat, SSR, #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 51; 72pp; English.
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04-MAY-2000; 2000AU-00007310.
                                         08-MAY-2002 (first entry)
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Best Local Similarity 95.0
Matches 19; Conservative
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AAH75569
ID AAH7556
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AC AAH7556
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Unidentified
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                         Mckay R,
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                                                                                                                                                                                                                                                                         The invention relates to control of telomere length in a cell by modifying the physiological activity of the Mrell protein in the cell, by transformation of the cell with DNA encoding a foreign Mrell protein which may be modified in the C-terminal and/or nuclease domain. The method is useful in gene therapy of telomere length-related diseases such as melanoma, liver cancer, breast cancer, bladder cancer and brain cancer. The present sequence is that of a Mrell related probe of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, antiinflammatory, cytostatic, antisense gene therapy;
phosphoenol pyruvate carboxykinase-cytosolic, PEPCK-cytosolic, infection,
inflammation, tumour formation; phosphorothioate; ss.
                                                                                                                                                                                                                             Controlling telomere length for gene therapy of telomere length related tumors comprises transformation using the modified Mrell protein.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                              88
                                            Yeast; Mre11; telomere length, nuclease; gene therapy; melanoma; liver cancer; brain cancer; probe.
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                                                                                                                                                                 (RIKE ) RIKEN KK.
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
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                                                                                                                              14-FEB-2001; 2001WO-JP001024
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           06-NOV-2001 (first entry)
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Matches 19; Conservative
                                                                                                                                                                                             Ohta K, Shibata T;
                                                                                                                                                                                                               WPI; 2001-541649/60
                              Mrell related probe
                                                                                           WO200160996-A1.
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                                                                                                             23-AUG-2001
                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                              invention
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The present sequence is one of a number of antisense compounds of up to 30 nucleobases in langth that are capable of inhibiting the expression of phosphoenol pyruvate carboxykinase-cytosolic (PEPCK-cytosolic). The antisense compounds are useful for inhibiting the expression of PEPCK-cytosolic in cells or tissues. They are commonly used as research reagents and in diagnostics. They are commonly used as research genes. They are distinguishing between functions of various members of a biological pathway and for research use. The antisense compounds are also useful prophylactically, e.g. to prevent or delay infection, inflammation or tumour formation. The present sequence is a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a
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                                                                                                                                                                                    Antisense compound capable of modulating the expression of phosphoenol pyruvate carboxykinase-cytosolic, useful for preventing or delaying infection, inflammation or tumor formation.
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                                                                Cowsert
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                                                                Wyatt J,
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99US-00347443.
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(ISIS-) ISIS PHARM INC.
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                                                                        Butler MM,
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les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA oligomer #5.
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ន្តដូច្ច 셤 윤 ਨੇ ઠ The present sequence was used to demonstrate the ability of deoxynucleic S-Methythiourea (DNmt) compounds to form triplexes with DNA oligomers. An increase in the C content of the oligos resulted in a large decrease in binding. This experiment was performed as an example of a method for preparing oligonucleotides comprising a backbone of alkyl or alkoxy thiourea linkages. The method is useful for preparing oligonucleotides for use in antisense or antigene therapy, to inhibit production of proteins associated with genetic diseases, cardiovascular, inflammatory and neurocellular diseases, and for antiviral therapy, e.g. to treat unan immunodeficiency virus, human-cytomegalovirus, influenza and herpes infections. The compounds are also useful as diagnostic reagents to detect the presence or absence of the target DNA or RNA sequences to which they specifically bind, and by antagonising the normal biological activity of a target protein, they can be used in the manipulation of tissue e.g. The method provides an efficient and rapid solid-phase method for the synthesis of thiourea and S-methylthiourea ö The present invention describes a method of treating systemic lupus erythematosus and lupus nephritis, involving administering a conjugate comprising a non-immunosenic valency platform molecule and 2 double stranded DNA epitopes which specifically bind to dsDNA-binding antibodies. Affinity of the epitopes for the antibody is used as a basis Gaps Treating systemic lupus erythematosus in individual comprises e.g. administering conjugate comprising non-immunogenic valency platform molecule and double stranded DNA epitopes which specifically bind to antibody from individual. Antibody affinity; DNA epitope; anti-DNA antibody; lupus nephritis; systemic lupus erythematosus; immunotolerance; ds. ö 0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; 1; Indels Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other; 0; Mismatches 2318 TGTGTGTGTGTGTGCGTG 2337 Example 7; Fig 16; 48pp; English Antibody binding oligonucleotide Claim 4; Page 57; 87pp; English. 20 TGTGTGTGTGTGTGTGTG 1 AAH48201 standard; DNA; 20 BP 99US-0167716P. 28-NOV-2000; 2000WO-US042307 (first entry) (LJOL-) LA JOLLA PHARM CO. 19; Conservative Linnik MD, Mcnealy PA; Query Match Best Local Similarity WPI; 2001-451601/48. WO200141813-A2 28-NOV-1999; 20-SEP-2001 14-JUN-2001, Synthetic AAH48201; RESULT 487 Matches

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for selecting individuals to receive treatment. The present sequence is an antibody binding dsDNA sequence described in the exemplification of the invention
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28-MAR-2000; 2000AU-0006520.
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Matches 19, Conservative
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Best Local Similarity
Matches 19; Conserv
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್ Matches
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AAI64445/c
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US2002115097-A1

489

RESULT 46 AAI64449

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The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidine-adenine (TA) repeats in the promoter - as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene
                                                                                                                                                                                                                                                                                Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity.
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                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 9; 13pp; English.
                                                                                                                                                                                                                 Ratain MJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00251274
                                                                                           01-FEB-2002; 2002US-00061693
                                                                                                                                  99US-00251274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TA repeat polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ARCH-) ARCH DEV CORP.
                                                                                                                                                                          (ARCH-) ARCH DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-740095/80
                                                                                                                                                                                                                 Rienzo AD, Iyer L,
                                                                                                                                                                                                                                                       WPI; 2002-740095/80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-2003
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                                                                                                                                       16-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rienzo AD,
                                                        22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL50667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAL50667/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNs. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs may be purity of legume seed batches. The present sequence is a dSR motif, which was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel simple sequence repeats in clover species useful for selection of genes in legume breeding, for profiling legume species varieties and for testing the purity of legume seed batches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human uridine diphosphate glucuronosyltransferase gene polymorphism #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gabs
                                                                                                                                                                                         Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat; uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1; drug dosage optimisation; xenobiotic sensitivity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.5%; Score 18.4; DB 1; Length 20; Best Local Similarity 95.0%; Pred. No. 6.7e+02; Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2319 GIGIGIGIGIGIGIGIGI 2338
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                                                 B.
                                                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2001; 2001NZ-00509194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                24-DEC-1999; 99AU-00004907
28-MAR-2000; 2000AU-00006520
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                                                 AA164449 standard; DNA; 20
                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Forster JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-431058/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koelliker R,
                                                                                                                                                                      SSR motif #9
                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                            23-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001
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RESULT 490

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                                                                                                             The invention comprises a method for detecting polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter (preferably UGT1A1). The method involves determining the number of thymidiahe-adenine (TA) repeats in the promoter — as the number of TA repeats correlates with expression of the UGT gene. The method of the invention is useful for detecting polymorphisms in a UGT gene promoter. The method of the invention is also useful in optimising drug dosages and predicting an individual's sensitivity to xenobiotics for drugs and xenobiotics that are glucuronidated by UGT. The present DNA sequence represents a UGT gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for the synthesis of a polynucleotide which involves coupling a second nucleoside to a first nucleoside through a phosphite linkage, where the second nucleoside has a non-carbonate protecting group protecting a hydroxyl, and exposing the product to a composition which concurrently oxidizes the phosphite formed to a phosphate and deprotects the protected hydroxyl of the second nucleoside. The method is useful for synthesizing the polynucleotides, for carrying out either 3' to 5' to 3' synthesis and for fabricating an addressable array of polynucleotides on a substrate. The
Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, involves determining number of thymidine-adenine repeats in the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthesis of polynucleotide useful during fabrication of an array involves coupling nucleoside phosphoramidite and a solid-supported nucleoside and treating the product with an oxidation/deprotection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide synthesis; polynucleotide array; protecting group;
                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caruthers M;
                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide synthesis method related DNA #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Betley JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2823 TATATATACATATATATA 2842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 15; 36pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Page 9; 13pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           19; Conservative
                                                                                                                                                                                                                                                                                           TA repeat polymorphism
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Best Local Similarity
Matches 19; Conserv
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present sequence is an oligonucleotide produced to demonstrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New method for immobilizing a molecule on a support comprises reacting derivatized molecule with a derivatized support via a cycloaddition reaction, shows high selectivity and efficiency.
                                                                                                        Gaps
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Pred. No. 6.7e+02;
0; Mismatches 1; Indels
                                                                          Score 18.4; DB 1; Length 20;
Pred. No. 6.7e+02;
                                                                                                      Indels
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                                               Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fluorescein label"
                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Immobilisation; Diels-Alder reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                    2318 TGTGTGTGTGTGTGCGTG 2337
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/mod_base= OTHER
/note= "5' fluores
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30-JAN-2001; 2001US-0265020P.
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                                                                                                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 2.
                                                                                                                                                                                                                                     ABA96307 standard; DNA; 20
                                                                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity 95.0
Matches 19, Conservative
                                                                                                        Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Husar GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-114155/15
                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           modified base
                                                                                                                                                                                                                                                                                              18-MAR-2002
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                                                                                                                                                                                                                                                                 ABA96307;
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                                                                                                                                                                                                          RESULT 493
ABA96307/c
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Synthetic.

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The invention relates to a method for immobilising a molecule on a support comparing reacting a derivatised molecule with a derivatised support capable of reacting with the molecule via a cycloaddition reaction. The method is used for immobilising molecules on a support method shows better chemoselectivity, functional groups do not need to be protected and it is highly efficient for immobilising molecules compared to other methods. The present sequence is that of an oligonucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New method for immobilizing a molecule on a support comprises reacting derivatized molecule with a derivatized support via a cycloaddition reaction, shows high selectivity and efficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid detection; hybridisation; microarray; thermistor; microcalorimetry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide (CA)10 used in nucleic acid hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sebesta DP, Leuck M,
                                                                                                                                                                                                                                                                             Immobilisation; Diels-Alder reaction; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2318 TGTGTGTGTGTGTGCGTG 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 31; 86pp; English.
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ID ABZ24438 standard; DNA; 20 BP.
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30-JAN-2001; 2001US-0265020P.
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                                                                                                                                                                                                              Oligonucleotide SEQ ID NO 1.
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                             ABA96306 standard; DNA; 20
                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·useful to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Wolter A,
Husar GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-114155/15.
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                                                                                                                                                                                                                                                                                                                                                                                                         WO200184234-A1
                                                                                                                                                       18-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                                                               ABA96306;
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Matches
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ABA96306

IID ABA9

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Latham-Timmons HA;

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The present sequence is that of a (CA)10 oligonucleotide used to contract the method of the invention. The invention provides methods illustrate the method of the invention. The invention provides methods condetecting specific binding pairs interact with condition and an ambers of specific binding pairs interact with careful of the heat of binding or reaction generated control of the manalytes methods to detect analytes in a colution through measurement of the heat of binding or reaction generated from the interaction of the analytes with binding or reaction partners. Control of the manalytes with binding or reaction partners of thermistors, which are useful in the multiparallel thermal arrays of thermistors, which are useful in the multiparallel thermal canalysis of samples. The methods and devices are particularly in the analysis of mucleic acid, respecially DNA/DNA, DNA/RNA, DNA/RNA (linear uncleic acid). The binding between the analyte and its binding partner comparises part of an enzymatic amplification reaction, especially PCR or primer extension reaction. The detection device provides a real time, comparises part of an enzymatic amplification reaction, using the binding or reaction between the analyte and its binding or reaction partner. An example from the invention, using the present oligonucleotide, showed that the thermal detection technique is constant of the distinguish between perfectly matched and mismatched DNA.
                                                                                                                                                                                                                                                                                                       Detection device useful for detecting binding between members of specific binding pair, and for multiparallel thermal analysis of samples, has an array of addressable thermistors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide (TG)10 used in nucleic acid hybridisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2318 TGTGTGTGTGTGTGCGTG 2337
                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 36; 60pp; English
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                                                                                                                                                                                                                                           Roach JS, Wolter A;
                                                                                                                                                                                                                                                                             WPI; 2003-148685/14.
                                                                                                                                                                                                        (PROL-) PROLIGO LLC
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                                                       WO200299386-A2.
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Gaps ö 12-DEC-2002.

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The present sequence is that of a (TG)10 oligonuclectide used to illustrate the method of the invention. The invention provides methods of illustrate the method of the invention. The invention provides methods so for detecting specific binding the heat of binding generated when members of specific binding pairs interact with each other. The invention also provides methods to detect analytes in a continuous the interaction of the heat of binding or reaction generated from the interaction of the analytes with binding or reaction partners. Detection devices are provided that consist of spatially addressable arrays of thermistors, which are useful in the multiparallel thermal analysis of samples. The methods and devices are particularly in the analysis of nucleic acids, sepecially DNA/DNA, DNA/RNA, DNA/RNA, ONA/RNA, ONA/RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection device useful for detecting binding between members of specific binding pair, and for multiparallel thermal analysis of samples, has an array of addressable thermistors.
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/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
1. .5
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developmental disorder; hyperproliferative disorder; antisense therapy;
FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 able to distinguish between perfectly matched and mismatched DNA
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Pred. No. 6.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human FGFR-3 antisense oligonucleotide, ISIS #125119.
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                                      07-JUN-2002; 2002WO-US018200
                                                                                                                   07-JUN-2001; 2001US-0296685P
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Best Local Similarity 95.0%;
Matches 19; Conservative
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/*tag=
                                                                                                                                                                                                                                                                                      Wolter A;
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-148685/14.
                                                                                                                                                                                                     (PROL-) PROLIGO LLC
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Synthetic.
                                                                                                                                                                                                                                                                                      Roach JS,
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Gaps

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The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential analyor combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Systemic lupus erythematosus; SLB; impaired renal function; LJP 394 conjugate; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                              Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental
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0
               /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                            16. 20
/*tag= c
/*tag= c
/note= "2 -methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 0.5%; Score 18.4; DB 1; Length 20; Local Similarity 95.0%; Pred. No. 6.7e+02; les 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense oligonucleotide targetted to human FGFR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 78; 120pp; English.
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                                                                                                                                                                                              06-SEP-2002; 2002WO-US028549.
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 /*tag=
                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                               Monia BP, Wyatt JR;
                                                                                                                                                                                                                                                                                                                                WPI; 2003-313244/30.
                                                                                                                               WO2003023004-A2
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Novel polynucleotide useful for detecting single nucleotide polymorphisms

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The present invention relates to a method of treating systemic lupus erythematosus (SLB) in an individual. The method comprises selecting an individual having SLE, significantly impaired renal function, and antibodies with high affinity to a polymuclectide epitope by administering a conjugate comprising non-immunogenic valency platform molecules and two or more double stranded DNA (dsDNA) epitopes that are polymucleotides. Also disclosed is a kit comprising the conjugate, LJP 394. The conjugate is administered in an amount effective to reduce incidence of renal flares in the individual. A medication chosen from corticosteroids and cyclophosphamide is also administered to the individual. The conjugate is administered in an amount effective to reduce the amount of a corticosteroid or cyclophosphamide shall shall a ministered to the individual. The present sequence represents a polynucleotide (dsDNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating systemic lupus erythematosus comprises selecting an individual having significantly impaired renal function and administering conjugate having non-immunogenic valency platform molecule and double stranded DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 18; 22pp; English.
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13-AUG-2002; 2002US-00219238
                                                                                                            13-AUG-2001; 2001US-0311858P. 22-AUG-2001; 2001US-0314281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linnik MD, Hepburn B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-810915/76
                                                                                                                                                                                                                                                                            (LINN/) LINNIK M D. (HEPB/) HEPBURN B.
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0.5%;
              Best Local Similarity 95.0
Matches 19, Conservative
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human; single nucleotide polymorphism; microarray; side effect; ss; Single nucleotide polymorphism detection primer, SEQ ID No 1671. ADF88088 standard; DNA; 20 BP. (first entry) Homo sapiens. 26-FEB-2004 primer; PCR Synthetic. ADF88088

Claim 2; SEQ ID NO 2088; 704pp; Japanese. in human gene.

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN,

WPI; 2003-820454/77.

12-FEB-2002; 2002JP-00034717.

12-FEB-2002; 2002JP-00034717

JP2003235571-A.

26-AUG-2003

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The invention relates to a novel polymucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention turther relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 120 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo; an anicroarray equipped with the SNP containing oligo. The isolated human gene information is useful for detecting the single nucleotide polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effecting single nucleotide polymorphisms in a human gene is also effecting single nucleotide polymorphisms in a human gene. This polymorleotide sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel polynucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo, and a microarray equipped with the SNP containing oligo. The isolated human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotide useful for detecting single nucleotide polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; single nucleotide polymorphism; microarray; side effect; ss; primer; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single nucleotide polymorphism detection primer, SEQ ID No 2088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.5%; Score 18.4; DB 1; Length 20; Best Local Similarity 95.0%; Pred. No. 6.7e+02; Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 1 A; 1 C; 10 G; 8 T; 0 U; 0 Other;
                                                      SEQ ID NO 1671; 704pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2322 TGTGTGTGTGCGTGTGTG 2341
                                                                                                                                                                                                                                                                                                                                                                                 detection method of the invention.
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                     in human gene.
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Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomedulator; cardiant; neuroprotective; antifilammathory; neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological; immunomedulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; sa
               polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymucleotide sequence represents one of the PCR primers used in the single nucleotide polymorphism detection method of the invention.
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                                                                                                                                                                                                                                                       Gaps
the invention is useful for detecting the single nucleotide
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                                                                                                                                                                                                       0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                 Sequence 20 BP; 0 A; 2 C; 9 G; 9 T; 0 U; 0 Other;
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/note= "2'-O-methocyethyls"
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les 19; Conservative
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Matches 19
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to og 9434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of complexed in cells or tissues; and (3) a method of treating an animal companies oligonucleotides and antisense compounds have cytostatic, antisinglammatory, neuroprotective, nootropic, antisinflammatory, neuroprotective, nootropic, antisinflammatory, neuroprotective, antisinflammatory, neuroprotective, and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's condition associated with mPGES-1 e.g., inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ischaemia or reperfusion injury, or
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.4; DB 1; Length 20;
Pred. No. 6.7e+02;
0; Mismatches 1; Indels
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/note= "2'-O-methoxyethyls"
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/note= "2'-0-methocyethyls"
                                                                                                       Claim 4; SEQ ID NO 141; 132pp; English.
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ADM14546 standard; DNA; 20
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                    (PHAA ) PHARMACIA CORP
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to day 1.3. The present invention also describes: (1) antisense compounds, gay 1.3. The present invention also describes: (1) antisense compounds, compGES-1, which specifically whybridise with the nucleic acid encoding compGES-1 in cells or tissues; and (3) a method of inhibiting the expression of mpGES-1 in cells or tissues; and (3) a method of treating an animal comparison associated with meGES-1. MpGES-1 chimeric antidiabetic, immunomodulator, cardiant, neuroprotective, controlic, antidiabetic, immunomodulator, and cardiovascular activities, and can be used for preparing a composition for treating a disease or composition of the used compound condition associated with mpGES-1 chimeric can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound condition associated with mpGES-1 e.g., inflammation, Alheimer's condition associated with mpGES-1 e.g., inflammation, Alheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or computable; immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                           /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines" % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1
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Pred. No. 6.7e+02;
0; Mismatches 1; Indels
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/note= "2'-O-methoxyethyls"
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16. .20
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                                            Location/Qualifiers
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Matches 19, Conservative
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*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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Gaps

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BP.

ADM13955 standard; DNA; 20

ADM13955/

ADM13955;

EXXX

Gaps

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Indels Length

sapiens.

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(PHAA ) PHARMACIA CORP
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                                Key
modified_base
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01-JUL-2004
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                            Synthetic.
                                                                                Gierse JK,
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chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; imPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cardiati; antidibitor; cardiant; neuroprotective; antidiflammatory; neuroprotective; antidiflammatory; neuroprotective; assotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; se.
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/note= "phosphorothioate linkages and all cytidine
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                                  Score 18.4; DB 1;
Pred. No. 6.7e+02;
0; Mismatches 1;
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Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                                                                         chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; antiinflammation; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; acrdiovascular disorder; neurological disorder; se.
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                                                                        Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:142.
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having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mpcBS-1, which specifically hybridise with the nucleic acid mPGBS-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGBS-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGBS-1. MPGBS-1 chimeric antisanse oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, antiinflammatory, neuroprotective, nootropic, antiinflammatory, neuroprotective, notropic, antianflammatory in immunomodulatory and cardiovascular activities, and can ophthalmological, immunomodulatory and extitovation activities, and can be used for preparing a composition for treating a disease or condition associated with mPGBS-1 e.g., inflammatory, and cardiovascular activities, and can be used for preparing a composition for treating a disease or condition associated with mPGBS-1 e.g., inflammatory.
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                                                                                                                                                                                                                      disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                                            Score 18.4; DB 1; Length 20; Pred. No. 6.7e+02;
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//*tag= a
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16. .20
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to gaz4.3. The present invention also describes: (1) antisense compounds, or a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and mPGES-1 in cells or tissues; and (3) a method of inhibiting the expression of mPGES-1 in cells or tissues; and antisense compounds have cytostatic, antisense oligonucleotides and antisense compounds have cytostatic, antidifiammatory, neuroprotective, nootropic, antistic; vasotropic, antidifiammatory, neuroprotective, nootropic, antistic; vasotropic, cophthalmological; immunomodulatory and cardiovascular activities, and can compound to be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., infilammation, inime, or condition and antisense compound condition associated with mPGES-1 e.g., infilammation, inime, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; yrOstatic; antidiabetic; imcrosomal prostaglandin E2 synthase inhibitor; yrOstatic; antidiabetic; imcunomodulator; cardiant; neuroprotective; antidiammatory; ineuroprotective; notropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
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                                                                                       New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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55.0%; Pred. No. 6.7e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                     Claim 4; SEQ ID NO 600; 132pp; English.
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Matches 19, Conservative
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antidiabetic, immunomodulator, cardiant, neuroprotective, antidiabetic, immunomodulator, cardiant, neuroprotective, ophthalmological, immunomodulatory and cardiavascular activities, and can cophthalmological, immunomodulatory and cardiavascular activities, and can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's
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/note= "2'-O-methoxyethyls"
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can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
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/mod_base= OTHER
/note= "2'-0-methoxyethyls"
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16. 20
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                                                                                                                                   chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; notinglammatory;
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
                                                                                                                                                                                               immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
                                                                                                             Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:138.
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/mod_base= OTHER
/note= "2'-0-methoxyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                               note= "2'-0-methocyethyls"
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                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  base= OTHER
                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-2003; 2003WO-US030374
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                                      ADM13951 standard; DNA; 20
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/mod_base=
                                                                                     01-JUL-2004 (first entry)
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                                                               ADM13951;
              RESULT 509
ADM13951/c
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be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                                     Gaps
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:317.
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                                                                                                                                                                                                                                    0.5%; Score 18.4; DB 1; Length 20;
ilarity 95.0%; Pred. No. 6.7e+02;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                               Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
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note= "2'-O-methocyethyls"
6. .20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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les 19; Conserv
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGE-1). The human mRGES-1 gene is located on chromosome 9, more specifically to oga4.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding mPGES-1 in cells or tissues, and clinhibiting the expression of mPGES-1 in cells or tissues, and method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antidiabetic immunomodulator, cardiant, neuroprotective, antidiabetic immunomodulator, cardiant, neuroprotective, antidiabetic immunomodulatory and cardiavascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder:
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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/note= "2'-0-methocyethyls"
16. .20
                                      Claim 4; SEQ ID NO 317; 132pp; English.
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to compound also describes: (1) antisense compounds, daving a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of inhibits a disease or condition associated with mPGES-1. MPGES-1 and antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, cantinflammatory, neuroprotective, nootropic, antianflammatory, neuroprotective, nootropic, antianflammatory, neuroprotective, and cardiovascular activities, and can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's condition associated with mPGES-1 e.g., inflammation, Alzheimer's
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Pred. No. 6.7e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 353; 132pp; English.
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                                                                   25-SEP-2003; 2003WO-US030374.
                                                                                                                                           25-SEP-2002; 2002US-0413549P.
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Best Local Similarity 95.07
Watches 19; Conservative
                                                                                                                                                                                                               (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-305094/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding mPGES-1,
   08-APR-2004.
                                                                                                                                                                                                                                                                                          Gierse JK;
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1; Indels

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Gaps

Location/Qualifiers

Key

Homo sapiens. Synthetic.

/note= "2'-0-methoxyethyls"

WO2004028458-A2

/*tag= c /mod_base= OTHER

modified base

chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mFGES-1; mFGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; antiarthritic; vasotropic; ophthalmological;

Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:484.

immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetees; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.

note = "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"

Location/Qualifiers

'mod_base= OTHER

...20 *tag=

modified base

Homo sapiens

Synthetic

modified base

/*tag= a /*tag= /mod_base= OTHER /note= "2'-O-methocyethyls" | 16..20 /*tag= c /mod_base= OTHER /note= "2'-O-methoxyethyls"

modified base

25-SEP-2003; 2003WO-US030374. 25-SEP-2002; 2002US-0413549P.

WO2004028458-A2

08-APR-2004

(PHAA) PHARMACIA CORP

WPI; 2004-305094/28.

Gierse JK;

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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to pag44.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisaberic, immunomodulator, cardiant, neuroprotective, antinflammatory, neuroprotective, nootropic, antiathatic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound of can be used for preparing a composition for treating a disease or condition associated with mPGES-1. Althaner's condition associated with mPGES-1 e.g., inflammation, Althaner's condition associated with mPGES-1 e.g., inflammation, Althaner's condition associated with mPGES-1 e.g., inflammation, Althaner's condition associated with mPGES-1 e.g., inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ischaemia or reperfusion injury, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ophthalmic, immunological, cardiovascular or neurological disorder.
                                                    /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense compound, having a sequence targeted to a nucleic ac
encoding mPGES-1, useful for preparing a composition for treating
inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                         /mod_base= OTHER
/note= "2'-O-methocyethyls"
16. .20
                                                                                                                                                                                                                            /mod_base= OTHER
/note= "2'-0-methoxyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 176; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes, cancer,
                                        /mod base= OTHER
                                                                                                                                                                                                       /*tag= c
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2003; 2003WO-US030374.
                                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-2002; 2002US-0413549P
                                                                                                                        /*tag= a
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Best Local Similarity 95.0
Matches 19; Conservative
                     *tag=
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                                                                                                                                                                                                                                                                                     WO2004028458-A2
modified base
                                                                                                   modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gierse JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ischemia.
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 by targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and mPGES-1 in cells or tissues; and (3) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antidisense oligonucleotides and antisense compounds have cytostatic, antidiflammatory, neuroprotective, neuroprotective, antidialmanatory, neuroprotective, notropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g. inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
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Gaps

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Score 18.4; DB 1; Length 20; Pred. No. 6.7e+02; 0; Mismatches 1; Indels

0.5%;

2319 GTGTGTGTGTGTGCGTGT 2338

CTGTGTGTGTGTGTGTGT 1

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ADM14297 standard; DNA; 20

(first entry)

01-JUL-2004

ADM14297;

RESULT 513
ADM14297/C
ID ADM1428
XX
AC ADM1428
XX

0.5%; Score 18.4; DB 1; Length 20;

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                                                                                                                                                                                                                                                                            chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "phosphorothioate linkages and all cytidine
                                                                                                                                                                                                                                                  Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:533.
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                 1; Indels
95.0%; Pred. No. 6.7e+02; ive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residues are 5-methylcytidines
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16. .20
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                                              2318 TGTGTGTGTGTGTGCGTG 2337
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                                                                                                                                                          ADM14346 standard; DNA; 20
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/mod_base=
                                                                                                                                                                                                                    (first entry)
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Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                                                        RESULT 51
ADM14346/
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inhibits its expression; (2) a method of inhibiting the expression of mPGBS-1 in cells or tissues; and (3) a method of treating an animal maying a disease or condition associated with mPGES-1. Underso, antisense oligonuclectides and antisense compounds have cytostatic, antishflammatory, neuroprotective, neotropic, antishflammatory, neuroprotective, nootropic, antiarthitic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microsomal prostaglandin E2 synthase; mpGES-1; mpGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostataic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; halbaleiner; disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; se.
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chimeric; antisense oligonucleotide; phosphorothioate; human;
                                                                                                                                                                                                                                                              Score 18.4; DB.1; Length 20;
Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                              Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
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/mod_base= OTHER
/note= "2'-O-methoxyethyls"
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/note= "2'-O-methocyethyls"
                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                   20 GTGTGTGTGTGTGTGTGT 1
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Best Local Similarity 95.0%;
Matches 19; Conservative
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/*tag= a
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modified base
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Synthetic.
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Claim 4; SEQ ID NO 319; 132pp; English
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                       WPI; 2004-305094/28
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modified_base
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                                                                                                                                                                      schemia.
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modified_base

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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mpCES-1). The human mpCES-1 gene is located on chromosome 9, more specifically to G1944.3. The present invention also describes: (1) antisense compounds, daying a sequence comprising 8-30 bp targeted to a nucleic acid encoding mpCES-1, which specifically hybridise with the nucleic acid mPCES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPCES-1 in cells or tissues; and (3) a method of treating an animal continuation and disease or condition associated with mPGES-1. MPGES-1 chimeric antidiabetic, immunomodulator, cardiant, neuroprotective, corruptic, antidiabetic, immunomodulatory and cardiavathritic, vasotropic, ophthalmological, immunomodulatory and cardiavaccular activities, and can be used for preparing a composition for treating a disease or condition associated with mPCES-1 inhibitors and in gene therapy. The antisense compound condition associated with mPCES-1 is inhibitors and in gene therapy. The antisense compound disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 18.4; DB 1; Length 20; 5.0%; Pred. No. 6.7e+02;
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                                                                                /note= "2'-0-methoxyethyls"
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/mod base= OTHER
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16. .20
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modified_base
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                                                                                                                                                                                                                                                                              The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to 9434.3. The present invention also describes: (1) antisense compounds, 9434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal comparison a disease or condition associated with mPGES-1. MPGES-1 chimeric antidabetic, immunomodulator, cardiant, neuroprotective, cardiant, neuroprotective, antidiabetic, immunomodulatory and cardiovascular activities, and can compute as mPGES-1 inhibitors and in gene therapy. The antisense compound be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Altheimer's condition associated with mPGES-1 e.g., inflammation, Altheimer's condition associated with mPGES-1 e.g., inflammation, injury, or optimalial, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; notropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer; disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
                                                                                   New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g. inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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Pred. No. 6.7e+02;
0; Mismatches 1; Indels
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/mod_base= OTHER
/note= "2'-0-methocyethyls"
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Gaps

chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGBS-1; mPGBS-1 inhibitor; microsomal prostaglandin E2 synthase; hPGBS-1; mPGBS-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antitinflammatory; neuroprotective; antidinflammatory; neuroprotective; asthritic; year therapy; inflammation; almunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder;

Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:321.

01-JUL-2004 (first entry)

ADM14134;

ADM14134 standard; DNA; 20 BP.

vivlemore401-10.rng

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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to add 343. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1, which specifically hybridise with he mucleic acid mPGES-1 and inhibits a disease or condition associated with mPGES-1. MPGES-1 chimeric antidiabetic immunomodulator, cardiant, neuroprotective, antidiabetic immunomodulator, and artiforms and infinity inmunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's
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reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
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/mod_base= OTHER
/note= "2'-O-methoxyethyls"
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'note= "2'-0-methocyethyls"
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                                                                                                           Location/Qualifiers
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                                                        Homo sapiens
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                                                                          Synthetic
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schemia. ö Gaps .. 0 0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; tive 0; Mismatches 1; Indels GTGTGTGTGTGTGCGTGT 2338

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RESULT 518

19; Conservative

Matches

2319 20

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Query Match Best Local Similarity

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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The tuman mEGES-1 gene is located on chromosome 9, more specifically to offers of a more present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal more antisense or condition associated with mPGES-1. MPGES-1 chimeric antishabetic, immunomodulator, cardiant, neuroprotective, antishamatory, neuroprotective, nootropic, antishamatory, neuroprotective, nootropic, antishamatory, neuroprotective, nootropic, antishamatory, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
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                                                                                                                                                                                                 /mod_base= OTHER
/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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/mod_base= OTHER
/note= "2'-O-methocyethyls"
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/note= "2'-O-methoxyethyls"
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                                                                                               Location/Qualifiers
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                                      Synthetic.
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Matches
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            or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, ophthalmic, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                 Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:483.
                                                          0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; ive 0; Mismatches 1; Indels
                                       Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
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16. .20
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/note= "2'-0-methoxyethyls"
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                                                                                                   2319 GTGTGTGTGTGTGCGTGT 2338
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                                                                                                               20 GTGTGTGTGTGTGTGTGT 1
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to ogd 4.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal continuation adisease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antisense oligonucleotides and antisense compounds have cytostatic, antistlammatory, neuroprotective, nootropic, antisthritic, vasotropic, antislammatory, neuroprotective, nootropic, antisthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound con be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or copithalmic, immunological, cardiovascular or neurological disorder.
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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16. .20
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/mod_base= OTHER
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vivlemore401-10.rng

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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to 9934.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mpGES-1, which specifically hybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mpGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mpGES-1. MpGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antialnamatory, neuroprotective, nootropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mpGES-1 e.g., inflammation, Alzheimer's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g. inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                 /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
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/mod_base= OTHER
/note= "2'-O-methoxyethyls"
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16. .20
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                                                                                                                                                                                               New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or ischemia.
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Pred. No. 6.7e+02;
0; Mismatches 1; Indels
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25-SEP-2003; 2003WO-US030374
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25-SEP-2003; 2003WO-US030374.
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                          Homo sapiens.
Synthetic.
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                                                                                                     Gierse JK;
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                      2318 TGTGTGTGTGTGTGCGTG
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chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; inmicrosomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antidiffiammatory; neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder;
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chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mFGES-1; mFGES-1 inhibitor; microsomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; immunomodulatory; cardiant; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiavascular; gene therapy; inflammation; Alzheimer; disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
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Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:482.
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/mod_base= OTHER
/note= "2'-O-methoxyethyls"
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/note= "2'-0-methocyethyls"
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01-JUL-2004
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having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetee, cancer, ischaemia or repertusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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                                                                                                                                             0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; ive 0; Mismatches 1; Indels
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/mod_base= OTHER
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                                                                                                                                              Query Match
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mpcES-1). The human mpcES-1 gene is located on chromosome 9, more specifically to gene is located on chromosome 9, more specifically to mere specifically to mere specifically to mere specifically hybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mpcES-1, which specifically hybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of mpcES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mpcES-1. MpcES-1 chimeric antisense oligonuclectides and antisense compounds have cytostatic, antisflabetic, immunomodulator, cardiant, neuroprotective, antisflabetic, immunomodulatory and cardiovascular activities, and can be used as mpcES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mpcES-1 e.g., inflammation, Alzheimer's
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New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.giflammation, Alzheimer's disease, arthritis, diabetes, cancer or
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (MPGES-1). The targeted to human microsomal prostaglandin E2 synthase (MPGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to operate invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mpGES-1, which specifically hybridise with the nucleic acid mpGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mpGES-1 in cells or tissues; and (3) a method of treating an animal cartisense oligonucleotides and antisense compounds have cytostatic, antisense oligonucleotides and antisense compounds have cytostatic, antisense oligonucleotides and antisense compounds have cytostatic, antisinflammatory, neuroprotective, nootropic, antistriritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound condition associated with mpGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or opththalmic, immunological, cardiovascular or neurological disorder.
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               /note= "2'-0-methoxyethyls"
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The present invention also describes: (1) antisense compounds, og 434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and mPGES-1, in cells or tissues; and (3) a method of inhibiting the expression of inhibite its expression; (2) a method of inhibiting the expression of maying a disease or condition associated with mPGES-1. MPGES-1 chimeric antisense oligonucleotides and antisense compounds have cytostatic, antidialmantory, neuroprotective, nouroprotective, contininflammatory, neuroprotective, nouropic, antiantlammatory, neuroprotective, nouropic, antiantlammatory, neuroprotective, nouropic, antiantlammatory, neuroprotective, nouropic, antiantlammatory, neuroprotective, notropic, antiantlammatory, neuroprotective, conditions associated with mPGES-1 e.g., inflammation, Alzheimer's condition associated with a cancer, isonaemia or reperfusion injury, or condition associated with antiantland and a cancer, isonaemia or reperfusion injury, or content in the condition associated with antiantland and an
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/note= "2'-O-methoxyethyls"
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Controlled by transcription factors. The method is simpler, quicker and particularly less expensive than known methods based on sequencing. This protein (PrP) comprising a polymorphic microsatellite locus.
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                                                                                                                                                                                                                                                                                                                                                                              Typing genes that contain polymorphic microsatellite loci, useful for identifying predisposition to disease, by amplification and determining length of amplicons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                 disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; cow; microsatellite; PCR; primer; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 6.7e+02; ive 0; Mismatches 1; Indels
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                                                                                        gene typing; polymorphic microsatellite loci; PML;
                                                               Cow prion protein microsatellite locus primer #64.
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                                     29-JUL-2004 (first entry)
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The invention describes a method of typing (M1) a gene (1) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one bNA region of (1) that includes PML, using as template a DNA sample containing at least one segment of (1); and determining the length of the resulting amplicon(s). Also described are: c determining the length of the resulting amplicon(s). Also described are: c method of determining (M2) microsatellite markers (MM) for predisposition to a disease, associated with a gene that includes one or more PML, and prediagnosis (M3) of diseases associated with a gene that include PML. The method is used to identify microsatellite markers, in a disease related gene, that are associated with a prediapsosition to diseases and for prediagnosis of such diseases, especially prion diseases of use associated with a prediapsosition to diseases and for prediagnosis, malignan hyperthermia syndrome in pigs and metabolic diseases; also to type genes that encode milk proteins.

C metabolic diseases; also to type genes that encode milk proteins.

C metabolic diseases; also to type genes that encode milk proteins.

C protein (PrP) comprising a polymorphic microsatellite locus.
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gene typing; polymorphic microsatellite loci; PML; disease; tedsipposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; sheep;
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                                                                                                                                                                                                                                                                                                                                                             The invention describes a new compound, having a sequence comprising 8-80 bp targeted to a nucleic acid encoding CDK9, specifically hybridises with the nucleic acid encoding CDK9 comprising 7018-bp sequence and inhibits expression of CDK9. Also described are: inhibiting the expression of CDK9 in cells or tissues; screening for a modulator of CDK9; a diagnostic the compound; and treating an animal having a disease or condition associated with CDK9. The oligonucleotide compound is useful for preparing a composition for treating hyperproliferative disorder, e.g. cancer. This sequence represents a human cyclin-dependent kinase 9 (CDK9) antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                       useful for
                                          mod base= OTHER
note= "OTHER= Phosphorothioate backbone. All cytidines
are 5-methylcytidines"
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15. .20
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                                                                                                                                                                                                                                                                                                      New oligonucleotide compound that inhibits expression of CDK9, useful preparing a composition for treating hyperproliferative disorder, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; human; non-muscle myosin-family heavy chain protein; MYH14; chromosome 19q13.3; Charcot-Marie-Tooth syndrome; brain; peripheral nerve; ovary; intestine; primer; PCR.
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              Location/Qualifiers
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This invention describes a novel non-muscle, human myosin-family heavy chain protein, designated MYH14 which maps to chromosome 19q13.3, a region associated with Charcot-Marie-Tooth syndrome. MYH14 is associated with Drain, peripheral nerves, ovary and intestines and has closest homology with the myosin family proteins MYH0, MYH10 and MHC11. The product of the invention is used to identify mutations and alteration in nucleic acids, by Mybridisation. Computer-based comparison of the human nucle myosin heavy chain B) indicated a potential human homologue. A set muscle myosin heavy chain B) indicated a potential human homologue. A set sometic primers was designed and used to amplify cDNA derived from mRNA isolated from the sciatic nerve. The 13 amplicons were sequenced and assembled to form an approximately skb sequence that included an open reading frame for MYH14, but lacked the polyadenylation signal. The corresponding gene contains 40 exons (about 100 kb), entirely present within the bacterial artificial chromosomes Acolosobé, Acolosis and Aconosomes The MYH14 protein corresponds to the hypothetical protein FLJ MYH14 protein corresponds to the hypothetical protein FLJ MYH14 protein corresponds to the hypothetical protein FLJ MYH14 protein corresponds to the hypothetical protein human approximately a PCR primer used to amplify the human approximately approximately approximately approximately approximately and approximately approximately approximately approximately approximately artificial chromosomes Aconosomes Aco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid encoding the human myosin heavy chain protein MYH14, useful for identifying mutations or alterations in nucleic acid,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        derived from chromosome 19q 13.3.
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                                                                                                                                                                                                                                                                      16-DEC-2002; 2002DE-01060633.
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                            (RAUT/) RAUTENSTRAUSS B.
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Best Local Similarity
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modified base
DE10260633-A1.
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                                                                                          24 - JUN - 2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN88973;
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The present invention describes a phosphoramidite compound (I) comprising two or more nucleoside moieties linked by one or more internucleoside phosphorus atoms, where the internucleoside phosphorus atoms are phosphorus (III) atoms. Also described: (I) preparing a trivalent phosphorus multimer or its stereoisomer (I); (2) a trivalent phosphorus multimer derivatised solid support (II); and (3) preparing (II). (I) or seed for the synthesis of oligonucleotides. The present sequence represents a phosphorothioate 21mer oligonucleotide which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; ss; short interfering RNA; siRNA; angiogenesis; vascular endothelial growth factor; VEGF, VEGF receptor; Flt-1; Flk-1/KDR; kinase domain region; diabetic retinopathy; age-related macular degeneration; inflammatory disease; psoriasis; rheumatoid arthritis; cancer; breast; retinoblastoma; Wilm's tumour; lymphoma; cytostatic; antidiabetic; ophthalmological; antiinflammatory; antipsoriatic; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel short interfering RNA (siRNA) comprises sense and antisense RNA strands, useful for inhibiting expression of human vascular endothelial growth factor mRNA, for treating angiogenic disease, e.g. diabetic
                                                              Novel phosphoramidite compound, useful for the synthesis of oligonucleotides, comprising nucleoside moieties linked by one or more internucleoside phosphorus atoms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Flt-1 DNA sequence, a target for siRNA inhibition SeqID 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 0.5%; Score 18.4; DB 1; Length 21; Local Similarity 95.0%; Pred. No. 7.1e+02; nes 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                             synthesised in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 10 A; 10 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2319 GTGTGTGTGTGTGTGTGT 2338
                                                                                                                                                      Example 4; Page 28; 67pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-2002; 2002US-0398417P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-NOV-2002; 2002US-00294228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ97603 standard; DNA; 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tolentino MJ, Reich SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retinopathy and cancer
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                    WPI; 2002-479457/51
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a phosphoramidite compound (I) comprising two or more nucleoside moieties linked by one or more internucleoside phosphorus atoms are the internucleoside phosphorus atoms are phosphorus (III) atoms. Also described: (I) preparing a trivalent phosphorus multimer or its stereoisomer (I); (2) a trivalent phosphorus multimer derivatised solid support (II); and (3) preparing (II). (I) or (II) can be used for the synthesis of oligonucleotides. The present sequence represents a phosphorothioate 21mer oligonucleotide which is synthesised in an example from the present invention
                                                                                                                                                                                                                                                                                                        Novel phosphoramidite compound, useful for the synthesis of oligonucleotides, comprising nucleoside moieties linked by one or more internucleoside phosphorus atoms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 18.4; DB 1; Length 21; 95.0%; Pred. No. 7.1e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
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/note= "phosphorothioate linkages"
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                                                                                                                                                    (AVEC-) AVECIA BIOTECHNOLOGY INC. (AVEC-) AVECIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AVEC-) AVECIA BIOTECHNOLOGY INC. (AVEC-) AVECIA LID.
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                                                              06-SEP-2001; 2001WO-GB003973
                                                                                                            07-SEP-2000; 2000US-0230685P
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                WPI; 2002-479457/51.
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modified_base
                       14-MAR-2002
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RESULT 532

ò 셤 cc interfering RNA (siRNA) molecules, which can be used to inhibit corpuses. Specifically, it refers to siRNAs that target and cause RNA1-induced degradation of mRNA from human vascular endochelial growth factor (VEGF), the VEGF receptor (FIt-1) and the FIk-1/KDR (kinase domain corpus) genes, as well as mutants derived thereof. The present invention constructs sense and antisense RNA strands that form an RNA duplex and describes sense and antisense RNA strands that form an RNA duplex and compared to the target mRNA, such that expression is inhibited and the target constructs as such, siRNA administered in combination with a therapeutic agent is useful for treating diseases associated with angiogenesis and the overexpression of VEGF, which include diabetic rethiopathy, agence related macular degeneration, inflammatory disease, psoriasis and concers including breast, retinoblastoma, Wilm's tumour and lymphoma. CC rheumatoid arthritis. Furthermore, it can be used to treat various concers including breast, retinoblastoma, Wilm's tumour and lymphoma. CC phthalmological, antiinflammatory, antipsoriatic, antiinflammatory, antipsoriatic, antiinflammatory, antipsoriatic, antiinflammatory, antipsoriatic, antiinflammatory, coligo, a target for siRNA inhibition of the invention. 8 \pm 8

Sequence 21 BP; 4 A; 8 C; 6 G; 3 T; 0 U; 0 Other;

Gaps ; 0.5%; Score 18.4; DB 1; Length 21; 95.0%; Pred. No. 7.1e+02; tive 0; Mismatches 1; Indel8 Query Match Best Local Similarity 95.0¹ Matches 19; Conservative

1393 AACCTGCTGGGCGCCTGCAC 1412

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ADJ98000 standard; DNA; 21 BP. RESULT 534 ADJ98000

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ADJ98000;

06-MAY-2004 (first entry)

Human Flk-1/KDR DNA sequence, a target for siRNA inhibition SeqID 773.

human; 88; short interfering RNA; siRNA; angiogenesis; vascular endothelial growth factor; VEGF, VEGF receptor; Flt-1; Flk-1/KDR; kinase domain region; diabetic retinopathy; age-related meaular degeneration; inflammatory disease; psoriasis; rheumatoid arthritis; cancer; breast; retinoblastoma; Wilm's tumour; lymphoma; cytostatic; antidiabetic; ophthalmological; antiinflammatory; antipsoriatic; antirheumatic; antiathritic.

Homo sapiens.

WO2004009769-A2

29-JAN-2004.

18-JUL-2003; 2003WO-US022444

2002US-0398417P. 2002US-00294228. 24-JUL-2002; 14-NOV-2002;

(UYPE-) UNIV PENNSYLVANIA.

SJ; Folentino MJ, Reich WPI; 2004-203472/19.

Novel short interfering RNA (siRNA) comprises sense and antisense RNA strands, useful for inhibiting expression of human vascular endothelial growth factor mRNA, for treating angiogenic disease, e.g. diabetic retinopathy and cancer.

Disclosure, SEQ ID NO 773; 218pp; English.

This invention relates to novel compositions that comprise short interfering RNA (siRNA) molecules, which can be used to inhibit

angiogenesis. Specifically, it refers to siRNAs that target and cause RNAi-induced degradation of mRNA from human vascular endothelial growth factor (VEGF), the VEGF receptor (Filt-1) and the Fik-I/KDR (kinsee domain region) genes, as well as mutants derived thereof. The present invention describes sense and antisense RNA strands that form an RNA duplex and bind to the target mRNA, such that expression is inhibited and the target bind to the target mRNA, such that expression is inhibited and the target capraded. As such, siRNA administered in combination with a therapeutic agent is useful for treating diseases associated with anglogenesis and the overexpression of VEGF, which include diabetic retinopathy, agenelated macular degeneration, inflammatory disease, psoriasis and renumatoid arthritis. Furthermore, it can be used to treat various cancers including breast, retinoblastoma, Wilm's tumour and lymphoma. Accordingly, these compositions exhibit cytostatic, antidiabetic, ophthalmological, antiinflammatory, antippsoriatic, antidiabetic and antiarthritic activities. This oligonucleotide is a human Flk-1/KDR DNA oligo, a target for siRNA inhibition of the invention. \$

Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Gaps ö cch 0.5%; Score 18.4; DB 1; Length 21; al Similarity 95.0%; Pred. No. 7.1e+02; 19; Conservative 0; Mismatches 1; Indels Query Match Best Local Similarity Matches 19; Conserv

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RESULT 535 ADD69446/

ADD69446 standard; DNA; 24 BP

ADD69446;

(first entry) 15-JAN-2004

(ISSR)-PCR primer - SEQ ID 4. 5' anchored

inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant; animal; Basmati rice; ss.

Synthetic.

WO2003085133-A2.

16-OCT-2003.

09-JAN-2003; 2003WO-IB000041.

(DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.

08-APR-2002; 2002IN-CH000260.

Nagaraju JG;

WPI; 2003-804317/75.

New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and animal systems

Claim 1; SEQ ID NO 4; 60pp; English.

The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the 5' anchored (ISSR)-PCR primer of the invention.

Sequence 24 BP; 8 A; 10 C; 3 G; 3 T; 0 U; 0 Other;

(first entry)

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Human IL-3 receptor antisense oligonucleotide fragment
 05-JUL-1999
                                                                                                                                                                      Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the human IL3 receptor. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                               Asthma; airway epithelium; adenosine free; cystic fibrosis; chronic obstructive pulmonary disease; bronchitis; interleukin; ss.
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0.5%; Score 18.4; DB 1; Length 24; llarity 95.0%; Pred. No. 8.2e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 0.5%; Score 18.2; DB 1; Length 23; I Similarity 87.0%; Pred. No. 8.3e+02; 20; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23 BP; 0 A; 11 C; 10 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                            Human IL3 receptor antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1477 CGGCGCGCGCCCCCCGGCCT 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cercceceeeeccccceeeccr 23
                                             2335 GTGTGTGTGTGTGCAC 2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 29; 71pp; English.
                                                                  24 Grererererererekes 5
                                                                                                                           ВÞ.
                                                                                                                                                                                                                                                                                                                                           95US-00474497.
                                                                                                                                                                                                                                                                                                                     96WO-US009306.
                                                                                                                                                                                                                                                                                                                                                               (UYEC-) UNIV EAST CAROLINA.
                                                                                                                         AAT76174 standard; DNA; 23
                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Nyce JW, Metzger WJ;
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-051871/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
            Best Local Similarity
Matches 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reactive airways
                                                                                                                                                                                                                                                                          WO9640162-A1.
                                                                                                                                                                                                                                                                                                                     06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                     12-SEP-1997
                                                                                                                                                                                                                                                                                               19-DEC-1996
                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                AAT76174;
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         subject.
                                                                                                   RESULT 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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AAX53971 standard; DNA; 23 BP.

RESULT 537

AAX53971

AAX53971;

SXXX

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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
con-coding regions of RNAs corresponding to target genes, gene initiation
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
coding regions of RNAs encoding intron-exon borders, the 5'-end, the 3'
conditions or mixtures. The antisense oligonucleotides may be derived
from sequences AAX5512-74. These multiple target oligonucleotides
conditions or mixtures multiple target oligonucleotides
from sequences AAX55180-271) can be used for the antisense treatment of
diseases and conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
acute asthma, allergies, asthma, impeded respiration, respiratory
disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
colon cancer, breast cancer, lung cancer, pancreatic cancer,
colon cancer, breast cancer, lung cancer, pancreatic cancer,
colon cancer, breast cancer, lung cancer, pancreatic cancer,
colon cancer, breast cancer, lung cancer, metastases,
colon cancer, breast cancer, lung cancer, pancreatic metastases,
as all types of cancers which may metastasize or have metastasized
colon cancer, breast cancer which may metastasize or have metastasized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 87.0%; Pred. No. 8.3e
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1477 CGGCGCGCGCCCCCCGGGCCT 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 48; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0059160P.
98US-00093972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYEC-) UNIV EAST CAROLINA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-229400/19.
                                                                                                                                                                                                                                                                                                                                                                                                prostate cancer; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9913886-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5-MAR-1999
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AAF19538
ID AAF1953
XX
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(first entry)

AAF19538;

and/or

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; businfacture depletion; respiratory; bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain, cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; Human IL3 receptor polynucleotide fragment #1105. WO200062736-A2 Homo sapiens 14-MAR-2001 cancer; 88. 26-OCT-2000 Nyce JW;

The present invention describes low adenosine (A) content antisense oligonuclectides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonuclectides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activity of target polypeptides associated with lung/respiratory disorders and transmitters, transcription factors, immunoglobulins and antibodies antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and nervous system (CNS) and peripheral nervous and non-nervous system peripheral nervous and non-nervous system peripheral nervous and non-nervous system creceptors, defensins, growth factors, vascociated proteins. The antisense oligonuclectides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactors binding respiratory obstruction and/or bronchoconstriction and/or lung inflammation, allergy(ies) and/or surfactors binding are sessible and alsease or surfactors become and suspense or surfactors binding respirators associated with a disease or surfactors binding respirators and surfactors associated with a disease or surfactors binding are associated with a disease or surfactors binding respirators associated with a disease or surfactors binding respirators associated with a disease or surfactors binding respirators binding are associated with a disease or surfactors binding respirators associated with a disease or surfactors binding respirators associated with a disease or surfactors binding respirators associated win this way to treat disorders and surfactors between the surfacto Low adenosine (A) content antisense oligonucleotides which do not trigge adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions. fragments and antisense oligonucleotides used in the exemplification of infections, bronchitis, condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary emphysema, chronic obstructive pulmonary disease (COPD) ary transplantation rejection, pulmonary infections, bronchil cancer. AAF18434 to AAF21543 represent human polynucleotide Claim 14; Page 207; 1592pp; English. 99US-0127958P. 24-MAR-2000; 2000WO-US008020 EAST CAROLINA the present invention WPI; 2000-679539/66. (UYEC-) UNIV EAST (NYCE/) NYCE J W. pulmonary transpl hypertension, 06-APR-1999;

Sequence 23 BP; 0 A; 11 C; 10 G; 2 T; 0 U; 0 Other;

DB 1; Length 23; 0.5%; Score 18.2;

Query Match

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              Gaps
              ;
              Indels
87.0%; Pred. No. 8.3e+02;
tive 0; Mismatches 3;
                                       1477 CGGGCGCGCCCCCCGGGCCT 1499
                                                                   1 CGTCCGCGGGGCCCCCGGGCCT 23
            20; Conservative
 Best Local Similarity
              Matches
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Human, antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. Human IL3 receptor antisense fragment no.1095. BP. ABZ95232 standard; DNA; 23 (first entry) 17-OCT-2003 ABZ95232; RESULT 539 ABZ95232

24-APR-2001; 2001US-0286137P. 23-APR-2002; 2002WO-US013135. WO200285308-A2. Homo sapiens. 31-OCT-2002.

(EPIG-) EPIGENESIS PHARM INC

Katz E, Pabalan J, Aguilar D; Sandrasagra A, K L, Shahabuddin S; Li Y, San Tang L, Miller S, Nyce JW,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 10474; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antisense to the initiation coodon, coding region, 5 or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 muclectides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entitificammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of, or reducing sensitivity to adenosine, reducing levels of edenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 23 BP; 0 A; 11 C; 10 G; 2 T; 0 U; 0 Other;

Query Match

Score 18.2; DB 1; Length 23; 0.5%;

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This invention describes a novel composition, all rist active agent, comprising oligonucleotides, effective for alleviating to the composition, respiratory tract inflammation, allergies and bronchoconstriction, respiratory tract inflammation, allergies and composition of a target polypeptide associated with lung airway or lung dysfunction or cancer polypeptide associated with lung airway or lung dysfunction also describes a kit, that comprises: (a) a delivery of entructions according a carrier and for use of the kit. The composition of the invention has antiallargic, antiinflammatory, antiathmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition of the target manalgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition of the target manalgesic and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory
                      ö
                                                                                                                                                                                                                                                                                                                                                        Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distresses syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention describes a novel composition (a) a first active agent,
                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted trucleic acids associated with lung airway or lung dysfunction, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aguilar D;
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                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pabalan J,
  Pred. No. 8.3e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Katz E,
                                                           1477 CGGCGCGCGCCCCCGGCCT 1499
                                                                                                                                                                                                                                                                                                                   Human IL3 receptor DNA fragment 1095.
                                                                                              23
                                                                                            1 CGTCCGCGGGGCCCCCCGGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li Y, Sandrasagra A,
Tang L, Shahabuddin
                                                                                                                                                                                                    BP.
l Similarity 87.0%;
20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                                                    ABD19194 standard; DNA; 23
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bronchodilating agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-093058/08.
Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                              29-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nyce JW, I
Miller S,
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ABD19194
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distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonuclectides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it.
                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAH43222-23 are primers which were used to amplify the CDNA encoding human kelch protein 19; Human Kelch protein 19 and its corresponding polynucleotide may be used in the diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, kelch protein 19; diagnosis; malignant tumor; hemopathy; PCR; HIV; inflammation; polymerase chain reaction; primer; amplify; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human kelch protein 19 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological diseases and various inflammations.
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                              0.5%; Score 18.2; DB 1; Length 23; 87.0%; Pred. No. 8.3e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                           Sequence 23 BP; 0 A; 11 C; 10 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 24 BP; 9 A; 10 C; 5 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                      1477 CGGGGGGGGGGCCT 1499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human kelch protein 19 primer 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-2000; 2000CN-00111516
                                                                                                                                                                                                                                                                                                                                                                                               AAH43222 standard; cDNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                 Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  various inflammations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483267/52.
                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH43222;
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Matches
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EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;

cross-species comparison.

US2003104410-A1. Homo sapiens.

05-JUN-2003

Human microarray DNA oligonucleotide SEQ ID NO 55473.

(first entry)

13-OCT-2003

vivlemore401-10.rng

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The invention relates to a replicase complex comprising a hepatitis C virus (HCV) NSSB replicase protein, a linear nucleic acid template and a complementary nucleic acid primer which is annealed to the 3' terminus of the template, where the template is at least three nucleotides and the primer is two or three nucleotides, and the template and primer do not form a stable duplex in solution in the absence of the HCV NSSB protein. The complex is useful for detecting HCV replicase activity and permits establishment of sensitive RNA-dependent RNA polymerase assays to screen and evaluate antiviral inhibitors and to improve the specificity and efficacy of the inhibitors. The complex is also useful in the development of a reliable system for determining kinetic and thermodynamic constants of HCV NSSB-catalysed nucleotide incorporation and investigation of mechanistic inhibitors for mis-incorporation or chain termination.

Specifically, the short RNA template and primer pairs are useful in screening assays which are used for determining kinetic, thermodynamic and mechanistic properties of NSSB replication and ultimately in the replicase activity may be used for developing anti-HCV pharmaccuticals.

Sequences ABK99271-ABK99296 represent HCV NSSB replicase RNA synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel replicase complex comprising hepatitis C virus NSSB replicase, a 3 nucleotide-long template to which a 2 nucleotide-long primer is annealed, and template and primer which do not form a stable duplex in the absence of HCV NSSB.
                                                                                                                                                                          Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 25;
                                                                                                                                                                                                                               Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 0 A; 20 C; 5 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18.2; DB 1;
Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 6; 17pp; English.
                            ABK99282 standard; RNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ferrari E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2001; 2001US-00828034,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-APR-2000; 2000US-0195852P
                                                                                                                              21-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-582330/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HONG/) HONG Z.
(FERR/) FERRARI E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hong Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZHON/) ZHONG W.
                                                                                                                                                                                                                                                                                                                                   US2002064771-A1
                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2002
                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhong W,
                                                                              ABK99282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
ABK99282/C
11D ABK992.X
AC ABK992.X
XX ABK992.X
XX ABK992.X
XX Hepati
XX Hepati
XX Synthe
XX Synthe
XX JO-MAY
XX D1-APR
XX D1-
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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

16-MAR-2001; 2001US-0276759P. 15-MAR-2002; 2002US-00098263.

(AFFY-) AFFYMETRIX INC

WPI; 2003-567953/53.

Mittmann MP;

Claim 1; SEQ ID NO 55473; 9pp; English

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison.

Cor family members of a gene and a cross-species comparison.

Cor family members of a gene and a cross-species comparison.

Cor family members of a gene and a cross-species comparison.

Cor family members of a gene and a cross-species comparison.

Cor family members of a gene and a cross-species comparison.

Cor family methors of any gene, in mapping the 5' termini of mRNA molecules by primer extensions of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the solute for this patent can also be obtained in electronic format directly from USPTO at sequence thml
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 5 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1328 ACCTGTCGGACCTGGTGTCTGAG 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ACCTGACGGACCACGTGTCTGAG 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 87.0 les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL99557;
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Gaps

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3; Indels

0; Mismatches

20; Conservative

Matches

2920 GGGCGGGCGTGGGGGCGTGG 2942 24 descedesecedesecedes

ACIS5482 standard; DNA; 25 BP

RESULT 543 ACI55482

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ACI55482

Hodgkin disease; Von Hippel-Lindau syndrome; Alzheimer's disease; stroke; tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; leukodystrophy; anxiety; pain; obesity; Crohn's disease; osteoporosis; inflammatory bowel disease; infertility; inflammatory bowel disease; scleroderma; haemophilia; diabetes; pancreatitis; autoimmune disease; asthma; arthritis; immunodeficiency; HIV; viral infection; neurogenesis; bacterial infection; paramitic infection; graff-versus-host disease; angiogenesis; probe; ss.

Human; NOVX; human disease; NOVX-associated disorder; cancer; addiction;

16-DEC-2002 (first entry) Human NOVX probe Ag3765.

ABS78791;

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The invention describes a multimeric molecular complex comprising at least 2 compounds, each of which has at least one targeting element directed to a ligand that confers transcytofic or paracellular transporting properties to a molecular complex specifically bound to the ligand. Also described are: a compound comprising at least 2 targeting elements directed to the ligand, a protein compusiang a composition polypeptide having a chemical linkage to at least one targeting element directed to the ligand; a pharmaceutical composition comprising the compound; delivering a biologically active agent to an animal; transporting a biologically active agent through an epithelial barrier; treating a disease in an animal; and identifying a disease in an animal. The complex is useful for preparing a composition for for diagnosing or treating diseases, e.g., osteoporosis, renal failure, collits, gastroenteriis, inflammatory bowel disease, psoriasis, Alzheimer's disease, optic neuropathy or ophthalmoplegia. This sequence represents a linker associated with the isolation of heavy chain regions compensate an animal antibody sysAF polypeptide, that targets the polyimmunoglobulin receptor (pigR) mediator of endocytosis and forward and reverse transcytosis in epithelial cells,
                                                             antipsoriatic; antiinflammatory; neuroprotective; ophthalmological; gastrointestinal; ostoopathic; nephrotropic; gene therapy; multimeric molecular complex; transcytotic transport; paracellular transport; calcitonin; osteoporosis; renal failure; colitis; gastroenteritis; inflammatory bowel disease; psoriasis; Alzheimer's disease; optic neuropathy; ophthalmoplegia; single chain antibody; sFv5AF; linker; heavy chain region; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New multimeric molecular complex, useful for preparing a composition for diagnosing or treating e.g. osteoporosis, renal failure, colitis, gastroenteritis, inflammatory bowel disease, psoriasis or Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 18.2; DB 1; Length 25; 13.9%; Pred. No. 9.1e+02; ve 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sheridan PL, Houston LL, Glynn JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25 BP; 0 A; 0 C; 20 G; 0 T; 0 U; 5 Other;
                      Single chain antibody sFv5AF related linker #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 51; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2001; 2001US-00949039
                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-2001; 2001US-00949039
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HAWL/) HAWLEY S B.
(CHAP/) CHAPIN S.
(SHER/) SHERIDAN P L.
(HOUS/) HOUSTON L L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hawley SB, Chapin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-898076/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYNN J M.
                                                                                                                                                                                                                                                                                     US2003166160-A1.
                                                                                                                                                                                                                                                                                                                              04-SEP-2003
                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease.
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2001US-0275601P 2001US-027600P 2001US-0277239P 2001US-0277338P 2001US-0277338P 2001US-0277338P 2001US-0278152P 2001US-0278152P 2001US-0278154P 2001US-0278152P 2001US-0278152P 2001US-0278152P

28-MAR-2001;

2001US-0294821P 2001US-0335302P

02-MAY-2001; 31-MAY-2001; 07-MAR-2002; 2002US-00094466

2001US-0274849P. 2001US-0275235P. 2001US-0275579P.

13-MAR-2001;

13-MAR-2001;

20-MAR-2001; 20-MAR-2001; 21-MAR-2001; 22-MAR-2001;

08-MAR-2002; 2002WO-US007283

08-MAR-2001;

WO200272770-A2. Homo sapiens.

19-SEP-2002

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New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, multiple sclerosis, atherosclerosis, cancer, infections, osteoporosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a new polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful in the manufacture of endicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX nucleic acids, polypeptides and antibodies are useful for treating, preventing or polypeptides and antibodies, the NOVX nucleic acids, solypeptides and antibodies, the nucleic acids, syndrome, Alzheimer's disease, stroke, tuberous aclarosis, by mippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous aclarosis, cerebral hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerlach VL;
a R, Pena CEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Malyankar UM, Gerla
Gusev VY, Kekuda R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tchernev VT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example C; Page 231; 266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patturajan M,
1, Taupier RJ;
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I, Gangolli EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vernet CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-713508/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spytek KA,
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Gaps

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2920 GGGCGGGCGTGGGGGCGTGG 2942

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Best Local Similarity 73.9%; Matches 17; Conservative

ABS78791 standard; DNA; 26 BP

ABS78791/c ID ABS787 XX RESULT 545

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palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia-
telangicctasia, leukodystrophies, addiction, anxiety, depression, pain,
c besity, Crohn's disease, osteoporosis, inflammatory bowel disease,
c netrility, inflammatory bowel disease, atherosclerosis, hypertension,
c cleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease,
c asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic
infections, or graft-versus-host disease. The nucleic acids and
c polypeptides may also be used as targets for the identification of small
molecules that modulate or inhibit e.g. neurogenesis, cell
c molecules that modulate or inhibit e.g. neurogenesis, cell
c molecules that modulate or inhibit e.g. neurogenesis, cell
c molecules that modulate or inhibit e.g. neurogenesis, cell
c molecules in constant or inhibit e.g. neurogenesis, cell
c molecules that modulate or inhibit e.g. neurogenesis, cell
c molecules that modulate or inhibit e.g. neurogenesis, cell
c molecules that modulate or inhibit e.g. neurogenesis, cell
c molecules that modulate or inhibit e.g. neurogenesis, cell
c molecules that modulate or inhibit e.g. neurogenesis, cell
c molecules that modulate or inhibit e.g. neurogenesis, cell
c molecules that modulate or inhibit e.g. neurogenesis, cell
c munnospecifically to NOVX substances for use in therapeutic or
diagnostic methods. The nucleic acids are further used as hybridisation
c probes, in chromosome mapping, tissue typing, preventive medicine, and
plax macogeneomics. The present nucleic acid sequence represents a probe
that was used in the methods of the invention for detection of human NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tunour cells and genomic DNA from normal cells. The method involves the cells from the same individual with oligonuclectide primers selected from (i) a nucleotide sequence (CG)xRG, where R is a purine selected from adenine and guanine and x = 3-7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and Y is a pyrimidiane selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG)xRY, where R is as in (i) and X = 3-7, (iv) a nucleotide sequence (CG)xYY, where X is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRG, where X is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 BP; 8 A; 14 C; 0 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.2; DB 1;
Pred. No. 9.5e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTGTGTGTGTGTGTGTG 2343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity 87.0
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-357197/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USS912147 primer 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5912147-A.
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AAX774685/
LID AAX774685/
XXX AAX774685/
XXX AAX7
XXX DE USS9
XXX Prim
XXX Synt
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The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer suitable for amplifying an SSR, identifying (MI) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the MI, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSRs in the breeding, a
                                                                                                                                                                                                                                                               ö
16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from adenine and guanine and Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR, where R is a purine selected from adenine and guanine and x = 6-16, (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat; cereal profiling; grass profiling; seed batch purity testing.
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                                                                                                                                                                                                                           Score 18; DB 1; Length 18;
Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                       Sequence 18 BP; 9 A; 8 C; 1 G; 0 T; 0 U; 0 Other;
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STATE VICTORIA DEPT NATURAL RES & ENVIRO.
                                                                                                                                                                                                                     0.5%; Sco.
100.0%; Pred. No. o...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simple sequence repeat, SSR, #36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-DEC-1999; 99A0-00004900.
04-MAY-2000; 2000AU-00007310.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS13764 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                    Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-2002
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Gaps

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method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profiling to establish the distinct identity, uniformity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New transgenic mice having a genetically modified fibroblast growth factor receptor gene, useful as a model for human chondrodysplasia, e.g. achondroplasia characterized by shortening of the limbs, midface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an animal model for chondrodysplasia, more particularly, to a transgenic mouse model for achondroplasia. This transgenic mouse contains a fibroblast growth factor receptor 3 (FGFR3) gene including a G to A point mutation changing Gly to Arg in codon 380 in its genome. The transgenic mouse is useful as a model for FGFR associated chondrodysplasia, particularly FGFR3 achondroplasia, e.g. shortening of the limbs, midface hypoplasia and large skull. This model may be exploited to gain better understanding of the disease and as an experimental model with which experimental therapy to chondrodysplasias can be exercised. The transgenic mouse is particularly useful as a tool for screening, developing and evaluating drugs with a potential of relieving or abolishing chondrodysplasia syndromes and/or symptoms. The present sequence is a PCR primer used to detect human FGFR3 allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chondrodysplasia; achondroplasia; transgenic mouse; therapy; fibroblast growth factor receptor 3; FGFR3; limb; midface hypoplasia; large skull; drug screening; drug development; transgenic; PCR; primer;
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                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 6.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human FGFR3 allele detecting antisense PCR primer.
                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 0 A; 1 C; 8 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTCTGTGTGTGTGTGT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2315 GTCTGTGTGTGTGTGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD34804 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUL-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-AUG-1999;
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AAD34804/A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining presence of a tumor cell or angiogenesis, and the effectiveness of treatment, by detecting the presence of marker genes is useful to detect and monitor treatment of Karposi's Sarcoma.
                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                 Human; Kaposi's sarcoma; tumour; angiogenesis; PCR primer; ss.
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                                Score 18; DB 1; Length 18;
Pred. No. 6.6e+02;
                                                                0; Indels
Seguence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                             Kaposi's Sarcoma TAG PCR primer SEQ ID NO:142.
                     0.5%; sco...
100.0%; Pred. No. co...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 10; Page 24; 38pp; English.
                                                                                                    1048 CTGGAGTCCAACGCGTCC 1065
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                                                                                                                        18 CTGGAGTCCAACGCGTCC 1
                                                                                                                                                                                                                           ABQ81992 standard; DNA; 18 BP
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28-SEP-2001; 2001EP-00203703.
28-SEP-2001; 2001US-0325722P.
                                                                                                                                                                                                                                                                                              19-NOV-2002 (first entry)
                            Query Match
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1225233-A2
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                                                                                                                                                                                         RESULT 549
                                                                                                                                                                                                           ABQ81992,
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degenerative nervous system disease, graft versus host disease, hypersensitivity disease; infectious disease; neoplastic disease; hadison's disease; atrophic gastritis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; Goodpasture's syndrome; Hype IV hypersensitivity; infections disease; viral infection; HiV; fungal infection; Mycobacterium; neoplastic disease; lilaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;

breast cancer; ds

JS2002150891-A1. Homo sapiens.

human; T-cell associated disease; Vbeta; autoimmune disease;

Human Vbeta gene repeat sequence #567.

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marker gene; tumour; Kaposi's Sarcoma; peripheral blood mononuclear cell; PBMC; expressed keratin 14; TIE 1; Salioadhesin; Siglec 1; angiogenesis; drug target; tag; SAGE library; KS3; KS4; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                     Determining whether a treatment is effective in changing a status of a certain set of target cells in an individual comprises determining whether the sample comprises an expression product of at least one marker
                                                                       Kaposi's sarcoma tag PCR primer, SEQ ID No 144.
                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 144; 94pp; English
                                                                                                                                                                                                                                                               Van Der Kuyl AC, Cornelissen M;
                                                                                                                                                                                                 28-SEP-2001; 2001EP-00203703.
                                                                                                                                                                                                                      28-SEP-2001; 2001EP-00203703
                                                                                                                                                                                                                                          (PRIM-) PRIMAGEN HOLDING BV
           ADC13477 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence of the invention.
                                                    (first entry)
                                                                                                                                                                                                                                                                                    WPI; 2003-589342/56.
                                                                                                                                                         EP1298221-A1
                                                    18-DEC-2003
                                                                                                                                    Unidentified
                                                                                                                                                                              02-APR-2003.
                                ADC13477;
ADC13477/
ID ADC1
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autoimmune, degenerative nervoŭs system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a

Disclosure; SEQ ID NO 971; 164pp; English.

Vbeta gene.

Kit for diagnozing and treating T-cell associated diseases e.g.

WPI; 2004-059052/06. Hood LE, Rowen L;

94US-00309335. 95US-00531241.

05-MAR-1999; 19-SEP-1994; 19-SEP-1995;

17-OCT-2002

HOOD/) HOOD L E. ROWE/) ROWEN L.

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The invention relates to a novel method for determining whether a treatment is effective in changing a status of a certain set of target cells in an individual. The method comprises obtaining a sample from an individual after initiation of the treatment; and determining whether the sample comprises an expression product of at least one marker gene. The marker gene and a proteinaceous molecule (which can bind to the protein derived from the marker gene of the invention) are useful for determining whether a treatment is effective in counteracting a tumour in an individual, especially Kaposi's Sarcoma. Peripheral blood mononuclear cell (PBMC) expressed keratin 14, TIE I, Salioadhesin, or Siglec I caquences or a fully defined sequence given in the specification, or their analogues are useful as indicators for angiogenesis and for detecting the presence of a tumour cell in an individual. The expression product of a gene comprising a marker gene of the invention is useful as a drug target. The compound is useful for preparing a medicament. This polynucleotide sequence represents a PCR primer of a Kaposi's Sarcoma tag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 2 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
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1888 AAGCTGCTGAAGGAGGC 1905

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18 AAGCTGCTGAAGGAGGGC 1

ADH70777 standard; DNA; 18 BP.

25-MAR-2004 (first entry)

ADH70777;

RESULT 551
ADH70777/C
ID ADH707
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AC ADH707
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TO ADH707
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TO ADH707

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The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers composition of each Vbeta gene, where and allowing amplification of each Vbeta gene, vbetaRNA or CDNA. The kit is useful for diagnosing organ transplant crejection and diagnosing and treating T-cell associated diseases including autoimmune disease, degenerative nervous system diseases, crejection and diagnosing and treating T-cell associated diseases. Creditorially diseases, infectious diseases, and neoplastic disease. Autoimmune diseases include Addison's disease. Creditorial and Alzahamer's disease. Hypersensitivity diseases include multiple actoris and Alzahamer's disease. Hypersensitivity diseases include multiple credit hypersensitivities such as those present in allargies, Type II hypersensitivities such as those caused to allargies, Type II hypersensitivities such as those caused by viruses such as midections such as those caused by the yeast genus Candida, parasitic infections such as those caused by confined and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases confined as Longe as those caused by hypersensitivity and bacterial infections such as those caused by hypersensity and bacterial infections such as those caused by hypersensity and bacterial infections such as those caused by hypersensity and bacterial infections such as those caused by hypersensity and bacterial infections such as those caused by hypersensity and bacterial infections and cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
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Pred. No. 6.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08; Prec. ...
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Matches
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Sequence 19 BP; 6 A; 5 C; 5 G; 0 T; 3 U; 0 Other;

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vivlemore401-10.rng

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The invention relates to short interfering nucleic acids (sinA) which downregulate expression of the human platelet-derived growth factor receptor (PDGFY) gene by RNA interference. The sinAs may or may not comprise ribonucleotides and may be double or single stranded. They turther comprise sense and may be double or single stranded. They turther comprise sense oligonucleotide and an antisense oligonucleotide. Specifically, the sinAs include short interfering RNA (siRNA, double-stranded RNA, micro-RNA (miRNA) and short hairpin RNA (siRNA). The sinAs can be unmodified or chemically modified, can contain contain and stranded for the in vitro or in vivo delivery of siRNA; conjugates and/or complexes of siRNA; and vectors that express siNA. The siNAs are used to modulate expression of the PDGFr gene in cells, tissue explants or conjudate expression of the PDGFr gene in cells, tissue explants or conjudate expression of the PDGFr gene in cells, tissue explants or treating leukacemia and solid tumours, restenosis, polycystic kidney disease, bronchiolitis, glomerulomephritis and stroke. The siNAs are also useful for drug screening, diagnosis, therapeutic target identification and validation, genetic engineering, pharmacogenomics, studying gene function, and gene mapping (e.g., of single mucleotide polymorphisms).

The present sequence represents the lower strand of a human PDGFr transcript
                                                                                                                                                                                                                       cytostatic; vasotropic; nephrotropic; cerebroprotective; treating leukaemia; solid tumors; restenosis; polycystic kidney disease; bronchiolitis; glomerulnonphritis; stroke; RNA interference; short interfering nucleic acid; siNA; short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New short interfering nucleic acid, useful e.g. for treatment and diagnosis of tumors, downregulates expression of the platelet-derived
                                                                                                                                                                                                                                                                                                                                         expression modulation; gene therapy; drug screening; diagnosis; therapeutic target identification; pharmacogenomics; gene function analysis; gene mapping; human; platelet derived growth factor receptor; POGFr; ss.
                                                                                                                                                                                Human PDGFr-targeted sinA lower strand SEQ ID NO:480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; SEQ ID NO 480; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcswiggen J, Beigelman L, Chowrira B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAR-2002; 2002US-0363124P.
06-JUN-2002; 2002US-0386782P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-040929P.
15-JAN-2003; 2003US-0440129P.
                                           ADO15049 standard; RNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-2003; 2003WO-US003473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002US-0358580P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      growth factor receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003072704-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2002;
                                                                                                                                   01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-2003
                                                                                        AD015049;
RESULT 552
                       ADO15049/
ID ADO1
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target sequence

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The invention relates to short interfering nucleic acids (siNA) which downregulate expression of the human platelet-derived growth factor receptor (PDGFr) gene by RNA interference. The siNAs may or may not comprise ribonuclectides and may be double or single stranded. They further comprise sense and antisense regions, or alternatively are assembled from a sense oligonuclectide and an antisense oligonuclectide. Specifically, the siNAs include short interfering RNA (siRNA, double-stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified, can contain deoxyribonuclectides, and can be chemically synthesised, expressed from a vector or enzymatically synthesised. The invention also relates to kits to the in vitro or in vivo delivery of siRNA; conjugates and/or complexes of siRNA, and vectors that express siNA. The siNAs are used to modulate expression of the PDGFr gene in cells, tissue explants or
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                          treating leukaemia; Solid tumors; restenosis; polycystic kidney disease; bronchiolitis; glomerulonephritis; stroke; RNA interference; short interfering RNA; siRNA; double-stranded RNA; micro-RNA; mikNA; short interfering RNA; siRNA; expression modulation; gene therapy; drug screening; diagnosis; therapeutic target identification; pharmacogenomics; diagnosis; gene function analysis; gene ampping; human; pulman; platelet derived growth factor receptor; PDGFr; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New short interfering nucleic acid, useful e.g. for treatment and diagnosis of tumors, downregulates expression of the platelet-derived
                                        Gaps
                                            ö
Query Match 0.5%; Score 18; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             cytostatic; vasotropic; nephrotropic; cerebroprotective;
                                                                                                                                                                                                                                                                                                                        Human PDGFr-targeted siNA upper strand SEQ ID NO:169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; SEQ ID NO 169; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chowrira B;
                                                                               1820 TCCTGCTCTGGGAGATCT 1837
                                                                                                            18 TCCTGCTCTGGGAGATCT 1
                                                                                                                                                                                                                      ВР
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0S-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0409293P.
1S-JAN-2003; 2003US-0440129P.
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2002US-0386782P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2003; 2003WO-US003473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-2002; 2002US-0358580P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth factor receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcswiggen J, Beigelman L,
                                                                                                                                                                                                                      ADO14738 standard; RNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                  01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-731605/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003072704-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-2003
                                                                                                                                                                                                                                                             ADO14738;
                                                                                                                                                                                 RESULT 553
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chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antiinflammatory; neuroprotective; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer; disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; se.

Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:586.

(first entry)

01-JUL-2004

ADM14399;

note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"

Cocation/Qualifiers

.50 *tag=

modified base

Homo sapiens

Synthetic

mod base= OTHER

/mod_base= OTHER /note= "2'-O-methoxyethyls"

*tag= c .20

modified base

25-SEP-2003; 2003WO-US030374. 25-SEP-2002; 2002US-0413549P.

WO2004028458-A2.

(PHAA) PHARMACIA CORP

'note= "2'-0-methocyethyls"

/mod_base= OTHER

...5 ′*tag≖ a

modified base

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organisms (e.g., by ex vivo gene therapy), or in grafts and transplants for the treatment of a variety of conditions. They may be used for treating leukaemia and solid tumours, restenosis, polycystic kidney disease, bronchiolitis, glomerulonephritis and stroke. The siNAs are also useful for drug screening, diagnosis, therapeutic target identification and validation, genetic engineering, pharmacogenomics, studying gene function, and gene mapping (e.g., of single nucleotide polymorphisms). The present sequence represents the upper strand of a human pDGFrtargeted double-stranded siNA, which is identical to the PDGFr transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymorphisms among highly interrelated rice plants or among plants of family Brassicae. They can also be used for genetic fingerprinting of plants, allowing detection of polymorphism within one or the same species of plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer - for detecting polymorphism in DNA among highly interrelated rice plants or plants of family Brassicae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer for detecting polymorphisms among highly related plant species.
                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection; polymorphism; genetic fingerprinting; primer; ss.
                                                                                                                                                                                                                 Score 18; DB 1; Length 19;
Pred. No. 7e+02;
6; Mismatches 0; Indels
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Pred. No. 7.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 0 A; 2 C; 9 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                    Sequence 19 BP; 3 A; 5 C; 5 G; 0 T; 6 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 5; 6pp; Japanese.
                                                                                                                                                                                                                                                                                     1820 TCCTGCTCTGGGAGATCT 1837
                                                                                                                                                                                                                                                                                                        2 UCCUGCUCUGGGAGAUCU 19
                                                                                                                                                                                                                                                                                                                                                                                                    AAQ49455 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91JP-00243122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-338949/43.
                                                                                                                                                       target sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP05244995-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ49455;
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                                                                                                                                                                                                                                                                                                                                                                     RESULT 554
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ID AAQ4
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mpCES-1). The human megES-1 gene is located on chromosome 9, more specifically to compare the present invention also describes: (1) antisense compounds, 9434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mpCES-1, which specifically hybridise with the nucleic acid mpCES-1 and inhibits its expression; (2) a method of inhibiting the expression of inhibits a disease or condition associated with mPGES-1. MPGES-1 and caridiabetic, immunomodulator, cardiant, neuroprotective, articlabetic, immunomodulator, cardiant, neuroprotective, antidiabetic, immunomodulatory and cardiovascular activities, and can cophinal mological, immunomodulatory and cardiovascular activities, and can be used as mPCES-1 inhibitors and in gene therapy. The antisease compound con be used as mPCES-1 inhibitors and in gene therapy. The antisease compound condition associated with mPGES-1 eg., inflammation, Alzheimer's condition associated with mPGES-1 is chaemia or reperfusion injury, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 586; 132pp; English.
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Gaps

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0; Indels

GIGIGIGIGIGIGC 2352

2335

Local Similarity 100. ses 18; Conservative

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BP.

ADM14399 standard; DNA; 20

RESULT 555

ADM14399/ ID ADM1

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Synthetic.
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                                                                                                                                                                                                                               chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antidifammatory; neuroprotective; antidifammatory; neuroprotective; assotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; acrdiovascular disorder; neurological disorder; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a chimeric antisense oligonucleotide
ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                         /note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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                                                                                                                                                                                                              Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:531.
                                      DB 1; Length 20; 7.4e+02;
                                                        0; Indels
                  Sequence 20 BP; 9 A; 10 C; 1 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                /mod_base= OTHER
/note= "2'-O-methocyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mod_base= OTHER
/note= "2'-O-methoxyethyls"
                                     0.5%; Score 18; DB
100.0%; Pred. No. 7.4
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID NO 531; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                base= OTHER
                                                                              2334 CGTGTGTGTGTGTGTG 2351
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                                                                                                                                                    ADM14344 standard; DNA; 20
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                                               Local Similarity 100.
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*tag=
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                                                                                                                                                                                                                                                                                                                                                                          modified base
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                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                20
                                                                                                                                                                       ADM14344;
                                      Query Match
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                                                 Best Loca
Matches
                                                                                                                                RESULT 556
                                                                                                                                         ADM14344,
SXS
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targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mPGES-1 gene is located on chromosome 9, more specifically to gq34.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of inhibits its expression; (2) a method of threating an animal comparation associated with mPGES-1. MPGES-1 and inhibits its expression; (2) a method of treating an animal contisense oligonucleotides and antisense compounds have cytostatic, antisense oligonucleotides and antisense compounds have cytostatic, antishifammatory, neuroprotective, nootropic, antiantialmamatory, neuroprotective, nootropic, antiantialmamatory, neuroprotective, nootropic, antianthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or continuous immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotide useful for PCR amplification along with two DNA fragment from another set of sequences, or for detecting single nucleotide polymorphism in human gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2334 CGTGTGTGTGTGTGT 2351
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Best Local Similarity 100.0
Matches 18; Conservative
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ADJ98020 standard; DNA; 21

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ADJ98020;

(first entry) 06-MAY-2004 Human Flk-1/KDR DNA sequence, a target for siRNA inhibition SeqID 793

human; ss; short interfering RNA; siRNA; angiogenesis; vascular endothabial growth factor; VEGF; VEGF receptor; Flt-1; Flt-1/KDR; kinase domain region; diabetic retinopathy; age-related macular degeneration; inflammatory disease; psoriasis; rheumatoid arthritis; cancer; breast; retinoblastoma; Wilm's tumour; lymphoma; cytostatic; antidiabetic; ophthalmological; antiinflammatory; antipsoriatic; antiarthritic.

Homo sapiens.

WO2004009769-A2.

29-JAN-2004.

18-JUL-2003; 2003WO-US022444.

24-JUL-2002; 2002US-0398417P.

(UYPE-) UNIV PENNSYLVANIA.

Tolentino MJ, Reich SJ;

WPI; 2004-203472/19.

Novel short interfering RNA (siRNA) comprises sense and antisense RNA strands, useful for inhibiting expression of human vascular endothelial growth factor mRNA, for treating angiogenic disease, e.g. diabetic retinopathy and cancer.

Disclosure, SEQ ID NO 793; 218pp; English.

This invention relates to novel compositions that comprise short interfering RNA (siRNA) molecules, which can be used to inhibit angiogenesis a Specifically, it refers to siRNAs that target and cause RNAi-induced degradation of mRNA from human vascular endothelial growth factor (VEGF), the VEGF receptor (Fit-1) and the Fik-1KCDR (Kinase Gomain region) genes, as well as mutants derived thereof. The present invention describes sense and antisense RNA strands that form an RNA duplex and bind to the target mRNA, such that expression is inhibited and the target degraded. As such, siRNA administered in combination with a therapeutic gene to the overexpression of VEGF, which include diabetic retinopathy, agether account degeneration, inflammatory disease, psoriasis and the thematoid arthritis. Furthermore, it can be used to treat various cancers including breast, retinoblastoma, wilm's tumour and lymphoma. Accordingly, these compositions exhibit cytostatic, antidiabetic, ophthalmological, antidiffammatory, antipsoriatic, antidiabetic activities. This oligonucleotide is a human Fik-1/KDR DNA coligo, a target for siRNA inhibition of the invention. RESULT 558
ADU98020
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ADU98020
ADU99020
ADU9902

Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

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0.5%; Score 18; DB 1; Length 21; 100.0%; Pred. No. 7.9e+02; ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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4 CCAGAGTGACGTCTGGTC 21
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AAX00049

BP. AAX00049 standard; DNA; 22

AAX00049;

(first entry) 16-MAR-1999

FGFR PCR sense primer.

oligodendrocyte; self-renewal; neuron; differentiation; neural crest cell; fibroblast growth factor; FGF; FGFR; receptor; CNS; central nervous system; glial cell; PCR primer; amplification; ss. Neuroepithelial stem cell; lineage restricted intermediate precursor;

Synthetic.

Homo sapiens

WO9850526-A1

12-NOV-1998.

98WO-US009630. 07-MAY-1998;

97US-00852744. 07-MAY-1997;

98US-00073881. 06-MAY-1998; (UTAH) UNIV UTAH RES FOUND

Rao MS, Mayer-Proschel M, Mujtaba T;

WPI; 1999-070093/06.

Mammalian neuroepithelial stem cells and glial restricted precursor - car self renew and differentiate into central nervous system cells, used for generating various types of cells.

Example 26; Page 61; 78pp; English

The present invention describes an isolated, pure population of mammalian neuroepithelial stem cells, which are capable of self-renewal in adherent cededar-cell-independent (AFCI) culture medium and differentiation to central nervous system (CNS) neuronal or glial cells and to neuronal central nervous system (CNS) neuronal or glial cells and to neuronal crest stem cells. Also described is an isolated population of mammalian correctivated precursor (GRP) cells which can self-renew in the AFCI culture medium and can differentiate to CNS glial cells but not to CNS neuronal cells. The stem cells can be used to generate a population of mammalian mnotor neurons by incubating the stem cells but not to CNS neurons and NEP medium lacking chick embryo comprises laminin-coated plates and NEP medium lacking chick embryo cartract. The stem cells can also produce neural crest stem cells by inducing the cells to differentiate in vitro. The inducing step comprises caplating the cells on a laminin-coated substrate and preferably comprises chick embryo extract. Inducing can also comprise adding a dorsalizing capant to the cells, preferably fibroblast growth factor; FGF) and control chick embryo extract. Inducing can also comprise adding a dorsalizing capant to the cells, preferably a bone morphogenetic protein (BMP) such gentiferentiate. At or -7. The stem cells can be used to produce cells to differentiate in vitro to neural creek stem cells, and inducing these cells to differentiate in vitro to neural creek stem cells, and inducing these cells to differentiate in the cap comprise cells or also comprise cells to differentiate in the cells or also comprise cells to differentiate in the cells or also comprise cells to differentiate or cells, and inducing these cells to differentiate or cells to a cells, and inducing these cells to cells and cells, and inducing these cells to cells in the cells, and inducing these cells to cells to cells, and cells, and inducing these cells to cells to cells to cells, and inducing these cells to c in an example from the present invention to amplify different FGF and FGFR genes

Sequence 22 BP; 8 A; 1 C; 8 G; 5 T; 0 U; 0 Other;

Gaps ; 0.5%; Score 18; DB 1; Length 22; 100.0%; Pred. No. 8.3e+02; tive 0; Mismatches 0; Indels 18; Conservative Best Local Similarity Matches 18; Conserv Query Match

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Genetic proximity, gene expression; cell characterisation; homeobox gene; genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR; kinase gene; protein phosphatase; P450; steroid receptor; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory component, e.g. acne, psoriasis, arthritis, organ rejection, wounds, burns, septic shock or inflammatory complications of septic shock
                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of an antisense oligonucleotide which is substantially complementary to at least a portion of the pre- or mature RNA transcript of human intracellular adhesion molecule (TCAM). Eselectin or vascular cell adhesion molecule (VCAM). It can be used to inhibit expression of these proteins. Inhibition of these proteins forms the basis for treatment of conditions and diseases that have an
                                                                                                                                                                                                                                                                                                               Antisense oligonucleotides to ICAM-1, E-selectin or VCAM-1 - useful for treating diseases having an inflammatory component, e.g. psoriasis, wounds and septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
vascular cell adhesion molecule-1; antisense; inflammatory; disease treatment; septic shock; psoriasis; wounds; burns; acne; arthritis; organ rejection; inhibition; expression; ss.
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98IL-00126627.
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                  WPI; 1998-333253/29
                                                                       Homo sapiens
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16-OCT-1998;
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                                                            Synthetic.
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AAZ18102/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-sense oligo:nucleotide(s) for blocking ICAM-1 mRNA translation - for treating septic shock, adult respiratory distress syndrome etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antisense to sequences contained in the pre-mRNA or mature mRNA transcript of human intercellular adhesion molecule-1 (ICAM-1). These oligonucleotides may be used for treating septic shock and the manifestations of septic shock, e.g. inflammation, and vascular and tissue defects. They are also useful in the treatment of septic shock associated diseases, e.g. adult respiratory distress syndrome, multiple organ failure etc. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAT58071-85 represent oligonucleotides which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                      Antisense; pre-mRNA; mature mRNA; vascular defect; tissue defect; human intercellular adhesion molecule-1; ICAM-1; inflammation; adult respiratory distress syndrome; multiple organ failure; GM1594; septic shock; ss.
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                                                                                                                                                                                                          ICAM-1 antisense oligonucleotide #10.
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TGAGATGGAGATGAA 1364
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               Claim 1; Col 21; 16pp; English.
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                                                                                                      ВР
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                                                                                                      AAT58080 standard; DNA; 21
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                                                                                                                                                               (revised)
(first entry)
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les 19; Conservative
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18-MAR-1997
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1347
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                                                                                                                                                                                                          cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell; (c) cell; (d) cell the pattern of expression of genes in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characteristing cells, e.g. for determining the origin of a cell; its genetic status, whether it carries a genetic defect, or whether it is transformed. They can be used for determining the an individual, e.g. a fecus. They can also be used for determining the ceffect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired containing cells capable of expressing an homeobox related desired containing the property. The method uses reverse transcriptes polymerase chain reaction gene family. Sequences AA21803-21842 represent primers that can be used in the RT-PCR reactions to determine the pattern of gene expression. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetic proximity, gene expression, cell characterisation, homeobox gene, genetic defect, reverse transcriptase polymerase chain reaction, RT-PCR; kinase gene, protein phosphatase, P450, steroid receptor, cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                          family can be selected from a set of homeobox genes, kinase genes, ain phosphatase genes, P450 enzyme genes, steroid receptor
                                                                                                                                                                                                 The invention provides a new method for identifying and characterising
                                                                                                                       Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        superfamily genes or cadherin superfamily genes
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                                                                                                                                                                   Claim 4; Page 42; 102pp; English.
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ID AAZ18094 standard; DNA; 21 BP.
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98IL-00126627
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                                                                           WPI; 1999-419113/35.
P-PSDB; AAY14637.
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                 (GENE-) GENENA LTD
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16-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                             Vider B;
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The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell compises: (a) obtaining the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell; (c) determining in the first cell and the second cell; (c) calculating a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell, its contains whether it carries a genetic defect, or whether it is contained. They can also be used for determining the ceffect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired property. The method uses reverse transcriptuse polymerase chain reaction (RT-PCR) for determining the pattern of gene expression in a selected gene family. Sequences AAZI/R03-Z18342 represent primers that can be used in the RT-PCR reactions to determine the pattern of gene expression. The gene family can be selected from a set of homeobox genes, kinase genes, containing cells capable from a set of homeobox genes, kinase genes, containing cells capable from a set of homeobox genes, kinase genes, containing cells capable from a set of homeobox genes, kinase genes, containing cells capable from a set of homeobox genes, kinase genes, containing cells capable from a set of homeobox genes, kinase genes, containing cells capable containing cells capable containing cells containing cells cel
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                                                                                                                                                            Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           superfamily genes or cadherin superfamily genes
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                                                                                                                                                                                                                                                                      Claim 4; Page 42; 102pp; English
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                                                                                                   P-PSDB; AAY14629
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Vider B;
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                                                                                                                                                                The invention provides a new method for identifying and characterising
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                                          Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.
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                                                                                                                 Claim 4; Page 43; 102pp; English
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AAZ18110 standard; DNA; 21 BP
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P-PSDB; AAY14645.
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tes 19; Conserv
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  P-PSDB; AAY14653.
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16-OCT-1998;
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The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell comprises: (a) obtaining the first cell and the second cell the pattern co cell; (b) determining in the first cell and the second cell the pattern of expression of genes in a selected gene family; and (c) calculating a proximity index using a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell, its carniformed. They can be used for detecting a selected genetic defect in the ransformed. They can be used for detecting a selected genetic defect in ceffect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired cobtaining the pattern of gene expression in a selected compression in a selected compression in the RT-PCR reactions to determine the pattern of gene expression. The control of gene family can be selected from a set of homeobox genes, kinase genes, control of the control of control of the control of c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of homeobox genes, kinase genes, genes, steroid receptor
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expression in a selected gene family.
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                                                                                                    Claim 4; Page 42; 102pp; English.
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Best Local Similarity 90.5'
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Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or
different chemokines. The invention relates to the use of chemokines which are capable of directing dendritic cells, in the manufacture of a medicament for the treatment of a disease state. Wethods are included for treating diseases by facilitating or inhibiting the migration or activation of antigen-presenting dendritic cells. The chemokines can be used to initiate, amplify or modulate an immune response. The chemokines are useful for the treatment of disease states e.g. a bacterial, wiral, fungal or parasitic infection, cancer (especially melanomal, breast, pancreatic, colon, lung, glioma, hepatocellular, endometrial, gastric, intestinal, renal, protate, thyroid, ovarian, testicular, liver, head and neck, colorectal, oesophagus, stomach, eye, bladder, glioblastoma and metastatic carcinomas), autoimmune disease, tissue rejection or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPB; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfects; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
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                                                                                                                                                                                                                                                                                                                          Score 17.8; DB 1; Length 21; Pred. No. 8.3e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                      Sequence 21 BP; 8 A; 11 C; 0 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP specific lower PCR primer SEQ ID 1230.
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                                                                                                                                                                                                                                                                                                                                0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH38434 standard; DNA; 21
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Best Local S
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Gaps

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The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in multiwell plates numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker or sequence is added to the mixture to carry out an amplification reaction; sequence is added to the mixture to carry out an amplification reaction; sequence is corresponding to the marker is detected from the resultant (c) a signal corresponding to the marker is detected from the resultant corresponding the clones having said marker sequence; (d) the order plates containing the clones having said marker sequence; (d) the order of the maximum in the specified discrimination Nos. to array the multiwell plates of the specified discrimination in sor are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the and lateral directions; (f) the mixed clones are cultured and the multiwell care detected from the amplified by using the above primer; (g) signals are detected from the amplified products; (h) the clones in the multiwell
identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insiptius, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, costeogenesis imperfects and acute intermittent porphyria. Phenotypic craits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune cinflammation, cancer, nervous system diseases and infection by manamatical cancer in erwork and infection by multiple sclerosis, microorganism. The method is also useful.in forensic investigations and microorganism. The method is also useful.in forensic investigations and containing DNA sequence represents a PCR primer specific for a human SNP containing DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                          0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human chromosome 1p36-35 PCR primer SEQ ID NO:1418.
                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 0 A; 3 C; 8 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2320 TGTGTGTGTGTGTGTGT 2340
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(GENO-) GENOTEX YG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Conservative
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 568
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reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42957 to ABL45322 represent PCR primers for human chromosome 198-5-35 DNA, and ABL45323 to ABL45634 represent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention
are specified from the detected result; and (i) the clones are
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Sequence 21 BP; 0 A; 2 C; 9 G; 10 T; 0 U; 0 Other;

Gaps ö 0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02; tive 0; Mismatches 2; Indels Query Match
Best Local Similarity 90.5
Matches 19; Conservative

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ABS98544;

ABS98544 standard; DNA; 21 BP

(first entry) 23-DEC-2002

Human acetyl choline muscarinic receptor 3 polymorphic sequence #10.

Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRB3; NRIJ2;

Aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS; cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological;

W glutathione-S-transferase 1; GST12; histamine-N-methyl transferase;

HNMT; kallikrein 2; KIKZ; nicotinamide-N-methyl transferase;

W MADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;

W UDP-glucuronosyl transferase 284; UDP-glucuronosyl transferase 287;

W UDP-glucuronosyl transferase; UGT2B15; urokinase receptor;

W ultidrug resistance 1; lactotransferrin; orphan nuclear receptor;

W ultidrug resistance associated protein 3; cancer; prostate;

Multidrug resistance sasociated protein 3; cancer; prostate;

M altered drug metabolism; cardiovascular function; colorectal tumour;

CENTRAL DEPTOR DECTOR STANS AND S single nucleotide polymorphism. ABS98544

ABS98544

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Homo sapiens.

WO200257410-A2.

25-JUL-2002.

28-NOV-2001; 2001WO-US044838.

28-NOV-2000; 2000US-00724389.

(DNAS-) DNA SCI LAB INC.

Guida M, Hall J;

WPI; 2002-698522/75.

solated nucleic acid molecules having polymorphisms in known human genes .g. cytochrome p450 and cathepsin S useful as genetic linkage markers or locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 28; Page 160; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 Al (CYP4501Al), cytochrome P450 A2 (CYP4501Al), cytochrome P450 A2 (CYP4501Al), adrenergic receptor betal (ADBR1),

aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARWT), cathepsin 8 (CTSS) cyclooxgenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydroxylase 2 (EFHX2), 5-1ipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GST12), histenmine-N-methyl protein (FLAP), glutathione-S-transferase 12 (GST12), histenmine-N-methyl transferase (NWMT), (ABILIKrein 2) KLX2, incotinamide -N-methyl LOXC (Transferase (NWMT), NADPH quinone oxidoreductase 2 (NOC2), unsethyl transferase 10 (GTZBH), uDP-glucuronosyl transferase 2BH (GTZBH), GTHMR2), GTHMR3, GT

Sequence 21 BP; 10 A; 0 C; 1 G; 10 T; 0 U; 0 Other;

Gaps .; 0 0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02; 2; Indels 0; Mismatches Local Similarity 90.5 hes 19; Conservative Query Match Matches

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ABS98544 standard; DNA; 21 BP RESULT 570 ABS98544/

ABS98544;

23-DEC-2002 (first entry)

Human acetyl choline muscarinic receptor 3 polymorphic sequence #10

Human; ds; cytochrome P450 Al; CYP4501Al; UGT2B4; MDR1; cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002El; LTF; adrenegie receptor betal; ADBR1; aryl hydrocarbon; AHR; MRD3; NR12; aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CYS; cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; haematological; epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP; glutathione-S-transferase 12; GST12; histamine-N-methyl transferase; HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT; UDP-Glucuronosyl transferase 2; NQO2; sulfotransferase thermolabile; STM; UGT2B7; UDP-Glucuronosyl transferase 287; UDP-Glucuronosyl transferase 287; multidrug resistance 1; lactotransferzin; orphan nuclear receptor; uPA; multidrug resistance associated protein 3; cancer; prostate; acerylcholine muscarinic receptor; CHWR1; CHWR2; CHWR3; CHWR4; altered drug metabolism; cardiovascular function; colorectal tumour; central nervous system; pulmonary; immunological; SNP; single nucleotide polymorphism.

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28-NOV-2001; 2001WO-US044838
                  WPI; 2002-698522/75.
  WO200257410-A2
Homo sapiens.
     25-JUL-2002
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28-NOV-2000; 2000US-00724389 (DNAS-) DNA SCI LAB INC. Guida M, Hall J; Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 28; Page 160; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytcochrome P450 A2 (CYP4501A2), cytochrome P450 A2 (CYP4501A1), cytochrome P450 A2 (CYP4501A2), cytochrome P450 O2E1 (CYP4501A1), adrenation from that of a known human cytcochrome P450 O2E1 (CYP4501A1), adrenation from that of a known (ARN), aryl hydrocarbon receptor nuclear translocator (ARNY), cathepsin S (CTSS), cytlooxeenses 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydroxylase 2 (ERHZ2), 5-lipoxygenase activating protein (PLAP), glutachione-6-transferase 12 (GYT12), histenmine-N-methyl transferase (HNMY), NADPH quinone oxidoreductase 2 (MNO2), culfortansferase (HNMY), NADPH quinone oxidoreductase 2 (NNO2), sulfoctransferase (HNMY), NADPH quinone oxidoreductase 2 (NNO2), culfoctransferase (HNMY), NADPH quinone oxidoreductase 2 (NNO2), culfoctransferase (HNMY), NADPH quinone oxidoreductase 2 (NNO2), culfortansferase (HNMY), natotransferation (GYM), unltidrug resistance associated protein 3 (NMR), lactocransferatin (GYM), multidrug resistance 1 (MRP), lactocransferatin (GYM), multidrug resistance associated protein 3 (HNR), lactocransferatin (GYM), multidrug resistance 1 (MRP), lactocransferatin (GYM), multidrug resistance associated protein 3 (HNR), lactocransferatin (GYM), multidrug resistance associated for a result of their e.g. overexpression, constitutive cander for their e.g. overexpression, constitutive collymorphic sequences contained in CYP4501A1, CYP94501A2, CYP94501A3, CYP94501A3, CYP94501A3, CYP94501A3, CYP94501A3, CYP94501A3, nervous system function. The present sequence represents a polymorphic DNA sequence of the invention

Sequence 21 BP; 10 A; 0 C; 1 G; 10 T; 0 U; 0 Other;

Gaps ö 0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02; tive 0; Mismatches 2; Indels Ouery Match Best Local Similarity 90.5 Matches 19; Conservative

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ABS97829 standard; DNA; 21 BP ABS97829/c

ABS97829;

(first entry) 23-DEC-2002

Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #37.

Human, ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

CYCloxgenase 2; CXZ; diazepam binding inhibitor; DB1; haematological;

CXZ; diazepam binding inhibitor; DB1; haematological;

CXZ; diazepam binding inhibitor; DB1; haematological;

CXX; diazepam binding information incortanterase;

CXX; diazepam binding information incortans extinaterase;

CXX; diazepam consolutions associated protein 3; cancer; prostate;

CXX; diazepam metabolism; cardiovascular function; colorectal tumour;

CXX; diazepam consolution in munical informaty; immunological; SNP; single nucleotide polymorphism.

Homo sapiens.

WO200257410-A2.

25-JUL-2002

28-NOV-2001; 2001WO-US044838

28-NOV-2000; 2000US-00724389

(DNAS-) DNA SCI LAB INC.

Guida M, Hall J;

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 16; Page 130; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid

molecule comprising at least one base variation from that of a known

molecule comprising at least one base variation from that of a known

the molecule comprising at least one base variation from that of a known

but an expression (2012) (2016) (20

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Example 16; Page 131; 714pp; English.

disorder-related traits.

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Human, ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 028; CYP4501A1;

Cytochrome P450 A2; CYP4501A2; cytochrome P450 028; CYP4501B1;

Adrenergic receptor beta1; ADBR1; aryl hydrocarbon, AHR; MRP3; NRI12;

W adrenergic receptor muclear translocator; ARNT; cathepsin S; CTSs;

Cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

W epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

Glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;

W NADPH quinone oxidoreductase 2; NQO2; sulfoctransferase; NNMT;

W DP-glucuronosyl transferase 24; UDP-glucuronosyl transferase 287;

W UGT2B7; UDP-glucuronosyl transferase 287;

W multidrug resistance associated protein 3; cancer; prostate;

multidrug resistance associated protein 3; cancer; prostate;

acetylcholine muscarinic receptor; CHWR1; CHWR2; CHWR3; CHWR4; CHWR5;

w altered drug metabolism; cardiovascular function; colorectal tumour;

central nervous system; pulmonary; immunological; SNP;

single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502B1, ARNT, EPHX2, GST12, NNWT, NOO2, NR112, STW, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/Or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2, AHR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or GHRR2 are used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DB1 or CHRR1 for altered central nervous system function, in FLAP and HNWT for altered pulmonary, immunological or haematological function, in KLR2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHRR3 or CHRR5 for altered central haematological function, in CHRR3, CHRR4 or CHRR5 for altered central and peripheral nervous system function. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymorphic DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2316 TCTGTGTGTGTGTGTGCGT 2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 rargrerererererer 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABS97831 standard; DNA; 21 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-2000; 2000US-00724389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DNAS-) DNA SCI LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200257410-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 572
        8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8\pm8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 쇰
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This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CTP4501A1), cyrochrome P450 OZB1 (CTP4501A2), are present that the cytochrome P450 OZB1 (CTP4501A2), are present that the cytochrome P450 OZB1 (CTP4501A2), are present translocator cytochrome P450 OZB1 (CTP4501A2), are present translocator (ARNY), cathepsin S (CTS2), cyclooxgenase 2 (CXCZ), diazepam binding inhibitor (DB1), epoxide hydrocarbon receptor nuclear translocator (ARNY), cathepsin S (CTS2), cyclooxgenase 2 (CXCZ), diazepam binding transferase (HNWT), NADPH quinone oxidoreductase 2 (NQC2), histanine-N-methyl transferase (HNWT), NADPH quinone oxidoreductase 2 (NQC2), cransferase (UGT2B1S), urokinase receptor (UPA), multidrug resistance 1 (MDR1), lactorransferzin (LTF), multidrug resistance associated protein 3 (MDR1), cransferase (MDR1), or acetylcholine muscarinic creceptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3) CHMR4) cransferase (MDR1), prophan nuclear receptor (NRT12), or acetylcholine muscarinic crare resoponsible for specific traits within the genes are resoponsible for specific traits within the genes are resoponsible for avariety of disorder-related craits as a result of their e.g., overexpression, constitutive captences contained in CTP4501A1, CTP450A1,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; tissue rejection; allergy; cancer; hepatocellular; melanoma; breast; pancreas; colon; glioma; endometrium; intestine; lung; prostate; thyrold; ovary; testis; liver; head; neck; colorectal; bladder; osephagus; stomach; eye; glioblastoma; gastric; metastatic carcinoma; immunosuppressive; antiallergic; cytostatic; rectum; RT-PCR; primer; reverse transcriptase; macrophage inflammatory protein 3 beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peripheral nervous system function. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chemokine; MCP-4; hMCP-4; ss; 6Ckine; dendritic cell; renal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.5%; Score 17.8; DB 1; Length 21; 0.5%; Pred No. 8.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human MIP-3 beta RT-PCR primer -439/MIP-3 beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymorphic DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2318 TGTGTGTGTGTGTGCGTGT 2338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK47993 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.5%;
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ABX47993/c
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Homo sapiens beta.

MIP-3

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for

WPI; 2002-698522/75. Hall J;

Guida M,

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The invention describes a method of predicting, diagnosing or prognosing a cardiovascular disease by detection of a polynucleotide in a biological sample comprises hybridising at least one of the polynucleotide to a nucleic acid material of a biological sample, thus forming a hybridisation complex, and detecting the hybridisation complex. The polynucleotides, polypeptides, antisense molecule, antibody and reagent are useful for preparing compositions for preventing, predicting or arteriosclerosis, isohaemnt for treating a cardiovascular disease, e.g. arteriosclerosis, isohaemia, angina pectoris, or myocardial infarction. This sequence represents a primer used to identify genes differentially regulated in individuals with cardiovascular disease
                                                                                                                               Predicting, diagnosing or prognosing a cardiovascular disease, e.g. angina, ischemia, myocardial infarction or arteriosclerosis by detection of a polynucleotide in a biological sample comprises detecting a hybridization complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; noctropic; antipaction anticonvulsant; osteopathic; antilipaemic; antiinflammatory; dermatological; antiasthmatic; antilipaemic; gene therapy; fibroblast growth factor receptor 4; FGFR4; occomplement factor I precursor; matrix metalloproteinase-15 precursor; fibroblast growth factor-21; FGF-21; fibroblast growth factor-21; FGF-21; antighnation in the polypebide variant; hardware and prove factor-21; FGF-21; antighnation in the polypebide variant; hardware and prove factor-21; FGF-21; antighnation in the polypeptide variant; hardware factor-21; FGF-21; antighnation factor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anilleukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1; transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NOV1 reverse real time quantitative PCR primer SEQ ID NO:148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 4 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                      Schmitz
                                                                                                                                                                                                                                                                                                  Example 3; Page 107; 454pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1796 AGAGTGACGTCTGGTCCTTTG 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGAGCGACGTCTGGTCCTATG 21
                      Wick M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2002US-0409145P.
; 2002US-0409544P.
; 2002US-0401320P.
; 2002US-0411060P.
; 2002US-041276F.
; 2002US-0412782P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.5
Best Local Similarity 90.5
Matches 19; Conservative
                         Gehrmann M,
                                                                               WPI; 2003-403108/38.
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10-SEP-2002;
12-SEP-2002;
16-SEP-2002;
23-SEP-2002;
24-SEP-2002;
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                         Munnes M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Using chemokine MCP-4 or 6Ckine to attract dendritic cells to the site of an antigen is useful to treat disease states, particularly autoimmune disease, tissue rejection, allergy and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cardiovascular disease differential gene expression related primer #163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for enhancing an immune response in a mammal, comprising administering chemokine MCP-4 or GCkine or their biologically active fragments. The chemokines are capable of directing the migration of dendritic calls to manufacture a medicament for a disease state. The invention is used to treat disease states, including an autoimmune disease, tissue rejection or an allergy, or a cancer, particularly melanoma, braset, pancreatic, colon, lung, glimma, hepatocellular, endometrial, gastric, intestinal, renal, prostate, thyroid, ovarian, testicular, liver, head and neck, colorectal, cesophagus, stomach, eye or bladder cancer, glioblastoma or metastatic carcinoma. This sequence represents an RT-PCR primer for macrophage inflammatory protein 3 beta (MIP-3 beta), used in analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cardiovascular disease, arteriosclerosis; ischaemia; angina pectoris; myocardial infarction; cardiant; antiarteriosclerotic; antianginal; gene therapy; differential gene expression; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 8 A; 11 C; 0 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2319 GTGTGTGTGTGTGTGTGTG 2339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 7; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        Laface D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACA90116 standard; DNA; 21 BP
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                                                                                                                                                         24-JAN-2001; 2001US-00768917
                                                                                                                                                                                                                  24-JAN-2001; 2001US-00768917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   responsiveness to chemokines
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                                                                                                                                                                                                                                                                                                                                                                                                           Vicari AP, Caux C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-351086/38
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Best Local Similarity
                                                                                                                                                                                                                                                                               (VICA/) VICARI A P. (CAUX/) CAUX C.
                                                                                                                                                                                                                                                                                                                                        (LAFA/) LAFACE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FARB ) BAYER AG
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                                   US2002034494-A1
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                                                                                               21-MAR-2002
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RESULT 574

Matches

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Gaps

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2; Indels

(first entry)

16-DEC-2002

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homology to MDC3; NOV3a-5c show homology to T-lymphocyte surface antigen Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21 Ly-9 precursor; NOV6a-6m show homology to fibroblast growth factor-21 polypeptide variant; NOV8a-8g show homology to alpha-2 macroglobulin-like polypeptide variant; NOV8a-8g show homology to antileukoproteinas 1 precursor; NOV9a-9i show homology to LIV-1 protein; NOV10a shows homology to nuclear hormone receptor NOR-1; NOV11a-11j show homology to transmembrane protein-like; NOV12a-12c show homology to beta-necendorphin-dynorphin precursor. The present sequence represents a PCR primer used in the exemplification of the invention.
                                                                                      New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
                                                   Ort T, Padigaru M, Rieger DK;
                                                                                                                                             Example 12; SEQ ID NO 148; 214pp; English.
                                                  Zhong M, Guo X, Anderson DW,
25-SEP-2002; 2002US-0413342P.
30-SEP-2002; 2002US-0414832P.
                               (CURA-) CURAGEN CORP.
                                                                      WPI; 2004-315567/29.
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Sequence 21 BP; 5 A; 8 C; 2 G; 6 T; 0 U; 0 Other;
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Gaps ô Query Match 0.5%; Score 17.8; DB 1; Length 21; Best Local Similarity 90.5%; Pred. No. 8.3e+02; Matches 19; Conservative 0; Mismatches 2; Indels

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ABS78792 standard; DNA; 22 ABS78792 RESULT 576 ABS78792 ID ABS7 XX AC ABS7

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Human; NOVX; human disease; NOVX-associated disorder; cancer; addiction; Hodgkin disease; Von Hippel-Lindau syndrome; Alzheimer's disease; stroke; tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; leukodystrophy; anxiety; pain; obsestly; Crohn's disease; osteoporosis; inflammatory bowel disease; infertility; frinflammatory bowel disease; scleroderma; haemophilia; diabetes; pancreatitis; autoimmune disease; sathma; arthritis; immunodeficiency; HIV; viral infection; neurogenesis; bacterial infection; parasitic infection; graft-versus-host disease; anglogenesis; PCR; primer; ss.
                    Human NOVX reverse primer Ag3765.
                                                                                                                                                                                                                                                                 2001US-0274281P.
2001US-0274849P.
2001US-0275235P.
2001US-0275579P.
2001US-0275601P.
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2001US-0279344P.
2001US-0280233P.
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2001US-0277833P.
2001US-0278152P.
2001US-0278894P.
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2001US-0288148P.
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2001US-0277327P.
2001US-0277338P.
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                                                                                                                                                                                                                                              08-MAR-2002; 2002WO-US007283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-0335302P
                                                                                                                                                                                                     WO200272770-A2
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      20-MAR-2001;
                                                                                                                                                                                                                                                                                                                       14-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAY-2001;
                                                                                                                                                                                                                         19-SEP-2002
                                                                                                                                                                                                                                                                                         12-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001
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KA, Vernet CA, Tchernev VT, Malyankar UM, Gerlach VL; Zerhusen BD, Patturajan M, Gusev VY, Kekuda R, Pena CEA; , Gangolli EA, Taupier RJ; Spytek KA, Zhong M,

2002US-00094466

07-MAR-2002;

(CURA-) CURAGEN CORP.

WPI; 2002-713508/77.

New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, multiple sclerosis, atherosclerosis, cancer, infections, osteoporosis or Parkinson's disease.

Example C; Page 231; 266pp; English.

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The present invention relates to a new polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The VOX nucleic acids, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hyperlamer's disease, Hutington's disease, recebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxiatelangiectasia, leukodystrophies, addiction, anxiety, depression, pain,

23 GTGTGTGTATGTGTTTGCACA 3

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AAQ5732
                                                                                                                      RESULT
obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, infertility, inflammatory bowel disease, atherosclerosis, hypertension, seleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versus-host disease. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind angiogenesis, in gene therapy, in generation of antibodies that bind diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present nucleic acid sequence represents a PCR primer that was used in the methods of the invention for amplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0.5%; Score 17.8; DB 1; Length 23;
Best Local Similarity 90.5%; Pred. No. 9.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 17.8; DB 1; Length 22;
llarity 90.5%; Pred. No. 8.7e+02;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; single nucleotide polymorphism; SNP; ss; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22 BP; 3 A; 0 C; 11 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23 BP; 9 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotide polymorphism in human gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer that
human NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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Matches
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XXX ADK9

XXX ADK9

XXX ADK9

XXX Huma

XXX Huma

XXX Synt.

XXX Synt.

XXX BD 16-S

PP 08-M

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PP 08-M

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is a ACE mRNA target sequence (nucleotide no. 491) of an enzymatic RNA molecule (ribozyme) which cleaves mRNA associated with the development or maintenance of a cardiovascular condition. The concn. of the ribozyme necessary to effect a therapeutic treatment is lower than that of an antisense oligonocleotide and the specificity of action is higher. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                   inhibitor; inhibition; ribozyme; treatment; prevention; psoriasis; asthma; inflammatory diseases; cardiovascular condition; hypertension; arthritis; restenosis; anglotensin converting enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzymatic RNA molecules which cleave mRNA - used to treat or prevent inflammatory, arthritic, stenotic or cardiovascular diseases or conditions.
                                                                                                                       Specific; cleavage; target RNA; protein; prophylaxis; expression;
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0.5%; Score 17.8; DB 1; Length 24;
Best Local Similarity 90.5%; Pred. No. 9.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multimerisation of minimal motifs using primer ZGR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24 BP; 3 A; 8 C; 10 G; 3 T; 0 U; 0 Other;
                                                                                             Enzymatic RNA molecule ACE mRNA target sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3187 CAGCCTGCCCGGAGCTGGAG 3207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 21; 65pp; English.
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ВP
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92US-00989848.
92US-00989849.
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AAQ57329 standard; mRNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV55817 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                         (RIBO-) RIBOZYME PHARM INC.
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                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Sullivan SM, Draper KG;
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                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-048853/06.
                                                                                                                                                                                                                                                                               02-JUL-1993;
                                                     25-MAR-2003
26-JUL-1994
                                                                                                                                                                                                                         WO9402595-A1
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18-NOV-1998
                                                                                                                                                                                                                                                                                                                         07-DEC-1992;
                                                                                                                                                                                                                                                                                                                                     07-DEC-1992;
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                                                                                                                                                                                                                                                     03-FEB-1994
                                                                                                                                                                                                Synthetic.
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                             AAQ57329;
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2335 GTGTGTGTGTGTGTGCACA 2355

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Sequences shown in AAV55812 to AAV55827 represent primers used in the course of the invention for the multimerisation of minimal motifs. The invention provides a method for increasing the resistence of a core protein to proteolytic degradation that comprises linking or inserting onto or into the core protein a stabilising polypeptide of formula conto or into the core protein a stabilising polypeptide of formula conto or into the core protein a stabilising polypeptide of formula can be anything between 1-66. X, Y and Z need not be identical from an can be anything between 1-66. X, Y and Z need not be identical from repeat to repeat. Alternatively a nucleic acid encoding a stabilising polypeptide can be linked onto or inserted into a nucleic acid encoding a core protein. The products can be used for treating autoimmune diseases, cancer and inflammation. In particular, the core protein may be an IkappaB regulator protein for the treatment of inflammatory bowel disease, or a nitroreductase protein which can activate nitro drugs in enzyme/prodrug therapy to treat cancer or other pathological conditions. The fusion proteins can also be used in diagnostic methods such as in vivo imaging. (Updated on 27-NUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion proteins resistant to proteolytic degradation - comprising a core protein with a stabilising polypeptide comprising a peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single nucleotide polymorphism; SNP; single nucleotide primer extension;
             Pusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; lkappab regulator protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therzapy; prodrug therapy; protease; cancer; pathological condition; minimal motif; PCR primer; ss.
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97US-0048945P.
                                                                                                                                                                                                                                                                     97WO-IB001508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        containing glycine repeats.
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                                                                                                                                                   Human herpesvirus 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-312463/27.
                                                                                                                                                                                                                                                                                                                                                                  (MASU/) MASUCCI M G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                           WO9822577-A1
                                                                                                                                                                                                                                                                     17-NOV-1997;
                                                                                                                                                                                                                                                                                                                          25-JUN-1997;
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                                                                                                                                                                                                                                                                                                         15-NOV-1996;
                                                                                                                                                                                                                               28-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                        Magucci MG;
                                                                                                                                 Synthetic
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ID AAH3
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Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the includes kits for determining the presence or absence of a SNP, using the coligonucleotides of the invention. The PCR primers are used to amplify a SNP farming the presence of a SNP, using the coligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insiphidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecte and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune craneze, including, rheumatoid arthritis, multiple sclerosis, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
               Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a PCR primer specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.8; DB 1; Length 24;
Pred. No. 9.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human microarray DNA oligonucleotide SEQ ID NO 70102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24 BP; 1 A; 0 C; 11 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for a human SNP containing DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 60; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2318 TGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                     (ORCH-) ORCHID BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rerererarerererer
                                                                                                                                                                                                                                                    13-OCT-2000; 2000WO-US028436.
                                                                                                                                                                                                                                                                                              99US-0160096P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                               Pohl
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-290930/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           paternity analysis.
                                                                                                                                                                                                                                                                                                                                                                               Picoult-Newburg L,
                                                                                                                                                                   WO200129262-A2
                                                                                                                                                                                                                                                                                            15-OCT-1999;
                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid sample.
                                                                                                                                                                                                           26-APR-2001
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                    The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in bybridisation to a DNA library, in analysis of genetic variation or in bybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring can expression levels, identifying bialplelic markers or polymorphisms, or family members of a gene and a gross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotbloc hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                              New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
EST; 88; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; resequence, genotype; disease; forensic; paternity testing; single nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.8; DB 1; Length 25;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human single nucleotide polymorphism (SNP) FGFR3 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 BP; 7 A; 4 C; 4 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 70102; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2783 AACTAGTGTACATTTCTATAA 2803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAAGTGTAGATTTCTATAA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI30472 standard; DNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%;
                                                                                                                                                                                16-MAR-2001; 2001US-0276759P
                                                                                                                                                   15-MAR-2002; 2002US-00098263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                            (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                       WPI; 2003-567953/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 19; Conserv
                                                                                         JS2003104410-A1
                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2001
                                                                                                                                                                                                                                          Mittmann MP;
                                                                                                                       05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
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AAI3047
IID AAX
XX
AC AA
AC AA
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DT 18
DD HU
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KW Sii
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The invention relates to the identification of nucleic acid molecules (AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zebrafiah; PTHIR receptor; PTH3R receptor; diagnosia; cancer; parathyroid hormone type 3 receptor; PCR primer; sa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                      /standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zebrafish PTH1R receptor coding sequence PCR primer For TM3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 17.8; DB 1; Length 31; larity 90.5%; Pred. No. 1.2e+03; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31 BP; 3 A; 11 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                      (WHED ), WHITEHEAD INST BIOMEDICAL RES.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3414 AGGGCCCCTGTGCAG 3434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lander ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 87; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 AGGGGCCGCCCTGCGTGCAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                  replace (16, T)
                                                                                                                                                                                                                                                                                                                            07-MAR-2000; 2000US-0187510P.
22-MAY-2000; 2000US-0206129P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US011883
                                                                                                                                                                                                                                                                    07-MAR-2001; 2001WO-US007268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA30842 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cargill M, Ireland JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-522952/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           particular genotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 19; Conserv
                                                                                                                                                 WO200166800-A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200032771-A1
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29-AUG-2000
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                                                                                                                                                                                                            13-SEP-2001
                               Variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA30842;
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PTH3R

New nucleic acids encoding parathyroid hormone receptors PTH1R and useful for treating diseases or disorders associated with impaired receptor functions comprises a specific nucleotide sequence.

98US-0110467P

30-NOV-1998;

Jueppner H, Rubin DA;

(JUEP/) JUEPPNER H. (RUBI/) RUBIN D A. WPI; 2000-412323/35.

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This sequence represents a PCR primer used to isolate DNA encoding the parathyroid hormone receptor type 1 (PTHIR) receptor protein of the invention. The invention also relates to a PTHIR receptor protein.

Antagonists of PTHIR or PTHIR can be used for the treatment of diseases associated with an increase in PTHIR or PTHIR activity, respectively. The peptides are used for diagnosis or prognosis of diseases and disorders associated with PTHIR or PTHIR, such as cancer. The polypeptides can be used as a molecular weight markers on sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or on molecular sieve polyacrylamide gel electrophoresis (SDS-PAGE) gels, or on molecular sieve polyacrylamide gel electrophoresis (SDS-PAGE) gels, or on molecular sieve polyacrylamide gel electrophoresis of such period monoclonal antibodies, that bind specifically to a polypeptide and poptides are useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide. The peptides are useful during diagnosis of diseases and disorders in mammals involving PTHIR or PTHIR sequence and/or expression. Mutations that affect to PTHIR sequence and/or expression levels of PTHIR or PTHIR curlogical nature. The nucleic acid molecules are valuable for chromosomes is an important first seep in correlating those sequences of the design of the discussion of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                  Novel zebrafish parathyroid hormone/parathyroid hormone related peptide receptor 3 and isolated nucleic acid encoding zebrafish parathyroid hormone receptor 1 for treating disorders associated with receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zebrafish; PTH1R; parathyroid hormone type-1 receptor;
developmental disorder; physiological disorder; neurological disorder;
PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 17.6; DB 1; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 5 A; 8 C; 2 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1e+03;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zebrafish PTHIR cDNA PCR primer For TM3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1344 GTCTGAGATGGAGATGAAGAT 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 GTCTGAGAAGAAGGTCATGAAGAT 1
                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 43; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA48458 standard; DNA; 24 BP.
                      98US-0110467P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity 83.3%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                          Jueppner H, Rubin DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-SEP-2003 (revised)
27-OCT-2000 (first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standardise OS field)
                                                                                                                                                                                      WPI; 2000-412319/35.
                                                                  (JUEP/) JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                           (RUBI/) RUBIN D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200032775-A1.
                      30-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio
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                                                                                                                                                                                                                                                                                                          function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA48458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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The present sequence is a PCR primer for the parathyroid hormone type-1 receptor (PTH1R) gene from the zebrafish. It was used to amplify and isolate cDNA encoding this protein. The gene and protein can be used to detect diseases in man where the receptor is either overexpressed or underexpressed, and they can be used to treat these diseases, which may be developmental, physiological or neurological disorders. They can also be used to identify agonists and antagonists which can be used in a similar manner. In addition, the gene can be used for chromosome identification. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; molecular chaperone 18; cytostatic; virucidal; immunomodulatory;
antiinflammatory; haemostatic; nootropic; neuroprotective; anti-HIV;
malignant neoplasm; HIV; infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide for the diagnosis and treatment of malignant neoplasm, hemopathy, HIV infection, immunological diseases and inflammations, comprises the human molecular chaperone 18 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 17.6; DB 1; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Seguence 24 BP; 5 A; 8 C; 2 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human molecular chaperone 18 PCR primer 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1344 GTCTGAGATGGAGATGAAGAT 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunological disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 46; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 12; 36pp; Chinese.
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                                                                                                                                                                                                                                                                                                                                                                                                                             83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI68170 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 83.3
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-611637/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200173072-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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8X44X1X8X111X8X2CCCCCCC
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ABA05945;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of human phosphoesterase 30. The sequences can be used in the treatment of cancer, nosohaemia, HIV infection, immunological diseases and inflammation. The present sequence is a PCR primer for the coding sequence of the invention
The invention relates to human molecular chaperone 18 with cytostatic, virucidal, immunomodulatory, antiinflammatory, haemostatic, nootropic, neuroprotective and anti-HIV activity. The polympeptide and encoded polymucleotide are applicable in diagnosis and treatment of malignant neoplasm, haemopathy, HIV infection, immunological diseases and various inflammations. The present sequence is that of a PCR primer, useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide-phosphoesterase 30 for treating various diseases, s malignant tumor, nosohemia, human immunodeficiency virus infection, immunological diseases and inflammations.
                                                                                                                                                                                                                                                                                                                                                           Human; phosphoesterase 30; cancer; nosohaemia; HIV infection; immunological disease; inflammation; gene therapy; PCR primer; ss.
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                                                                                                                       Score 17.6; DB 1; Length 24; Pred. No. 1e+03; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                     Human phosphoesterase 30 coding sequence PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24 BP; 5 A; 0 C; 4 G; 15 T; 0 U; 0 Other;
                                                                                                   Sequence 24 BP; 11 A; 2 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 16(Disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3311 TTTTCTTTAGGAGATTTATTTTT 3334
                                                                                                                                                                           2822 GIATATATACATATATATATAAA 2845
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                                                                                                                                                                                         TTTGATTTAGGAAGTTTATTTTT
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                                                                                                                         ch 0.5%;
il Similarity 83.3%;
20; Conservative (
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                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                             Query Match
Best Local Similarity
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                                                                              the invention
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                               22-FEB-2002
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BP.

ABA05945 standard; DNA; 24

RESULT 587

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ABA05945 ID ABA0

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                                                                      25; cancer; haemopathy; HIV; infection; enzyme; virus; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bpidermal growth factor receptor; tyrosine kinase receptor inhibitor;
epidermal growth factor receptor inhibitor; EGFR; mammary tumour;
cytostatic; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human endomannosidase 25 and encoding polynucleotide, useful for treating cancer, hemopathy and human immunodeficiency virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human epidermal growth factor receptor PCR primer SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.5%; Score 17.6; DB 1; Length 24; Best Local Similarity 83.3%; Pred. No. 1e+03; Matches 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24 BP; 6 A; 1 C; 4 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 18 (Disclosure); 32pp; Chinese.
                                  Human endomannosidase 25 PCR primer SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3314 TCTTTAGGAGATTTATTTTGGA 3337
                                                                                                                                                                                                                                                                                                                                             (BODE-) BODE GENE DEV CO LTD SHANGHAI
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                                                                                                                                                                                                                                                                                                        24-MAR-2000; 2000CN-00115107.
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                                                                               endomannosidase
                                                                                                  human immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                          Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
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                                                                                                                                           Homo sapiens
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                                                                                                                                                                                    CN1315551-A.
06-MAR-2002
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30-NOV-1998;
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अस्टिएकाम् Match
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Matches
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                                                                                                                                                                                                            RESULT
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                                                                         Composition for treating mammary tumors associated with aberrant tyrosine kinase receptor activity in nonhuman animals, comprises one or more substances that inhibit the aberrant activity.
                                                                                                                                                     tumours associated with aberrant tyrosine kinase receptor activity in nonhuman animals. (C) comprises one or more substances that inhibit the aberrant tyrosine kinase receptor activity. (C) has cytostacic activity. (C) can be used as a tyrosine kinase receptor inhibitor, and an epidermal growth factor receptor (BGFR) inhibitor. (C) is especially useful for treating canine mammary tumours. The present sequence represents a PCR primer for human EGFR, which is used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes an isolated nucleic acid (I) comprising a polynucleotide having a nucleotide sequence chosen from nucleotide sequence encoding a parathyroid hormone (PTH)/PTH-related peptide (PfHrP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parathyroid hormone; PTH; PTH-related peptide; PfHrP;
parathyroid hormone receptor; PTHR; chromosome identification; zebrafish;
PTH1R; receptor; ss; primer; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Full length zebrafish parathyroid hormone receptor PTHIR primer ForTM3
                                                                                                                                             mammary
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid comprising a polynucleotide encoding parathyroid hormone/parathyroid hormone-related peptide receptor, useful for chromosome identification.
                                                                                                                                           The present invention describes a composition (C) for treating
                                                                                                                                                                                                                                                                                                  ö
                                Kleemann
                                                                                                                                                                                                                                                                         Score 17.6; DB 1; Length 24;
Pred. No. 1e+03;
0; Mismatches 4; Indels
                                Bette P,
                                                                                                                                                                                                                                                      Sequence 24 BP; 6 A; 4 C; 7 G; 7 T; 0 U; 0 Other;
                                Van Meel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; SEQ ID NO 17; 52pp; English
                                                                                                                                                                                                                                                                                                                      1945 TACATGATCATGCGGGAGTGCTGG 1968
          (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
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                                                                                                                      Example 1; Page 21; 37pp; English
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                                F, Brandstetter I,
                                                                                                                                                                                                                                                                                                                                                                                                 ADC42320 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rubin DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-754511/71.
                                                    WPI; 2003-365180/35
                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jueppner H,
                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danio rerio
                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                                                                                                                                        ADC42320;
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                              Hilberg
                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zebrafish; parathyroid hormone; PTH; parathyroid hormone related protein; PTHPP; parathyroid hormone related protein receptor; PTHIR; PTHSR; diagnosis; prognosis; pharmaceutical composition; chromosome assay; RACE-PCR; rapid amplification of cDNA end; primer; ss.
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receptor (PTHIR receptor) having a fully defined sequence of 536 amino acids as given in the specification, PTHIR receptor, mature PTHIR receptor, PTHIR extracellular or transmembrane domain, and their complement. (I) is useful for diagnosing and treating decrease in the standard or normal level of PTHIR receptor activity in an individual, for chromosome identification. This sequence represents a primer used ioslate the full length cDNA encoding zebrafish PTHIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New parathyroid hormone receptors designated PTHIR and PTHIR isolated from zebrafish are useful to diagnose and treat parathyroid hormone receptor-related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 17.6; DB 1; Length 24; 33.3%; Pred. No. 1e+03; Ive 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zebrafish PTH1R cDNA amplifying For TM3 RACE-PCR primer.
                                                                                                                                                                                                                                                                                                          Sequence 24 BP; 5 A; 8 C; 2 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24 BP; 5 A; 8 C; 2 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; SEQ ID NO 17; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1344 GTCTGAGATGGAGATGATGAAGAT 1367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH61074 standard; DNA; 24 BP
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99US-00449632
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3%;
Marches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2004 (first entry)
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The invention comprises isolated human gene sequences and PCR primer sequences which can be used to detect single nucleotide polymorphisms (SNPs). The DNA sequences of the invention are useful for detecting SNPs existing in human genes and for the diagnosis of human disease. The present DNA sequence represents a human gene PCR primer of the invention.
                                                                                                                                                                                                                                                                                                                                                        Polynucleotide for detecting single nucleotide polymorphisms existing in human gene, contains isolated human gene having specified sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams syndrome cognitive profile; WSCP; cognition; LIM-kinase 1;
LIMK1 gene; supra-vascular aortic stenosis; protein kinase; human; PCR;
primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 0.5%; Score 17.6; DB 1; Length 24; l. Similarity 83.3%; Pred. No. 1e+03; 20; Conservative 0; Mismatches 4; Indel8
                                                                                                                   human; gene sequence; single nucleotide polymorphism; SNP; disease diagnosis; ss; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 1 A; 2 C; 9 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 1733; 529pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2329 GTGTGCGTGTGTGTGTGTGTGC 2352
                                                                                                                                                                                                                                                                                                     (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Grgrgrgrgrgrgrgrargrrrc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV05314 standard; DNA; 25 BP
           ADH93896 standard; DNA; 24 BP
                                                                                                                                                                                                                                             11-DEC-2001; 2001JP-00377637.
                                                                                                                                                                                                                                                                           11-DEC-2001; 2001JP-00377637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinase domain 3' PCR primer
                                                                                            Human gene PCR primer #741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                 WPI; 2003-819215/77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                            JP2003174883-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9801740-A2
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-1998
                                                                  22-APR-2004
                                                                                                                                                                                                                      24-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV05314;
                                     ADH93896;
ADH93896
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This oligonucleotide was designed to amplify the region of homology in the kinase domains of PDGF receptor, HER2, HER3, FGF-FLG, FGF-BEK, insulin receptor and IRR. It was used with another kinase homology domain—based primer (see AAV05313) in the amplification of human LIM-kinase 1 (LIMK1) sequences. The LIMK1 gene is composed of 16 exons (see AAV05315 and AAT95599-T99629) and is located 15.4 kb 3' of elastin in chromosome 7. It encodes a novel protein kinase (see AAM46576). Williams syndrome cognitive profile (WSCP) is detected by determining zygosity of the LIMK1 locus, with hemizygosity being indicative of impaired visuo-spatial constructive cognition. Chromosome 7 deletion analysis allows discrimination between WSCP, SVAS (supra-vascular aortic stenosis) and Williams syndrome
                                                                                                                                                      Diagnosing Williams syndrome cognitive profile from hemi-zygosity of LIMK1 - gene on chromosome 7 encoding new kinase, allowing differentiation from classic Williams syndrome and supra-vascular aortic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid encoding an isoform of human pregnancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 4 A; 10 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.6; DB 1;
Pred. No. 1.1e+03;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PAPP-Ea associated 25-mer SEQ ID 1206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1744 CCCGTGAAGTGGATGGCGCCTGAG 1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 ccacrcaacrecarecreces 1
                                                                                                                                                                                                                                        Example 3; Page 22; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-2000; 2000US-0207456P
97WO-US011687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2001; 2001US-00827998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match ( 0.5%;
Best Local Similarity 83.3%;
Matches 20; Conservative
                                                             (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABS75680 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-DEC-2002 (first entry)
                                                                                              Morris CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-697817/75.
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(SHAN/) SHANNON M E.
                                                                                                                              WPI; 1998-101185/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002102252-A1.
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 07-JUL-1997;
                                 10-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-2002
                                                                                                Keating MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS75680;
                                                                                                                                                                                                             stenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 593
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the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention

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                                                      This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, hPAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
                                                                                                                                                                                                                                                                                                                                         Gaps
associated plasma protein E, for preventing or aborting pregnancy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding an isoform of human pregnancy
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                         0.5%; Score 17.6; DB 1; Length 25;
                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                         Sequence 25 BP; 3 A; 0 C; 9 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                      1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PAPP-Ea associated 25-mer SEQ ID 1205.
                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                    2321 GTGTGTGTGTGCGTGTGTGTGT 2344
                                                                                                                                                                                                                                                                                                                                                                                                   25
                              Example 2; Page 233; 353pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       GTGTGTTTTGTGAGTGTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS75679 standard; DNA; 25 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2001; 2001US-00827998
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                                                                                                                                                                                                                                                                                                                      83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                      20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GUYY/) GU Y.
(SHAN/) SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-697817/75.
                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gu Y, Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002102252-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 594
ABS75679
                                                                                                                                                                                                                                                                                                                                        Matches
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This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein B. hPAPPP. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess

associated plasma protein E, for preventing or aborting pregnancy.

Example 2; Page 233; 353pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; 8s.
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                                                                                                                                                                                                                                                                                                                    Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                         Score 17.6; DB 1; Length
Pred. No. 1.1e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antenatally. This sequence represents an oligomer used
human PAPP-E genes described in the disclosure of the
                                                                                                                                                                                         Sequence 25 BP; 3 A; 0 C; 10 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 BP; 3 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
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0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PAPP-Ea associated 25-mer SEQ ID 1204.
                                                                                                                                                                                                                                                                                                                                                                           2319 GTGTGTGTGTGTGTGTGTGT 2342
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGTGTGTTTGTGAGTGTGTAT
                                                                                                                                                                                                                                                   0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2001; 2001US-00827998
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABS75678 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GUYY/) GU Y.
(SHAN/) SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-697817/75.
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 20, Conserv
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nes 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 595
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Matches
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11D ABS776

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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                   BST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
          Human microarray DNA oligonucleotide SEQ ID NO 87311
                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 87311; 9pp; English
                                                                                                                                                                          15-MAR-2002; 2002US-00098263.
                                                                                                                                                                                                     16-MAR-2001; 2001US-0276759P.
                                                                   cross-species comparison.
                                                                                                                                                                                                                                 (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                       WPI; 2003-567953/53.
                                                                                                                        US2003104410-A1.
                                                                                                Homo sapiens
                                                                                                                                                                                                                                                             Mittmann MP;
                                                                                                                                                   05-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, hpAPP-E. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the artibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence represents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention
                                                                                                                                                                                                        PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis; dysgenetic pregnancy; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 0.5%; Score 17.6; DB 1; Length 25; al Similarity 83.3%; Pred. No. 1.1e+03; 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25 BP; 3 A; 0 C; 9 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                 Human PAPP-Ea associated 25-mer SEQ ID 1208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2322 TGTGTGTGTGTGCGTGTGTGTGTG 2345
     2319 GIGIGIGIGIGIGIGIGI 2342
                    Example 2; Page 234; 353pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-2001; 2001US-00827998.
                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000; 2000US-0207456P.
                                                                                                  ABS75682 standard; DNA; 25
                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       (GUYY/) GU Y.
(SHAN/) SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-697817/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gu Y, Shannon ME;
                                                                                                                                                                                                                                                                                              JS2002102252-A1.
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                         01-AUG-2002.
                                                                                                                                                         27-DEC-2002
                                                                                                                              ABS75682;
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

CC perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation to a DNA library, of at least one target sequence. The method of analysis comprises

CC compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises

CC probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acids further comprises in Southern, Northern or dotor probes is useful in in situ hybridisation, in Southern, Northern or dotor mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions of any sene, in mapping the 5' termini of mRNA molecules by containing segments of DNA that have been consolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarary. Note: The sequence cut at for this patent can also be obtained in electronic format directly from USPTO at sequence. Thun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.5%; Score 17.6; DB 1; Length 25; 33.3%; Pred. No. 1.1e+03; Ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human microarray DNA oligonucleotide SEQ ID NO 80270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 4 A; 9 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 CGGATGGACAAGAAGCTGCTGGCC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cegaredaceadaadarectreac 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 83.3%;
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACI80279 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKAKAKA
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ACI87320 standard; DNA; 25

14-OCT-2003 (first entry)

ACI87320;

RESULT 597
ACI87320/c
ID ACI873;
XX
AC ACI873;
XX
DT 14-OCT

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acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises which is acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a grass-appeales comparison. Bach of the nucleic acids further comprises a grass-appeales comparison. Bach of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a grass-appeales or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence of the form the patent can also be obtained in electronic format directly form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention discloses a microarray comprising a plurality of nucleic
                     ss; probe; expressed sequence tag; microarray; gene expression; ic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25 BP; 4 A; 8 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from USPTO at segdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 80270; 9pp; English.
                                                                                                                                                                                                                                               15-MAR-2002; 2002US-00098263
                                                                                                                                                                                                                                                                                            16-MAR-2001; 2001US-0276759P
                                                                 cross-species comparison
                                                                                                                                                                                                                                                                                                                                      (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-567953/53.
                                                                                                                                                        US2003104410-A1.
                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     Mittmann MP;
                                                                                                                                                                                                   05-JUN-2003.
                     EST; 88;
genetic .
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ACH58465 standard; DNA; 25
                                                                                                                                                                                                                    16-OCT-2003 (first entry)
                                                                                                                                                                                       ACH58465;
                                                                                                                               RESULT 600
                                                                                                                                              ACH58465,
                                                                                     엄
                                                          ð
                                                                                                                                                              ö
                               Gaps
                                                                                                                                                                                                                                                                             Gene expression analysis; array; hybridisation; genetic variation;
                                                                                                                                                                                                                                               DNA target sequence #3326 useful in array for genetic analyses.
                               ö
0.5%; Score 17.6; DB 1; Length 25; 13.3%; Pred. No. 1.1e+03; ve 0; Mismatches 4; Indels
                                                          2569 CACGGGACATCACAGGGTGCGCTC 2592
                                                                                   cacedeaceacrcaeeerecere 1
                83.3%;
                                                                                                                                                              ACH54190 standard; DNA; 25
                                                                                                                                                                                                                    (first entry)
              Local Similarity 83.3 tes 20; Conservative
                                                                                                                                                                                                                    16-OCT-2003
                                                                                     24
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Query Match

Matches

ઠ 엄 ACH54190;

599

RESULT

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complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive mucleotides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, sense mismatch, antisense match or antisense mismatch oligonucleotides. The probes may be used in an array comprising at least 10 distinct.

The probes may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic variations, and in hybridising tag-labelled compounds. The probes are useful in in situ hybridisations, in screening cDNA or genomic libraries or useful in in situ hybridisations, in screening segments of DNA constructions subclones) for additional clones containing segments of DNA conserved subclones) for additional clones containing segments of DNA conserved subclones) for additional clones containing segments of the hard have been previously; solated and sequenced, in southern, northern, or dot-blot hybridisation of genomic DNA to identify or detect the sequence of any gene or detect specific mutations in any gene, and in nucleic acid sequences of the invention of nucleic acid sequences of the invention of nucleic acid sequences of the invention of nucleic acid sequences of the arage collection of any sequences of the invention of nucleic acid sequence data for this patent was obtained in electronic format the sequence data for this patent was obtained in electronic format the sequence and sequences of the invention of the sequence of any set e at sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New probe array useful e.g. for monitoring gene expression levels, for analyzing genetic variations, or for hybridizing tag-labeled compounds. comprises multiple nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
tag-labelled compound; gene family; in situ hybridisation; library screening; Southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection; target sequence; probe; PCR; primer; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene expression analysis; array; hybridisation; genetic variation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to nucleic acid sequences that are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA target sequence #7601 useful in array for genetic analyses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 17.6; DB 1; Length 25; 33.3%; Pred. No. 1.1e+03; ve 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 2 A; 7 C; 7 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3677 AGGGTGTCTTCTTGGGGCCCA 3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 3326; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ACGGICGICITCTICGGICCIA 25
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                                                                                                                                                                                                                                                                                            08-AUG-2002; 2002US-00215112
                                                                                                                                                                                                                                                                                                                                                08-AUG-2001; 2001US-0311040P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.5%;
Best Local Similarity 83.3%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-576608/54.
                                                                                                                                                                                                                                                                                                                                                                                                  (MITT/) MITTMANN M.
                                                                                                                                                                                       US2003082596-A1.
                                                                                                                                   Unidentified
                                                                                                                                                                                                                                        01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mittmann M;
        %XCCCCCCCCCCCCCCCCCX
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genetic alteration; pharmacogenetic reaction; genotyping; polymorphism; gene expression profiling.

single multiplex polymerase chain reaction; multifactorial disease;

vivlemore401-10.rng

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The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises such as gene expression analysis. Each probe mucle consecutive nucleotides from at least one of 14336 nucleotide sequences defined in the patent, or their perfect sense match, antisense match or antisense mismatch, antisense match or sense match or probes may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic variations, and in hybridisations, in screening compounds The probes are useful for identifying family members of a gene. The probes are also useful in in situ hybridisations, in screening cDNA or genomic libraries (or derived subclones) for additional clones containing segments of DNA that have been previously isolated and sequenced, in Southern, northern, or dot-blot hybridisation of genomic DNA to identify or detect the mapping the 5' termini of genomic DNA to identify or detect the mapping the 5' termini of mRNA molecules by primer extensions. The mapping the 5' termini of mRNA molecules by primer extensions. The mapping the 5' termini of mRNA molecules by primer extensions.

The invention provides a large collection of mcleic acid sequences of the invention were data genes with a wide range of analytical uses.

ACH50865-ACH65260 represent the target sequences of the invention. Note:

The sequence data gone spatent was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   directly from the USPTO web site at segdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New probe array useful e.g. for monitoring gene expression levels, for analyzing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.
tag-labelled compound, gene family, in situ hybridisation, library screening, Southern hybridisation; northern hybridisation; dot-blot hybridisation, gene sequence; mutation detection; target sequence; probe; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.5%; Score 17.6; DB 1; Length 25; Best Local Similarity 83.3%; Pred. No. 1.1e+03; Matches 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 BP; 9 A; 7 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3677 AGGGTGGTCTTCTTGGGGCCCA 3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 7601; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 ACGGTCGTCTTTTTTGGGTCCTA 1
                                                                                                                                                                                                                                                          08-AUG-2002; 2002US-00215112.
                                                                                                                                                                                                                                                                                                       08-AUG-2001; 2001US-0311040P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO10905 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-576608/54.
                                                                                                                                                                                                                                                                                                                                                 (MITT/) MITTMANN M.
                                                                                                                                                                     US2003082596-A1.
                                                                                                                          Unidentified.
                                                                                                                                                                                                                  01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                 Mittmann M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 601
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Designing primers for simultaneous amplification of target DNA fragments in a single multiplex polymerase chain reaction, for high throughput multiplex DNA sequence amplification, comprises aligning two primers.

Disclosure; Page 34; 120pp; English.

(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

WPI; 2004-340914/31.

Li J;

Li H,

07-OCT-2003; 2003WO-US031874 07-OCT-2002; 2002US-0417009P

WO2004033649-A2.

Synthetic

22-APR-2004

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Gaps
                             ;
0.5%; Score 17.6; DB 1; Length 25; 33.3%; Pred. No. 1.1e+03;
                             4; Indels
                                                                                                                                                                                                                                                                      Microsatellite sequence from clone TGLA147.
                             0; Mismatches
                                                              3361 ATACAAATTCTTCTAATTGCTGTG 3384
                                                                                         1 Aracacarrrrrrrrrrardrrardr 24
                                                                                                                                                                     AAQ33728 standard; DNA; 19 BP.
                  Local Similarity 83.3%;
les 20; Conservative
                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                 25-MAR-2003
02-FEB-1993
                                                                                                                                                                                                    AAQ33728;
       Query Match
                                                                                                                                        RESULT 602
                                     Matches
                                                                                                                                                          AAQ33728
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Gaps

ss; primer; simultaneous amplification;

Single multiplex PCR primer #277.

15-JUL-2004 (first entry)

ADO10905;

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The invention relates to a method of designing primers for simultaneous amplification of target DNA fragments in a single multiplex polymerase chain reaction by aligning a first primer and a second primer. The method comprises: (a) aligning a first primer and a second primer; and (b) comprises: (a) aligning a first primer and a second primer; and (b) contain four or more bases that are perfectly matching to the 3' end does not contain four or more bases that are perfectly matching contain four or more bases that are perfectly matching contain some no mismatch to the 3' end sequence of the first primer at its 3' end does not contain six or second primer, the first primer at its 3' end does not contain six or correct bases that are perfectly matching to a sequence anywhere of the first primer or the second primer, and the first primer or the second primer. The method is useful for designing primer or the second contain eleven or more bases that are perfectly matching except one mismatch to a sequence anywhere of the first primer or the second primer. The method is useful for designing primers for simultaneous amplification of target DNA fragments in a single multiplex polymerase contain reaction. It is also useful in the identification of multiple genes contain the primer or the denotyping that the primer or the denotyping that the primer or the denotyping that the denotyping that the process of the denotyping that the denotyping the denotyping the designing primer describers that the denotyping that the denotyping that the denotyping that the denotyping the designing primer describers that the denotyping that the denotyping that the denotyping that the denotyping the designing primer describers the designing primer describers that the denotyping the designing the describers the describers that the denotyping the describers the describers the describers the describers the den
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alterations, the studies in pharmacogenetic reactions, the genotyping genetic polymorphisms in a large population, the gene expression profiling in various samples and high throughput genotyping technologies. This sequence corresponds to an example of a primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 BP; 6 A; 4 C; 3 G; 12 T; 0 U; 0 Other;
AXXBXBXBXB
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The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. The sequences AAT66084-T66107 represent repeat sequences of low informativeness found in specific human genes. This repeat sequence is found in the haemoglobin gamma G gene located at chromosomal position 11p15.5. The sequence is amplified by primers AAT66094-5. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                                                                       Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n-using novel nucleic acid mols. as primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a hairpin or hammerhead ribozyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 17.4; DB 1; Length 19; 94.7%; Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 BP; 10 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robbins JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                 Example 9; Col 59-60; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclin B1 ribozyme binding site #135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 98; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2318 TGTGTGTGTGTGTGCGT 2336
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                 89US-00341562.
91US-00754351.
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                                                                               (MARS-) MARSHFIELD CLINIC.
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                                                                                                                                                            WPI; 1997-042299/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-412314/35.
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tes 18; Conserv
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                     21-APR-1989;
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                                    05-SEP-1991;
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                                                                                                                        Weber JL
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 by with an (ACIIs and a (TCI)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100,000. The sequence information of for ca. 230 such bovine microsatellites is summarised in the sequence information of specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the microsatellite (using the program OFTTRRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
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Pred. No. 8.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat sequence found in the haemoglobin gamma G gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                              Table 7; Page 221; 517pp; English
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(first entry)
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                                                                                                                                                                                                                                                                   Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                       WPI; 1992-284684/34.
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                                                                                                                                                                                                                            (GENM-) GENMARK
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                                                                                                                                                                                 15-JAN-1991;
                                                         WO9213102-A1
                                                                                                                                         15-JAN-1992;
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18-JUN-1997
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                                                                                                  06-AUG-1992
                     Bos taurus.
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Matches

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Gaps

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This invention describes a novel method for obtaining DNA of unknown sequence flanking a single site of known sequence involves single site of amplification of circular DNA template flanking a trarget DNA of known camplification of circular by the sequence using a polymerase having strand displacement capability. The method is used for obtaining a particular target DNA sequence that can be useful as templates that contain entire simple sequence repeat (SSR) alleles for amplification (SSA) procedures e.g. PCR or can be employed as molecular markers, e.g. in distinguishing between species, strains or varieties within species or identifying the presence of a disease condition. It also provides a marker for use in areas such as import and export regulation, variety and ecotype identification, marker condition. It created a linear DNA molecule containing two target sequences in sequences in sequences within a single stranded DNA template and flanking regions for these target sequences. It can also be used for e.g. for cloning cDNA or genomic DNA which flanks any known short target sequence. The present method can also be used to obtain entire coding regions of the present method can also be used to obtain entire coding regions of the present method can also be used to obtain entire coding regions of the present method can also be used to obtain entire coding regions of the present method can also be used to obtain entire coding regions of the present method can also be used to obtain entire coding regions of the present method son also be used to obtain entire coding regions of the present method son also be used to obtain entire coding regions of the present method son also be used to obtain entire coding regions of the present method son also be used to obtain entire coding a degenerate
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designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obtaining unknown DNA sequence flanking a single known sequence for use as PCR templates, involves single site amplification with polymerase having strand displacement capability.
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simple sequence repeat; SSR; single site amplification; SSA; disease;
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                                                                                                                                                                                                                                                Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSA primer 3 for amplifying A. thaliana and Z. mays DNA
                                                                                                                                                                                                      Sequence 19 BP; 2 A; 8 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  2550 TCGGCCTCTGCCTTTGCAC 2568
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nes 18; Conservative
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using a polymerase having strand displacement capability which can synthesize up to 10 kb fragments. This is especially useful for obtaining plant genes which are usually less than 10 kb in length. The method allows accelerated development of high resolution DNA markers that may be used for fingerprinting, mapping etc., using small amounts of tissue (less than 1 mug). It also allows the production of a PCR template with knowledge of only one region of target DNA sequence, the size of which is regulated only by the primer design. The present method also eliminates genomic DNA library preparation and screening which are the most time consuming steps, typically requiring no less than three months, with total time for target DNA development being between 4.6 months. AA289469-289474 represent primers used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Obtaining unknown DNA sequence flanking a single known sequence for use as PCR templates, involves single site amplification with polymerase having strand displacement capability.
nucleic acid sequence derived from amino acid sequence back translation
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Pred. No. 8.2e+02;
0; Mismatches 1; Indels
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Best Local Similarity 94.7
Matches 18; Conservative
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trom one sequence within a single stranded DNA template and flanking concessions for these target sequences. It can also be used for e.g. for coloning cDNA or genomic DNA which flanks any known short target sequence. The present method can also be used to obtain entire coding regions of genes based upon a known nucleic acid sequence or by using a degenerate nucleic acid sequence derived from amino acid sequence back translation using a polymerase having strand displacement capability which can using a polymerase having strand displacement capability which can using a polymerase having strand displacement capability which can using a polymerase having strand displacement capability which can using a polymerase which are usually less than 10 kb in length. The method also plant genes which are usually less than 10 kb in length. The method also plant genes which are usually apply the production DNA markers that may be used for fingerprinting, mapping etc., using small amounts of tissue the finally. It also allows the production of a PCR template with knowledge of only one region of target DNA sequence, the size of which is regulated only by the primer design. The present method also eliminates genomic DNA library preparation and screening which are the most time consuming steps, typically requiring no less than three months, with the total time for target DNA development being between 4-6 months, with the total time for target DNA development being between 4-6 months, with 85888888888888888888888888888888

Sequence 19 BP; 0 A; 0 C; 10 G; 9 T; 0 U; 0 Other;

Gaps . 0 Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02; 0; Mismatches 1; Indels 2315 GTCTGTGTGTGTGTGTG 2333 Grererererererere 0.5%; Query Match Best Local Similarity 94.7 Matches 18; Conservative 셤

AAC66739 standard; DNA; 19 BP (first entry) 15-FEB-2001 AAC66739; RESULT 607

Heterologous insert sequence #2.

Probe; cytostatic, antiviral; gene therapy; ss.

Unidentified

WO200063365-A1

26-OCT-2000.

21-APR-2000; 2000WO-US010909.

99US-0130345P 21-APR-1999;

(PANG-) PANGENE CORP.

Zarling D; Belotserkovskii B, Reddy G,

WPI; 2000-647516/62.

Composition for modulating transcription or replication of a pre-selected target sequence and for treating a plant or animal disease, comprises a recombinase and two probes, each containing a homology clamp and an anchoring sequence.

Disclosure, Fig 9, 103pp; English.

The present invention relates to a composition comprising a recombinase and two complementary single stranded probes each containing at least one homology clamp corresponding or complementary to a preselected target nucleic acid sequence and at least one annobring sequence. The present sequence is a heterologous insert sequence used to generate the probes that can be used in the present invention. The composition of the present invention can be used to modulate transcription or replication of a pre-

selected target sequence, treat a disease state of a plant or animal caused by expression of a disease gene, detect a double stranded nucleic acid target sequence, isolate either strand of a double stranded target sequence, isolate either strand of a gene family, produce a transgenic non-human organism or plant, determine the function of a double stranded nucleic acid target sequence and inhibit double stranded nucleic acid target sequence and inhibit composition may be used to produce animal models for genetic defects 8888888888888

Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;

Gaps . 0 Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02; 1; Indels 0; Mismatches Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative

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ઠે 셤 RESULT 608 AAC66738/

AAC66738 standard; DNA; 19 X4X4X8X8X8X8X8X4X4X4X4X4X4X4X6XX0X0X0X0X0X0XX8XX4X4X4X4X4X4X4X4X4X

AAC66738;

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15-FEB-2001 (first entry)

Heterologous insert sequence #1.

Probe; cytostatic; antiviral; gene therapy; ss.

Unidentified.

WO200063365-A1

26-OCT-2000

21-APR-2000; 2000WO-US010909

99US-0130345P 21-APR-1999;

(PANG-) PANGENE CORP.

Zarling Reddy G, Belotserkovskii B,

WPI; 2000-647516/62.

Composition for modulating transcription or replication of a pre-selected target sequence and for treating a plant or animal disease, comprises a recombinase and two probes, each containing a homology clamp and an anchoring sequence.

Disclosure, Fig 9; 103pp; English.

The present invention relates to a composition comprising a recombinase and two complementary single stranded probes each containing at least one thom two complementary single stranded probes each containing at least one and two complementary to a preselected target nucleic acid sequence and at least one anchoring sequence. The present sequence is a heterologous insert sequence used to generate the probes that can be used in the present invention. The composition of the present invention can be used to modulate transcription or replication of a preselected target sequence, treat a disease state of a plant or animal caused by expression of a disease strand of a double stranded nucleic acid target sequence, isolate either strand of a double stranded target sequence, isolate either strand of a member of a gene family, produce a transgenic non-human organism or plant, determine the function of a composition or nucleic acid rotation or branch migration. In addition, the composition may be used to produce animal models for genetic defects

Sequence 19 BP; 10 A; 9 C; 0 G; 0 T; 0 U; 0 Other;

ö Gaps ö Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02; 0; Mismatches 1; Indels 2318 TGTGTGTGTGTGTGCGT 2336 94.78; Query Match
Best Local Similarity 94.7
Matches 18; Conservative 8

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RESULT 609

ВР AAH60968 standard; DNA; 19

AAH60968;

(first entry) LO-SEP-2001 Cyclin B1 ribozyme binding site SEQ ID NO:3392.

Human, ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; porthasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP; matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral actopic dermattitis, actinic keratosis; squamous cell carcinoma; basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss

sapiens. Synthetic. Homo

WO200130362-A2.

03-MAY-2001.

26-OCT-2000; 2000WO-US029500

99US-0161532P. 26-OCT-1999;

(IMMU-) IMMUSOL INC.

Robbins JM, Tritz R;

WPI; 2001-300427/31.

Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.

Example 1; Page 318; 408pp; English.

The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (I) which cleaves RNA encoding a cytokine involved in callozyme (I) which cleaves RNA encoding a cytokine involved in information, matrix metalloproteinase (MMP), cyclin, cell-cycle callozed segment encoding (I) (I) comprising a promoter operably linked to a nucleic acid molecule (II) comprising a promoter operably linked to a concleic acid segment encoding (I) (I) can have antipsoriatic, and nucleic acid segment encoding (I) (I) can have antipsoriatic, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing sear and solved and such as keloid, adhesion and hypertrophic or hypertrophic burn scar. AMR57577 to AMH62099 represent sequences used in the complification of the present invention

Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02; Sequence 19 BP; 2 A; 8 C; 3 G; 6 T; 0 U; 0 Other; 0.5%; g

Gaps ; 0 1; Indels 0; Mismatches Ouery Match 0.5 Best Local Similarity 94.7 Matches 18; Conservative

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RESULT 610 ABK90423

ABK90423 standard; DNA; 19 BP

ABK90423;

05-NOV-2002 (first entry)

Human UGT1al promoter polymorphism (TA)8 repeat region.

Human; ds; UGTLAl; promoter; Gilbert's syndrome; hyperbilirubinaemia; uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome; UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan; TAS-103; xenobiotic.

Homo sapiens.

US6395481-B1.

28-MAY-2002.

99US-00251274. 16-FEB-1999;

99US-00251274

16-FEB-1999;

DEV CORP. (ARCH-) ARCH Di Rienzo A, Iyer L, Ratain MJ;

WPI; 2002-588597/63.

Detecting polymorphisms in uridine diphosphate glucuronosyltransferase gene promoter, useful for optimizing drug dosages for a patient, comprises determining the presence of five thymidine-adenine repeats in the promoter.

Example 6; Col 11; 13pp; English.

The invention relates to detecting (M1) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter by determining the prosence of five thymidine-adenine (TA) repeats in the promoter, where the presence of the five TA repeats correlates with increased expression of the gene. The method is used for detecting polymorphisms in a UGT gene promoter, the preferably a UGT 1 (UGTAI) gene promoter. (M1) is cativity, for optimising draugh desages for a patient, where the drugs cativity, for optimising draugh desages for a patient, where the drugs (e.g. Trinotecan or TAS-103) are glucuronidated by UGT (preferably UGTIAI) and the activity of the drug is effected by its level of glucurodination. The method preferably involves obtaining DNA from an individual, amplifying all or part of a UGT gene promoter (UGTIAI) gene promoter (UGTIAI) gene promoter. Thus the DNA being amplified comprises all or part of in the promoter. Thus the DNA being amplified comprises all or part of the number of TA repeats is determined by gel electrophoresis or by the number of five TA repeats (TA) is, TA repeats chain reaction and consisting of five TA repeats (TA) is, TA repeats or DNA repeats (TA) is, (TA) is also useful for predicting an individual an individual and uGT (preferably continity the number of TA repeats correlates custoff the number of TA repeats correlates

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The invention relates to detecting (MI) polymorphisms in a uridine diphosphate glucuronosyltransferase (UGT) gene promoter by determining the presence of five thymidine-adenine (TA) repeats in the promoter, where the presence of the five TA repeats correlates with increased expression of the gene. The method is used for detecting polymorphisms in a UGT gene promoter, preferably a UGT I (UGT1A1) gene promoter. (MI) is useful for screening individuals for variation in glucuronidation activity, for optimising drug desages for a patient, where the drugs (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably CUT1A1) and the activity of the drug is effected by its level of glucurodination. The method preferably involves obtaining DNA from an individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene promoter) contained in the DNA being amplified comprises all or part of UGT1A1 promoter. Thus the DNA being amplified comprises all or part of UGT1A1 promoter. The DNA is amplified by gel electrophoresis or by sequencing the amplified DNA. The polymorphism comprises an allele
with expression of the UGT gene, and the individuals sensitivity to xenobiotics is effected by glucuronidation activity. The methods preferrably involve determining the presence of five, six or seven TA repeats in the promoter. Defects in glucurodination is associated with Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The present sequence is the UGTIA1 promoter (TA)8 repeat region
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uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
TAS-103; xenobiotic.
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                                                                                                                                                                                                                                                                                                                                        Query Match 0.5%; Score 17.4; DB 1; Length 19; Best Local Similarity 94.7%; Pred. No. 8.2e+02; Matches 18; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                      Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
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LID ABK99

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consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA repeats (TA)7. The promoter has any one of the genotypes (TA)5, (TA)5, (TA)6, (TA)6, (TA)6, (TA)7, (TA)6, (TA)7, (TA)6, (TA)7, (TA)7, (TA)7, (TA)7, (TA)8 or TA)6, (TA)8. (TA)9, (TA)9, (TA)9 or TA)6, (TA)9, (TA)9 or TA)6, (TA)9, (TA)9 or TA)9 or TA
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14.7%; Pred. No. 8.2e+02;
ve 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
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Best Local Similarity 94.7%;
Matches 18; Conservative
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New set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes, useful for genotyping diverse genomes of plant and
                                                                       .nter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
                                                                                                                                                                                                                                                                                                  DNA FINGERPRINTING & DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 19; 60pp; English.
                                                                                                                                                                                                                                   09-JAN-2003; 2003WO-IB000041.
                                                                                                                                                                                                                                                                     08-APR-2002; 2002IN-CH000260.
                (first entry)
                                              ISSR-related PCR primer 4.
                                                                                                animal; Basmati rice; ss
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                                                                                                                                    Inidentified.
              15-JAN-2004
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                                                                                                                                                                                                       16-OCT-2003.
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                                                                                                                                                                                                                                                                                                             Human uridine diphosphate glucuronosyltransferase gene polymorphism #15.
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                         Length 19;
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                     Score 17.4; DB 1;
Pred. No. 8.2e+02;
0; Mismatches 1;
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                                                                                           2827 TATACATATATATAAA 2845
                                                                                                                    TATATATATATATATA 19
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                                                                                                                                                                                                                                                                                     (first entry)
                                                            Conservative
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                          Query Match
Best Local Similarity
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                                                              18;
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double-stranded short interfering nucleic acid; short interfering nucleic acid; siNA; downregulation; vasculation; ancient acid; siNA; downregulation; antiangiogenic; cytostatic; antidiabetic; ophthalmological; antiathritic; antipsoriatic; emphrotropic; gynaecological; angiogenesis-associated condition; cancer; diabetic retinopathy; macular degeneration; neovascular glaucoma; arthritis; psoriasis; endometriosis; angiofibroma;
                                                                                                                                                                                                                                                               ö
The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the ISSR-related PCR primer of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human VEGFR3 short interfering nucleic acid (siNA) SEQ ID NO:1676.
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                                                                                                                                                                                                    O.5%; Score 17.4; DB 1; Length 19; Local Similarity 94.7%; Pred. No. 8.2e+02; Pred. No. 8.2e+02; Pred. O; Mismatcher 1. rad.
                                                                                                                                                                             Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                   2318 TGTGTGTGTGTGTGCGT 2336
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ADD69517 standard; DNA; 19

RESULT 614

ADD69517;

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20-FEB-2002;
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                                                                                                                                                                               28-AUG-2003
                                                                                       Synthetic.
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ID ADF3
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candothelial growth factor receptor (VEGFR) gene. Also described: (1) a siNA that downregulates the VEGF gene; (2) kits for in vitro or in vit
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bort interfering nucleic acid; slNA; downregulation;
vascular endothelial growth factor receptor; VBGFR; antianglogenic;
cytostatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                 double-stranded interfering nucleic acid, useful e.g. for treatment diagnosis of cancer, downregulates the vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes a double-stranded short interfering
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14.2%; Pred. No. 8.2e+02;
ve 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                              Mcswiggen J, Beigelman L, Pavco P;
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                                                                                                                       06-JUN-2002; 2002US-0386782P.
03-JUL-2002; 2002US-0393796P.
29-JUL-2002; 2002US-0399348P.
                                                                                                                                                                           29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0409293P.
                                                                                                                                                                                                                                 04-NOV-2002; 2002US-00287949.
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                                   20-FEB-2003; 2003WO-US005022
                                                                                                        2002WO-US017674
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                                                                                                                                                                                                                                                                                                          (RIBO-) RIBOZYME PHARM INC
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor receptor gene.
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                                                                                                        29-MAY-2002;
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28-AUG-2003
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ID ADF3
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nucleic acid (siMa) that downregalates expression of the vascular endothelial growth factor receptor (VBGFR) gene. Also described: (1) a siNA that downregalates the VEGF gene; (2) kits for in vitro or or in vitro or in vit
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nephrotropic; gynaecological; angiogenesis-associated condition; cancer; diabetic retinopathy; macular degeneration; neovascular glaucoma; arthritis; psoriasis; endometriosis; angiofibroma; polycystic kidney disease; ss.
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09-SEP-2002; 2002US-0409293P-
04-NOV-2002; 2002US-00287949-
27-NOV-2002; 2002US-00306747-
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2002WO-US017674
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(first entry)

12-FEB-2004

ADF37400;

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double-stranded short interfering nucleic acid; short interfering nucleic acid; siNA; downregulation; vascular endothelial growth factor receptor; VEGFR; antiangiogenic; cytosteatic; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; nephrotropic; gynaecological; angiogenesis-associated condition; cancer; diabetic retinopsthy; macular degeneration; neovascular glaucoma; arthritis; psoriasis; endometriosis; angiofibroma; polycystic kidney disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (downregularing) the expression of VEGER genes. The siNA are potentially useful for treating a wide range of angiogenesis-associated conditions, particularly cancers, diabetic retinopathy, macular degeneration, neovascular glaucoma, arthritis, psoriasis, endometriosis, angiofibroma, and polycystic kidney disease. The siNA may also be useful for diagnosis, drug screening, target identification and validation, genetic engineering, studying gene function, and also for gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid (siNA) that downregulates expression of the vascular endothelial growth factor receptor (VEGFR) gene. Also described: (1) a siNA that downregulates the VEGFR) gene, (2) kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or complexes of siNA; (4) vectors that express siNA; and (5) single-stranded siNA with similar properties. The siNAs have antianglogenic, cytostatic, antidiabetic, ophthalmological, antiarbritic, antipsoriatic, nephrotropic and gynaecological activities. The siNA are useful for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double-stranded interfering nucleic acid, useful e.g. for treatment diagnosis of cancer, downregulates the vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes a double-stranded short interfering
                                                                        Human VEGFR3 short interfering nucleic acid (siNA) SEQ ID NO:1689
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06-JUN-2002; 2002US-0386782P.
03-JUL-2002; 2002US-0393796P.
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29-AUG-2002; 2002US-0406784P.
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15-JAN-2003; 2003US-0440129P
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                                                                                                                                                                                                                                                                                           Synthetic
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The present invention describes a double-stranded short interfering nucleic acid (siNh) that downregulates expression of the vascular endothelial growth factor receptor (VEGER) gene. Also described: (1) a sink that downregulates the VEGF gene; (2) kits for in vitro or in vitro and vitro or in vitro or in vitro or in vitro or or vitro or or vitro or or vitro vitro or vit
                                                                                                                                                                                                                                                                                                                                                                                  double-stranded short interfering nucleic acid; short interfering nucleic acid; slAA; downregulation; swearlar endothelial growth factor receptor; VEGFR; antiangiogenic; cytostatic; antidiabetic; ophthalmological; antiatchritic; antipsoriatic; nephrotropic; gynaecological; angiogenesis-associated condition; cancer; alabetic retinopathy; macular degeneration; neovascular glaucoma; arthritis; psoriasis; endometriosis; angiofibroma; polycystic kidney disease; ss.
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                                                                                                                                                                                                                                                                                                                                         Human VEGFR3 short interfering nucleic acid (siNA) SEQ ID NO:1923.
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1843 CTGGGGGCTCCCCGTACC 1861
                              1 CUGGGGCCUCCCCGUACC 19
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2002US-0393796P.
2002US-0399348P.
2002US-0406784P.
2002US-040878P.
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2002WO-US017674.
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2002US-00287949.
2002US-00306747.
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04-NOV-2002;
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Gaps

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0.5%; Score 17.4; DB 1; Length 19; 78.9%; Pred. No. 8.2e+02; tive 3; Mismatches 1; Indels

Query Match 0.5 Best Local Similarity 78.9 Matches 15; Conservative

Sequence. 19 BP; 1 A; 9 C; 6 G; 0 T; 3 U; 0 Other;

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WPI; 2003-679876/64
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11-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                         ADF36527;
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                                                                                                                                                                                                                                                                               RESULT 620
 888888888888888888888888888888888
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                                                                                                                                                                                                                                                                             double-stranded short interfering nucleic acid; short interfering nucleic acid; siNA; downregulation; vascular endothelial growth factor receptor; VEGFR; antiangiogenic; cytostatic; antidabetic; ophthalmological; antiarthritic; antipsoriatic; nephrotropic; gynaecological; angiogenesis-associated condition; cancer; abbetic retinopathy; macular degeneration; neovascular glaucoma; arthritis; psoriasis; endometriosis; angiofibroma; polycystic kidney disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a double-stranded short interfering nucleic acid (siNA) that downregulates expression of the vascular endothelial growth factor receptor (VEGFR) gene. Also described: (1) a siNA that downregulates the VEGF gene; (2) kits for in vitro or in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                double-stranded interfering nucleic acid, useful e.g. for treatment diagnosis of cancer, downregulates the vascular endothelial growth
            (e.g. c
in the
                                                                                              Gaps
                                                                                                                                                                                                                                                          Human VEGFR3 short interfering nucleic acid (siNA) SEQ ID NO:1936.
drug screening, target identification and validation, genetic engineering, studying gene function, and also for gene mapping single-nucleotide polymorphisms). The present sequence is used
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                                                                         0.5%; Score 17.4; DB 1; Length 19; 94.7%; Pred. No. 8.2e+02;
                                                                                              1; Indels
                                                  Sequence 19 BP; 2 A; 4 C; 6 G; 0 T; 7 U; 0 Other;
                                                                                              0; Mismatches
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                                the present invention.
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29-JUL-2002; 2002US-0399348P.
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04-NOV-2002; 2002US-00287949.
27-NOV-2002; 2002US-00306747.
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                                                                                                                                                                                           ADF37647 standard; RNA; 19
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                                                                                                                                                                                                                                      (first entry)
                                                                                   Local Similarity 94.7
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     factor receptor gene
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                                 exemplification of
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                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                         Query Match
                                                                                                                                                                                                                 ADF37647;
                                                                                                                                                                       619
                                                                                     Best Loc
Matches
                                                                                                                                                                       RESULT 61
ADF37647/
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that express siNA; (3) conjugates and/or complexes of siNA; (4) vectors that express siNA; and (5) single-stranded siNA with similar properties. The siNAs have antiangiogenic, cytostatic, antidiabetic, cophthalmological, antiarthritic, antipsoriatic, nephrotropic and synaecological activities. The siNA are useful for modulating (Gownregulating) the expression of VEGFR genes. The siNA are potentially useful for treating a wide range of angiogenesis-associated conditions, particularly cancers, diabetic retinopathy, macular degeneration, neovascular glaucoma, arthritis, psoriasis, endometriosis, angiofibroma, and polycystic Kidney disease. The siNA may also be useful for diagnosis, cand polycystic Kidney disease. The siNA may also be useful for diagnosis, cand polycystic studying gene function, and also for gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 3 A; 6 C; 9 G; 0 T; 1 U; 0 Other;
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2002US-0408378P.
2002US-0409293P.
2002US-00287949.
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2002US-0386782P.
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15-JAN-2003; 2003US-0440129P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.5
Best Local Similarity 94.7
Matches 18; Conservative
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The present inventions described according to the vascular endothelial growth factor receptor (VEGFR) gene. Also described: (1) a sink that downregulates the VEGF gene; (2) kits for in vitro or in vitro delivery of sink; (3) conjugates and/or complexes of sink; (4) vectors that downregulates the VEGF gene; (2) kits for in vitro or in vitro delivery of sink; (3) conjugates and/or complexes of sink; (4) vectors that express sink; and (5) single-stranded sink with similar properties. The sinks have antianglogenic, cytostatic, nephrotropic and gynacological, antiarthritic, antipsoriatic, nephrotropic and gynacological activities. The sink are useful for modulating convegulating the expression of VEGFR genes. The sink are potentially useful for treating wide range of angiogenesis—associated conditions, particularly cancers, diabetic retinopathy, macular degeneration, neovascular glaucoma, arthritis, psoriasis, endometriosis, angiofibroma, and polycystic kidney disease. The sink may also be useful for diagnosis, drug screening, target identification and validation, genetic congineering, studying gene function, and also for gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence is used in the exemplification of the present invention.
double-stranded interfering nucleic acid, useful e.g. for treatment diagnosis of cancer, downregulates the vascular endothelial growth
                                                                                                                                                                                               present invention describes a double-stranded short interfering
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                                                                                                                                  Example 3; SEQ ID NO 816; 207pp; English.
                                                                      factor receptor gene.
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; 0 Score 17.4; DB 1; Length 19; Pred. No. 8.2e+02; 0; Mismatches 1; Indels 2318 TGTGTGTGTGTGTGCGT 2336 rererererererer 0.5%; Query Match 0.5 Best Local Similarity 94.7 Matches 18; Conservative 19 셤 ò

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Gaps

ACC79668 standard; DNA; 19 27-AUG-2003 (first entry) ACC79668; RESULT

BP

Human fibroblast growth factor 3 mutagenesis primer SEQ ID NO:3.

Human, fibroblast growth factor 3; FGF3; flat epithelial cell; cancer; flat epithelial cell cancer; mutagenesis; primer; ss.

sapiens

Homo sapier Synthetic.

JP2002272474-A.

24-SEP-2002.

22-MAR-2001; 2001JP-00083352

(ZERI) ZERIA SHINYAKU KOGYO KK 22-MAR-2001; 2001JP-00083352.

WPI; 2003-345602/33

Inspection of flat epithelial cell, screening of treating or preventive agents for flat epithelial cancers, the treating or preventive agents for flat epithelial cancer.

Example; Page 8; 18pp; Japanese.

The present invention describes a method for the inspection of flat epithelial cells in which it is judged that flat epithelial cells separated from an organism can proceed to flat epithelial cancer when the

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2128th base in fibroblast growth factor receptor (FGFR) gene of the cells is mutated from quanine to thywine. Also described is a method for screening treating or preventive agents for flat epithelial cancers in which a candidate substance of treating agent for flat epithelial cancer is applied to flat epithelial cancer cells producing FGFR protein in which the 2128th (exon 17) amino acid in FGFR3 gene is mutated from guanine to thymine or the 697th amino acid is mutated from guanine to thymine or the 697th amino acid is selected by using the facts that the 2128th base in the flat epithelial cell FGFR3 gene after the application returned to quanine and that the 697th amino acid of FGFR3 protein produced returned to glycine as the indices. The method is used for the inspection of flat epithelial cells. The present sequence represents a mutagenesis primer for human FGFR3, which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful e.g. for treatment and down regulates expression of at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a short interfering nucleic acid (siNA) that down regulates expression of at least one cyclin gene by RNA interference, siNA are used to modulate expression of cyclin genes, in,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             short interfering nucleic acid; siNA; cyclin; Cytostatic; Vasotropic; cancer; cell-proliferation disorder; restenosis; drug screening; genetic engineering; pharmacogenomics; gene mapping; single nucleotide polymorphisms; ss.
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0
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                                                                                                                                                                                                                                                                                                              0.5%; Score 17.4; DB 1; Length 19; 94.7%; Pred. No. 8.2e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                Sequence 19 BP; 2 A; 10 C; 3 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                          1855 CCGTACCCCGGCATCCCTG 1873
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2002US-0408378P.
2002US-0409293P.
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2002US-0386782P.
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                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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06-JUN-2002;
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DB 1; Length 19;

Sequence 19 BP; 10 A; 9 C; 0 G; 0 T; 0 U; 0 Other;

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cells, tissue explants or organisms, e.g. for treating a wide range of cancers and other cell-proliferation disorders such as restenosis, but also for drug screening, diagnosis, target identification and validation; genetic engineering, pharmacogenomics, studying gene function and gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence represents the lower strand of cyclin D1 targeted double stranded siNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             short interfering mucleic acid; sINA; cyclin; Cytostatic; Vasotropic; cancer; cell-proliferation disorder; restenosis; drug screening; genetic engineering; pharmacogenomics; gene mapping; single nucleotide polymorphisms; se.
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06-JUN-2002, 2002US-0386782P.
29-AUG-2002, 2002US-0406784P.
05-SEP-2002, 2002US-0408378P.
09-SEP-2002, 2002US-040939P.
17-SEP-2002, 2002US-0411275P.
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                                                                                                                                                                                                                                                                                    0.5%;
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                                                                                                                                                                                                                                                                                                              Local Similarity 47.4 nes 9; Conservative
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The present invention relates to a short interfering nucleic acid (siNA) that down regulates expression of at least one cyclin gene by RNA interference. SINA are used to modulate expression of cyclin genes, in cells, tissue explants or organisms. e.g. for treating a wide range of cancers and other cell-proliferation disorders such as restenosis, but also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence represents the upper strand of cyclin D1 targeted double stranded sinA which is identical to the cyclin D1 transcript target sequence.

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The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Vbeta gene, VbetaRNA or CDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases. Concluding autoimmune disease, degenerative nervous system diseases, carefulous diseases include Addison's diseases. Cond neoplastic disease. Autoimmune diseases include Addison's disease. Cond neoplastic disease. Autoimmune diseases include Addison's disease. Cond neoplastic disease. Autoimmune diseases include Addison's disease. Cond neoplastic disease. Hypersensitivity diseases include Type: I hypersensitivities such as contact with allergens that lead to allergies. Type II hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infectious diseases include viral infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a
                                                                                                                                                                                                                                                                                                                                                                                   degenerative nervous system disease; graft versus host disease; hypersensitivity disease; infectious disease; neoplastic disease; Addison's disease; atrophic gastrilis; degenerative nervous system disease; multiple sclerosis; Alzheimer's disease; hypersensitivity disease; type I hypersensitivity; Goodpasture's syndrome; type II hypersensitivity; leprosy; infectious disease; viral infection; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection, Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                     human; T-cell associated disease; Vbeta; autoimmune disease;
                                      Indels
Score 17.4; DB 1;
Pred. No. 8.2e+02;
                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 836; 164pp; English.
                                                                                                                                                                                                                                                                                                                               Human Vbeta gene repeat sequence #432.
                                                                            2318 TGTGTGTGTGTGTGCGT 2336
                                                                                                              rerererererererer
                                                                                                                                                                                                              ADH70642 standard; DNA; 19 BP
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95US-00531241.
0.5%;
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                                                                                                                                                                                                                                                                                          25-MAR-2004 (first entry)
Query Match 0.5
Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breast cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hood LE, Rowen L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HOOD/) HOOD L E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROWE/) ROWEN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002150891-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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vivlemore401-10.rng

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caused by viruses such as HIV, fungal infections such as those caused by
                   the yeast genus Candida, parasitic infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                 Match 0.5%; Score 17.4; DB 1; Length 19; Local Similarity 94.7%; Pred. No. 8.2e+02; es 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                  Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                          Matches
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2823 TATATATACATATATAT 2841 TATATAAATATATAT 19 à

BP

Single stranded nucleic acid molecule (AT)4. AAZ88880 standard; DNA; 20 (first entry) 25-MAY-2000 11-DEC-1996; US6027884-A 22-FEB-2000 Synthetic. AAZ88880; RESULT 625 AAZ88880

Free energy parameter; thermodynamics; ss. 93US-00078759. 94US-00224840. 94US-00260200. 96US-00763417. 17-JUN-1993; 08-APR-1994;

(UYNY) UNIV NEW YORK STATE RES FOUND. Lane MJ; Benight AS, Faldasz BD, uncing double stranded nucleic acid molecules with preselected values free energy parameters such as affinity for nucleic acid binding Producing double stranded

WPI; 2000-194826/17

This invention describes novel methods of producing double stranded nucleic acid molecules with a preselected value for a free energy parameter (e.g. a preselected T m or a preselected affinity for a nucleic acid binding ligand). The method involves preparing a first double carid binding ligand. The first value of a first free energy parameter of the first redefence value of a first free energy parameter for a reference first reference value of a first free energy parameter for a reference double-stranded nucleic acid comprising a reference binding site for the light reference value of a first free energy parameter for a reference binding of a light than, equal to or lower than (sic). The method relationship is higher than, equal to or lower than (sic). The method comprises: (a) determining a test value for a test double stranded cucleic acid, comprising a test value for a test double stranded complementary strands of double stranded nucleic acid, (b) comparing the first value to a reference value) of the cacond free energy parameter for the reference value) of the cacond free energy parameter for the reference value) of the accond free energy parameter for the reference value) of the accond tree energy parameter for the reference value of the cacid, and (c) if the test value and the second reference value of the Disclosure; Col 71-72; 49pp; Énglish. ligands.

second free energy parameter exhibit a test relationship that is the same as the preselected relationship, then preparing a first double stranded nucleic acid comprising all or part of the test nucleic acid, but if the test relationship is different than the preselected relationship, repeating step (a) and (b) on one or more additional test double stranded nucleic acids until an additional test double stranded and is dentified in which the test relationship is the same as the preselected comprising all or part of the additional test nucleic acid. AZ288875ö a nucleic This invention describes novel methods of producing double stranded nucleic acid molecules with a preselected value for a free energy parameter (e.g. a preselected I m or a free energy parameter (e.g. a preselected I m or a preselected affinity for a nucleic acid binding ligand). The method involves preparing a first double stranded nucleic acid comprising a binding site for a nucleic acid binding ligand. The first value of a first free energy parameter of the first couble stranded nucleic acid has a preselected relationship with a first reference value of a first free energy parameter for a reference binding of a ligand uncleic acid comprising a reference binding site for the binding of a ligand of interest to its binding site and the preselected relationship is higher than, equal to or lower than (sic). The method comprises: (a) determining a test value for a test double stranded nucleic acid, comprising a test binding site for the ligand, of a second Producing double stranded nucleic acid molecules with preselected values for free energy parameters such as affinity for nucleic acid binding Gaps . 0 0.5%; Score 17.4; DB 1; Length 20; 94.7%; Pred. No. 8.7e+02; Indels Sequence 20 BP; 9 A; 1 C; 1 G; 9 T; 0 U; 0 Other; Single stranded nucleic acid molecule (AT) 4. Free energy parameter; thermodynamics; ss. 0; Mismatches (UYNY) UNIV NEW YORK STATE RES FOUND. Disclosure; Col 71-72; 49pp; English Benight AS, Lane MJ; 3463 TATATATATCTATATAT 3481 2 TATATATAGCTATATATA 20 93US-00078759. 94US-00224840. 94US-00260200. 96US-00763417. AAZ88880 standard; DNA; 20 (first entry) Best Local Similarity 94.7 Matches 18; Conservative method of the invention WPI; 2000-194826/17. 11-DEC-1996; 17-JUN-1993; 08-APR-1994; 16-JUN-1994; Faldasz BD, 25-MAY-2000 22-FEB-2000 Synthetic. AAZ88880; Query Match ligands. AAZ88880/c 8à

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free energy parameter that is characteristic of the hybridization of the two complementary strands of double stranded nucleic acid; (b) comparing the first value to a reference value (second reference value) of the second free energy parameter for the reference double stranded nucleic acid; and (c) if the test value and the second reference value of the second free energy parameter exhibit a test relationship that is the same as the preselected relationship, then preparing a first double stranded nucleic acid comprising all or part of the test nucleic acid, but if the test relationship is different than the preselected relationship, repeating step (a) and (b) on one or more additional test double stranded nucleic acids until an additional test double stranded nucleic acid is identified in which the test relationship is the same as the preselected relationship, and then preparing a first double stranded nucleic acid is centified in which the part of the additional test nucleic acid. AA288975-

Z88882 represent the single stranded DNA molecules used to illustrate the
                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; antiinflammatory; cytostatic; antisense gene therapy; phosphoenol pyruvate carboxykinase-cytosolic; PEPCK-cytosolic; infection; inflammation; tumour formation; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse PEPCK-cytosolic antisense oligonucleotide ISIS 113342.
                                                                                                                                                                                                                                                                                                                       Score 17.4; DB 1; Length 20;
Pred. No. 8.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                        Sequence 20 BP; 9 A; 1 C; 1 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                         3463 TATATATCTATATATAT 3481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mckay R, Butler MM, Wyatt J,
                                                                                                                                                                                                                                                                                                                                                                                                         TATATAGCTATATATA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF62964 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-2000; 2000US-00488671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-2000; 2000US-00488671.
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                         method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 627
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The present sequence is one of a number of antisense compounds of up to phosphenon pyruvate carboxykinaec-cytesolic (PECK-cytesolic). The antisense compounds are useful for inhibiting the expression of pytosolic in cells or tissues. They are commonly used as research reagents and in diagnostics, e.g. to elucidate the function of particular genes. They are also useful for distinguishing between functions of various members of a biological pathway and for research use. The antisense compounds are also useful prophylactically, e.g. to prevent or

Antisense compound capable of modulating the expression of phosphoenol pyruvate carboxykinase-cytosolic, useful for preventing or delaying infection, inflammation or tumor formation.

WPI; 2001-190979/19.

Example 17; Col 44; 64pp; English.

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The invention relates to a map of the bread wheat D genome comprising the genome location of a microsatellite marker selected from a group of 185 genome location of a microsatellite marker selected from a group of 185 of left (ABQ92131-ABQ92137). The invention also encompasses the use of left (ABQ92191-ABQ93103) and right (ABQ93103-ABQ93187) primers to amplify and detect the microsatellite markers, and to identify genes responsible for a phencypic trait of interest in wheat. Wheat is an allohexaploid species consisting of 3 diploid genomes designated A, B and a lohexaploid species of the prome is thought to have been introduced in the most recent intercrossing, between the amphipioid AABB and Triticum to the polyptoid genome, the large size of its genome, and its low level of polymorphism, the genetic mapping of wheat has to date been difficult. Microsatellites are tandemly repeated sequences the want of polymorphism, the genetic mapping in length, mainly due to polymerase slippage during replication. This high degree of polymorphism makes them especially suitable for the genetic mapping of polymorphism makes them especially suitable for the genetic mapping of
                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Map of wheat D genome comprising the genome location of a microsatellite marker, useful for e.g. identifying genes responsible for a desired phenotypic trait, especially quantitative trait loci in wheat, and
delay infection, inflammation or tumour formation. The present sequence is a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T. tauschii/wheat D genome microsatellite cfd67 right PCR primer.
                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsatellite marker; wheat; D genome; mapping; genotyping; polymorphism; phenotypic trait; OTL; quantitative trait locus; disease-associated gene; development factor; quality factor; resistance factor; wheat product; identification; detection; genetically modified wheat; PCR; primer; ss.
                                                                                                                  0.5%; Score 17.4; DB 1; Length 20; 94.7%; Pred. No. 8.7e+02;
                                                                                                                                                          1; Indels
                                                                         Sequence 20 BP; 2 A; 0 C; 10 G; 8 T; 0 U; 0 Other;
                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                  2325 GTGTGTGTGTGTGTG 2343
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                                                                                                                                                                                                                        GrerereAererere 19
                                                                                                                                                                                                                                                                                                                                         ABQ93169 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sourdille P,
                                                                                                                                     Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bernard M,
                                       deoxy gap
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                                                                                                                  Query Match
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species which show little intraspecies polymorphism, such as wheat. In addition, microsatellites are codominant, and exhibit Mendelian.

inheritance. The 185 microsatellite markers of the invention are developed from the ancestral diploid donor species Triticum tauschii and map to the wheat D genome, which is less polymorphic than the A or B genomes. These microsatellite markers thus help to overcome some of the problems associated with the genetic mapping of wheat. The wheat D genome invention are useful for identifying genes responsible for a phenotypic trait of interest, most notably OTLs (quantitative trait loci). In charticular they may be used for analysing genes and alleles implicated in disease and for identifying development factors, quality factors and factors conferring resistance to pathogens and xenobiotics. The microsatellite markers and associated primers may be used in microsatellite markers and associated primers may be also be used in microsatellite markers and associated primers may be also be used in mapping and genotyping diploid and polyphoid species of Triticum, particularly Aegilops, Triticum monococcum, Triticum durum, Triticum essetivum, or related species; for identifying cultivars and hybrids of Triticum and related species; to assess whether or not a product comprises wheat or a related species; and to assess whether or not a product comprises genetically modified wheat. The present sequence represents a specifically claimed Triticum tauschii/wheat genome D microsatellite marker right per primer of the invention. (Updated on 29-Sequence 20 BP; 0 A; 1 C; 8 G; 11 T; 0 U; 0 Other; 2330 TGTGCGTGTGTGTGTGT 2348 AUG-2003 to standardise Os field) 94.78; Query Match 0.5 Best Local Similarity 94.7 Matches 18; Conservative 88888888888888888888888888888888888 ð

ö Gaps ö Score 17.4; DB 1; Length 20; Pred. No. 8.7e+02; 0; Mismatches 1; Indels

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ABS97833 standard; DNA; 20 BP ABS97833;

(first entry) 23-DEC-2002

Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #41.

Human, ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

CW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

CW dronergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NRILS;

A aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

CYClooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

CYClooxgenase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

CYClooxgenase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

CYCLOOXGENACE, TRANSFERSE 3-Lipoxygenase activating protein; FLAP;

CYCLOOXGENACE, TRANSFERSE 3-Lipoxygenase activating protein; FLAP;

CYCLOOXGENACE, TRANSFERSE 3-Lipoxygenase activating protein;

CYCLOOXGENACE, Incotinamide-N-methyl transfersase;

CYCLOOXGENACE, Incotinamide-N-methyl transfersase;

CYCLOOXGENACE, INCOTINAMICAN, TRANSFERSE 2B7;

CYCLOOXGENACE, TRANSFERSE 2B4; UDP-Gloctnoseyl transfersase;

CYCLOOXGENACE, TRANSFERSE 2B4; UDP-GLOCK, TRANSFERSE 2B7;

CYCLOOXGENACE, TRANSFERSE 2B4; UDP-GLOCK, TRANSFERSE 2B7;

CYCLOOXGENACE, TRANSFERSE 2B4; UDP-GLOCK, TRANSFERSE 2B7;

CYCLOOXGENACE, TRANSFERSE 2B single nucleotide polymorphism

Homo sapiens

WO200257410-A2

28-NOV-2001; 2001WO-US044838.

28-NOV-2000; 2000US-00724389.

(DNAS-) DNA SCI LAB INC.

Hall J; Guida M,

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 16; Page 131; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known molecule comprising at least one base variation from that of a known molecule comprising at least one base variation from that of a known human cytochrome P450 OZEI (CTP450D12), cytochrome P450 OZEI (CTP450D12), adrenergic receptor betal (ADBRI), cytochrome P450 OZEI (CTP50D12), adrenergic receptor betal (ADBRI), cytochrome P450 OZEI (CTP50D12), adrenergic receptor unclear translocator (ARNT), cathepsin S (CTPS), cyclooxgenage 2 (CTP2), diazepam binding content (FLAP), plutathione-S-transferage 12 (GST2), histanie-N-methyl transferase (HNWT), NADPH quinone S-transferase 2 (GTP3), unchande -N-methyl cransferase (HNWT), NADPH quinone saidoreducase 2 (NOO2), cransferase (HNWT), NADPH quinone saidoreducase 2 (NOO2), alloctoransferase (HNWT), natochromatic 2) KIXI, nicothramide -N-methyl cransferase (HWTS181), urokinase receptor (MR12), upp-glucuronosyl transferase (MRP3), upp-glucuronosyl transferase (MRP3), orphan nuclear receptor (NR12), or acetylcholine muscarinic (MRP3), orphan nuclear receptor (NR12), or acetylcholine muscarinic (MRP3), orphan nuclear receptor (MR12), or acetylcholine muscarinic cransferase (MRP3), orphan nuclear receptor (MR12), or acetylcholine muscarinic cransferase (MRP3), orphan nuclear receptor (MR12), or acetylcholine muscaring and characterising the genes that care responsible for a variety of disorder-related craits as a result of traits and results of the compression, constitutive cransfersion, mutation or underexpression, which may be used in disquence contained in CYP4501A, CYP4501A, CYP4501A, CANT, EPHX2, GST12, NNMT, NOO2, NR112, STM, UGT284, UGT287, UGT284, UGT polymorphic DNA sequence of the invention

Sequence 20 BP; 10 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Gaps ö Score 17.4; DB 1; Length 20; Pred. No. 8.7e+02; 0; Mismatches 1; Indels 0.5%; Ouery Match
Best Local Similarity 94.7
Matches 18; Conservative

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ADH93178 standard; DNA; 20 BP. ADH93178; **XXXXXXXX**

RESULT 630

22-APR-2004 (first entry)

Human gene PCR primer #23.

human; gene sequence; single nucleotide polymorphism; SNP;

Gaps

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chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1; inhibitor; microsomal prostaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antilnflammatory; neuroprotective; antidinflammatory; neuroprotective; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder;
                    primer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or ischemia.
  human disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                             Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:967.
                                                                                      y Match 0.5%; Score 17.4; DB 1; Length 20; Local Similarity 94.7%; Pred. No. 8.7e+02; nes 18; Conservative 0; Mismatches 1; Indels
existing in human genes and for the diagnosis of present DNA sequence represents a human gene PCR
                                                      Sequence 20 BP; 2 A; 4 C; 7 G; 7 T; 0 U; 0 Other
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16. .20
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/note= "2'-0-methoxyethyls"
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/*tag= a
/mod_base= OTHER
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                                                                                                                                                                                                                                                                                                          Polynucleotide for detecting single nucleotide polymorphisms existing in human gene, contains isolated human gene having specified sequence.
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                                                                                                                                                                                                                                                                                                                                                                   Claim 2; SEQ ID NO 1015; 529pp; Japanese
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                                                                                                                                                                                                                                  (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
disease diagnosis; ss; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease diagnosis; ss; PCR; primer
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                                                                          JP2003174883-A.
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                                      Homo sapiens
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transpected to human microsomal prostaglandin E2 synthase (mFGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to human mpGES-1 gene is located on chromosome 9, more specifically to gas-3. The present invention also describes: (1) antisense compounds, compounds, which specifically hybridise with the nucleic acid encoding mpGES-1, which specifically hybridise with the nucleic acid mpGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mpGES-1 in cells or tissues; and (3) a method of treating an animal comparison of antisense oligonucleotides and antisense compounds have cytostatic, cophinalmological, immunomodulatory and cardiovascular activities, and can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound composition for treating a disease or condition associated with mpGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or cophinalmic, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; inhibitor; eytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; plateimer; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
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sequence represents a chimeric antisense oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                               / Match 0.5%; Score 17.4; DB 1; Length 20; Local Similarity 94.7%; Pred. No. 8.7e+02; neg 18; Conservative 0; Mismatches 1; Indels
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/note= "2'-O-methoxyethyls"
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Synthetic.
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ADM14772/c
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGBS-1). The targeted to human microsomal prostaglandin E2 synthase (mPGBS-1). The human mPGBS-1 gene is located on chromosome 9, more specifically to gasta. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGBS-1, which specifically hybridise with the nucleic acid encoding mPGBS-1, which specifically hybridise with the nucleic acid encoding mPGBS-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mPGBS-1. MPGBS-1 chimeric antidaheacid, immunomodulator, cardiant, neuroprotective, antidifiammatory, neuroprotective, notropic, antiarthritic, vasotropic, antidifiammatory, neuroprotective, notropic, antistrhities, and can ophthalmological, immunomodulatory and artiforascular activities, and can be used for preparing a composition for treating a disease or condition associated with mPGBS-1 e, inflammation, Alzheimer's compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                   New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 17.4; DB 1; Length 20; 94.7%; Pred. No. 8.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 9 A; 8 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse B7H antisense oligonucleotide ISIS 231397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B7H; autoimmune disease; ss; antisense; mouse.
                                                                                                                                                                                                                                                 claim 4; SEQ ID NO 959; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2332 TGCGTGTGTGTGTGTGT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 receigrererererer 1
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               25-SEP-2002; 2002US-0413549P.
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ID ADNS8895 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC.
                                               (PHAA ) PHARMACIA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dobie KW;
                                                                                                                          WPI; 2004-305094/28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAY-2004
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                                                                                        Gierse JK;
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                                                                                                                                                                                                                     ischemia
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The present invention relates to measuring the copy number of a locus by amplifying and comparing test and reference loci. The invention is useful as diagnostic and prognostic tools and in correlating abnormal copy number values for specific loci with disease and effectiveness of different treatment options. The present sequence is a CA repeat fluorogenic probe used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Measuring copy number of a polynucleotide locus in sample useful as diagnostic and prognostic tool, comprises quantifying amount of test locus and reference loci in test and control subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end attached to 6-carboxy fluorescein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 17.4; DB 1; Length 21;
14.7%; Pred. No. 9.2e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                    Probe; Fluorescein; tetramethyl rhodamine; copy number; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 0 A; 0 C; 10 G; 9 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mod_base= OTHER
/note= "3' end attached to TAMRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gray JW;
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jensen RH,
                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/mod_base= OTHER
/note= "5' end at!
                                      CTGGTGACCGAGGACAACG 1663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; Col 33; 27pp; English.
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                                                                                                                                                                           ВР
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                                                                         crecreacadadeacaace
                                                                                                                                                                                                                                                                                                CA repeat fluorogenic probe.
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                                                                                                                                                                           AAF85976 standard; DNA; 21
                                                                                                                                                                                                                                                           (first entry)
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    Conservative
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nes 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                    modified base
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                                                                                                                                                                                                                                                         20-JUN-2001
  18;
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                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                        1645
                                                                                                                                                                                                                    AAF85976;
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ID AAH49075
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Matches
  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                     The invention relates to a compound targeted to a nucleic acid molecule encoding B7H, where the compound specifically hybridises with the nucleic acid molecule encoding B7H and inhibits the expression of B7H. The compound is useful for modulating the expression of B7H. It is also useful for diagnosing or treating diseases associated with expression of B7H, e.g. an autoimmune disease. The present sequence represents a mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a compound targeted to a nucleic acid molecule encoding B7H, where the compound specifically hybridises with the nucleic acid molecule encoding B7H and inhibits the expression of B7H. The compound is useful for modulating the expression of B7H. It is also useful for diagnosing or treating diseases associated with expression of B7H, e.g. an autoimmune disease. The present sequence represents a mouse
                                    New compound targeted to a nucleic acid molecule encoding B7H and inhibits expression of B7H, useful for modulating the expression of B7H or for diagnosing or treating, e.g. autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New compound targeted to a nucleic acid molecule encoding B7H and inhibits expression of B7H, useful for modulating the expression of B7H or for diagnosing or treating, e.g. autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                     0.5%; Score 17.4; DB 1; Length 20; 94.7%; Pred. No. 8.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.4; DB 1; Length 20;
Pred. No. 8.7e+02;
                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sxample 16; SEQ ID NO 250; 97pp; English.
                                                                                                                    Example 16; SEQ ID NO 146; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse B7H target sequence ISIS 147955,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B7H; autoimmune disease; ss; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                    1645 CTGGTGACCGAGGACAACG 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGTGACAGAGGACAACG 1
                                                                                                                                                                                                                                                         B7H, e.g. an autoimmune disease
B7H antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
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Best Local Similarity 94.7
Matches 18, Conservative
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WPI; 2004-399728/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-399728/37.
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Monia BP,

Query Match

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RESULT 639
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                                                                             phenylketonuria; maple syrup disease; galactosemia; homocysteinuria; medium-chain acyl-CoA-dehydrogenase deficiency; blotinidase deficiency; familial hyperxholesterolemia; familial defective apolipoprotein-B; cystic fibrosis; Marfan syndrome; Smith-Lemil-Opitz syndrome; androgenital syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                             DNA chip, useful for neonatal or prenatal screening for many genetic diseases simultaneously, carries oligonucleotides complementary to phenotypically relevant reference sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                       Neonate screening; prenatal screening; gene chip; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.4; DB 1; Length 21;
Pred. No. 9.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 6 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arteriosclerosis-detecting probe from LDLR #42.
                                               gene associated primer #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3667 GCCATGGCTCAGGGTGGTC 3685
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 63; 101pp; German.
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                                                                                                                                                                                                                                                      21-JAN-2000; 2000DE-01002446
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                         (first entry)
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Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                 Cullen P, Seedorf U;
                                                                                                                                                                                                                                                                                                                                      WPI; 2001-457616/49.
                                                                                                                                                                                                                                                                                       (SEED/) SEEDORF U.
                                                                                                                                                                                                                                                                            (CULL/) CULLEN P.
                                                                                                                                                                                WO200153520-A2
                         12-NOV-2001
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-2003
                                                                                                                                                                                                        26-JUL-2001.
                                                  Human LDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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  AAH49075;
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This invention describes a novel method for determining the genetic risk of arteriosclerosis both for clinical diagnosis and for population studies. The method comprises: (i) selecting risk-associated reference nucleic acid sequences, including their functionally characterizing complements, to a carrier, (iii) hybridising the probes with a nucleic complements, to a carrier, (iii) hybridising the probes with a nucleic acid from (or synthesised from) a patient sample; and (iv) detecting and evaluating the hybridistion pattern. The method provides a quick, inexpensive and informative diagnosis, and makes possible a intractions or mutations that when present alone carry no risk but are risk mutations or mutations that when present alone carry no risk but are risk associated in presence of other mutations. The results may be combined with known risk-assessment methods to provide a more reliable diagnosis, completed against specific genes. All relevant mutations in a confinct are directed against specific genes. All relevant mutations in a reference sequence can be screened for in a single test and the method is not all interaction. Associated in a single test and the method is interaction and the method is all relevant probes used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ds; cytochrome P450 Al; CYP4501Al; UGT2B4; MDR1; cytochrome P450 Al; CYP4501A2; cytochrome P450 02E; CYP45002El; LTF; adrenergic receptor betal; ADBR1; aryl hydrocarbon; AHR; MRP3; NR112; aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS; cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological; epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP; glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining genetic risk of arteriosclerosis, for clinical diagnosis, comprises hybridizing patient nucleic acid with an array of probes derived from risk-associated reference genes and their mutations.
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Arteriosclerosis, diagnosis; hybridisation; synergism; gene therapy; mutation; probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 128; 146pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3667 GCCATGGCTCAGGGTGGTC 3685
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                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-2002; 2002WO-EP002780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2001; 2001DE-01011925.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seedorf U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-723374/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OGHA-) OGHAM GMBH
                                                                                                                                                                                                                                               WO200272882-A2.
                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                        19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cullen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
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HNWT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNWT; NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM; DDP-glucuronosyl transferase 287; UGT2B7; UDP-glucuronosyl transferase 287; UGT2B7; UDP-glucuronosyl transferase; UGT2B1; urokinase receptor; uPA; multidrug resistance 1; lactortransferrin; orphan nuclear receptor; multidrug resistance associated protein 3; cancer; prostate; acetylcholine muscarinic receptor; CHWR1; CHWR2; CHWR3; CHWR3; altered drug metabolism; cardiovascular function; colorectal tumour; central nervous system; pulmonary; immunological; SNP; single nucleotide polymorphism.

Homo sapiens.

WO200257410-A2

25-JUL-2002.

28-NOV-2001; 2001WO-US044838

28-NOV-2000; 2000US-00724389

(DNAS-) DNA SCI LAB INC.

Hall J; Guida M,

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 28; Page 159; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human of a known concorned page of a concorned page of a known cytochrome P450 A2 (CTP4501A2), acronded page variation from that of a known nuclear translocator cardy hydrocarbon (ARR), aryl bydrocarbon receptor nuclear translocator (ARRY), cathepsin S (CTSS), cyclooxeganse 2 (CCX2), diazepam binding inhibitor (DBI), epoxide hydroxylase 2 (EPHX2) 5-11poxygenase activating cransferase (HNWT), khallkten 2) KAK2, nicotinamide -N-methyl transferase (HNWT), khallkten 2) KAK2, nicotinamide -N-methyl transferase (HNWT), khallkten 2) KAK2, nicotinamide -N-methyl transferase (HOWT), uvokinase receptor (URD2), UDP-glucuronosyl transferase 2B (UGT2B1), UDP-glucuronosyl transferase 2B (UGT2B1), urokinase receptor (URD2), unlidatury resistance a seociated protein 3 (MRR), cardylam nuclear receptor (RRI12) or actylcholine muscarinic creeptor 1, 2, 3, 4, or 5 (CHRX), CHRX2, CHRX3, CHRX4 or CHRX5) sequence (C (MRP), orphan nuclear receptor (RRI12) or actylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHRX1, CHRX2, CHRX3, CHRX4 or CHRX5) sequence (C G creptor 1, 2, 3, 4, or 5 (CHRX1, CHRX2, CHRX3, CHRX4 or CHRX5) sequence (C c responsible for specific traits within the genome and eventually crare responsible for specific traits within the genome and eventually corresponsible for specific acid molecules comprising the genes responsible for a variety of disorder-related craft and/or MDR3 are useful for a variety of disorder and and eventually activated and and/or MDR3 and also be used to screen individuals for altered contained in CYPP4501A, CAHK, MDR1 and/or MDR3 may also be used to screen individuals for altered cauchors or altered contained in CYPP4501A, in munological or heematological function, in KHX2 for altered series and contained in CRM3, CHRM2 or precent sequence represents a numeror of h polymorphic DNA sequence of the invention

Sequence 21 BP; 9 A; 0 C; 2 G; 10 T; 0 U; 0 Other;

The invention relates to a kit for diagnosing and treating T-cell associated diseases which comprises a panel of nucleic acid primers specifically priming and allowing amplification of each Vbeta gene, VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant rejection and diagnosing and treating T-cell associated diseases including autoimmune diseases, degenerative nervous system diseases, and neoplastic disease, hypersensitivity diseases, infectious diseases and neoplastic diseases. Autoimmune diseases include Addison's disease, atrophic gastritis. Degenerative nervous system diseases include multiple sclerosis and Alzheimer's disease. Hypersensitivity diseases include multiple in hypersensitivities such as contact with allergens that lead to

allergies, Type II hypersensitivities such as those present in Goodpasture's syndrome and Type IV hypersensitivities such as those manifested in leprosy. Infectious diseases include viral infections caused by viruses such as HIV, fungal infections such as those caused by

Kit for diagnozing and treating T-cell associated diseases e.g. autoimmune, degenerative nervous system and infectious disease, comprises nucleic acid primers specifically priming and allowing amplification of a

WPI; 2004-059052/06 Hood LE, Rowen L;

94US-00309335. 95US-00531241. 99US-00263959

19-SEP-1995;

US2002150891-A1. Homo sapiens.

05-MAR-1999; 9-SEP-1994;

17-0CT-2002.

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(HOOD/) HOOD L E. (ROWE/) ROWEN L.

Disclosure, SEQ ID NO 753; 164pp; English

Vbeta gene

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                                                                                                                                                                                                                                                         Alzheimer's disease; hypersensitivity disease; type I hypersensitivity, allergy; type II hypersensitivity; Goodpasture's syndrome; type IV hypersensitivity; leprosy; infections disease; viral infection; HIV; fungal infection; Candida; parasitic infection; schistosome; filaria; bacterial infection; Mycobacterium; neoplastic disease; lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
                     Gaps
                                                                                                                                                                                                               degenerative nervous system disease, graft versus host disease, hypersensitivity disease, infectious disease, neoplastic disease, Addison's disease, atrophic gastritis, degenerative nervous system disease, multiple sclerosis;
                      ö
                                                                                                                                                                                                      human; T-cell associated disease; Vbeta; autoimmune disease;
 Length 21;
                     Indels
Score 17.4; DB 1;
Pred. No. 9.2e+02;
                      0; Mismatches
                                                                                                                                                                                 Human Vbeta gene repeat sequence #349.
                                         2823 TATATATACATATATAT 2841
                                                              19 TATATACACATATATA 1
                                                                                                                  ВР
 0.5%;
                                                                                                                  ADH70559 standard; DNA; 22
                                                                                                                                                             (first entry)
 Query Match 0.53
Best Local Similarity 94.73
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                           breast cancer; ds
                                                                                                                                                             25-MAR-2004
                                                                                                                                       ADH70559;
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Mao Y, Xie Y;
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                                                                       Homo sapiens
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                                                                                                             19-DEC-2001.
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                                                   primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer; ss.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ25283;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primers AAX34328-X34331 were used to PCR amplify the gene encoding a human brain-specific tyrosine kinase (Byk; AAX34327). The coding DNA can be used in drug applications, especially to detect a nervous skin syndrome (sic) related antigen
the yeast genus Candida, parasitic infections such as those caused by schistosomes, filaria and bacterial infections such as those caused by Mycobacterium. Neoplastic diseases include lymphoproliferative diseases such as leukaemias, lymphomas and cancers such as cancer of the brain, breast. The present sequence represents a Vbeta gene repeat sequence.
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene coding brain-specific tyrosine kinase - can be used to detect nervous skin syndrome related antigen.
                                                                                                                                                                                                                                                                        Human; brain, tyrosine kinase; Byk; drug application; antigen; se;
nervous skin syndrome; PCR; primer; amplification.
                                                                                                                                                                                                                                                       Primer PTK3YK for human brain-specific tyrosine kinase (Byk) gene.
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                                                                             0.5%; Score 17.4; DB 1; Length 22; 94.7%; Pred. No. 9.7e+02; tive 0; Mismatches 1; Indel8
                                                           Sequence 22 BP; 9 A; 0 C; 2 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23 BP; 4 A; 5 C; 5 G; 1 T; 0 U; 8 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1618 CACAGGGACCTGGCTGCCCGCAA 1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CACMGNGAYCTSGCNGCNMGNAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 7; 31pp; Japanese.
                                                                                                                       2826 ATATATATATATATA 2844
                                                                                                                                          22 ATATACATATACATATA 4
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                                                                                                                                                                                            AAX34331 standard; DNA; 23
                                                                                                                                                                                                                                    (first entry)
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                                                                                        Local Similarity 94.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL45613 standard;
                                                                                                                                                                                                                                                                                                                                    JP08256780-A.
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            17-MAR-1995;
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                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                 Query Match
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Matches
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AAL45613
ID AAL4
XX
AC AAL4
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DT 21-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; zinc finger protein 234-72.38; tumour; cytostatic; diabetes; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide-human ATP dependent membrane conjugated zinc proteinase 10.45 and polynucleotide for encoding such polypeptide.
                                                                        Human, ATP dependent membrane conjugated zinc proteinase 10.45; enzyme, development disturbance; lipid metabolism disease; gene therapy; PCR;
ATP dependent membrane conjugated zinc proteinase 10-45 PCR primer #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24 BP; 9 A; 3 C; 1 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human zinc finger protein 234-72.38 PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 17(Disclosure); 34pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BODE-) BODE GENE DEV CO LTD SHANGHAI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-2000; 2000CN-00116334.
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nucleic acid target, using a fluorescently labeled probe which produces reduced fluorescence emission when hybridised to the target nucleic acid. The method comprises measuring the reduction in emission caused by hybridisation. The new method is particularly used to quantify target nucleic acids by a real-time polymerase chain reaction, e.g. for quantifying microbial cells in co-cultures or symbiotic system. for detecting gene mutations or polymorphisms, and for analysing melting curves of target nucleic acids to determine a Tm value. Methods of the invention allow target nucleic acids to be quantified quickly, easily and accurately. Particularly there is no need to remove unbound probe, and no materials are introduced that inhibit amplification by Taq polymerase (so conventional PCR conditions can be used). The specificity of PCR is kept
                                                                                                                                                                                                              The present invention relates to human zinc finger protein 234-72.38 (see 8BS59122). The protein can be used for treating diseases such as tumours and diabetes. The present sequence is a PCR primer, which was used in an example from the invention
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                                     Polypeptide-human zinc finger protein 234-72.38 and polynucleotide for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
Furusho K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the determination of the concentration of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Concentration, quantification, mutation detection, polymorphic, polymerase chain reaction; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 17.4; DB 1; Length:24; 4.7%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24 BP; 10 A; 0 C; 4 G; 10 T; 0 U; 0 Other;
                                                                                                                                           Example 3; Page 17 (Disclosure); 34pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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(AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
(KANK-) KANKYO ENG CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3475 TATATATATATTGAGT 3493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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Koyama O,
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The invention relates to the determination of the concentration of a nucleic acid target, using a fluorescently labeled probe which produces cauched fluorescence emission when hybridised to the target nucleic acid. The method comprises measuring the reduction in emission caused by the real-time polymerase chain reaction, e.g. for nucleic acids by a real-time polymerase chain reaction, e.g. for analysing microbial cells in co-cultures or symbiotic systems, for detecting gene mutations or polymorphisms, and for analysing melting curves of target nucleic acids to determine a Tm value. Methods of the invention allow target nucleic acids to be quantified quickly, easily and accurately. Particularly there is no need to remove unbound probe, and no materials are introduced that inhibit amplification by Taq polymerase (so conventional PCR conditions can be used). The specificity of PCR is kept high (amplification of primer dimers is delayed), and the limit of quantitation is reduced. Complex probes are not needed, and amplification
                quantitation is reduced. Complex probes are not needed, and amplification can be monitored in real time. The working graph for data analysis dutomatically generated by a computer) has a higher correlation coefficient than conventional graphs so more accurate quantitation is possible. The current sequence represents a synthetic deoxyribooligonucleotide that was used for investigating the base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the concentration of a target nucleic acid, useful e.g. for detecting genetic mutations, comprises using a fluorescently labeled probe in which emission is reduced by binding to the target nucleic acid.
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                                                                                                                                                                                                                                                             Gaps
high (amplification of primer dimers is delayed), and the limit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Concentration, quantification, mutation detection, polymorphic, polymerase chain reaction; PCR, ss.
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                                                                                                                                                                                                                   0.5%; Score 17.4; DB 1; Length 30; 77.8%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                             Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
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Furusho K;
                                                                                                                                                                                                                                  77.8%; Pred ...
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                                                                                                                                        selectivity of a target nucleic acid
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Best Local Similarity 77.8
Matches 21, Conservative
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Koyama O,
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ABA97618 standard; DNA; 30 BP.

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can be monitored in real time. The working graph for data analysis (automatically generated by a computer) has a higher correlation coefficient than conventional graphs so more accurate quantitation is possible. The current sequence represents a synthetic deoxyribooligonucleotide that was used for investigating the base
                                                                                                                                                                                   Gaps
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                                                                                                                                             Query Match 0.5%; Score 17.4; DB 1; Length 30; Best Local Similarity 77.8%; Pred. No. 1.3e+03; Matches 21; Conservative 0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; fluorochrome; nucleic acid probe; fluorescence
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                                                                                                                  Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
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(KANK-) KANKYO ENG KK.
(KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN
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                                                                                   selectivity of a target nucleic acid
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24-AUG-1999; 99JP-00236666.
30-AUG-1999; 99JP-00242693.
31-AUG-1999; 2000JP-00028896.
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Best Local Similarity 77.8
Matches 21; Conservative
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3259 AGATATTTATTTGCTTTGTCCTTTTT 3285

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RESULT 647 ABA97618

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Measurement of nucleic acids, using a nucleic acid probe and analysis of
the obtained data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; polymorphism detection; mutation detection; disease diagnosis; microbial identification; ss.
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                                                                                               ss; fluorochrome; nucleic acid probe; fluorescence,
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                                                                                                                                                                                                                                                                                               (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe poly a for assaying nucleic acids
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                                                                                                                                                                                                                                  99JP-00236666.
99JP-00242693.
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                                                                     Poly g nucleotide sequence
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                                               (first entry)
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Matches 21; Conserv
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24-AUG-1999;
30-AUG-1999;
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                                                                                                                                                                                                                    Fluorescently-labeled nucleic acid probes for assaying nucleic acids and their polymorphism and mutation, particularly useful in science and medicine for e.g. analytical applications, disease diagnosis and microbial identification.
                                                                                                                        Yamada K;
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                                                                                                                        Kurata S,
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Pred. No. 1.3e+03;
0; Mismatches 6; Indels
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                                                                                                                        Torimura M,
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                                                          (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY (KANK-) KANKYO ENG CO LTD.
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                                                                                                                                                                                                                                                                                                                                  Example 12; Page 60; 152pp; Japanese.
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                                                                                                                      Kanagawa T, Kamagata Y,
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03-AUG-2000; 2000JP-00236115.
26-SEP-2000; 2000JP-00292483.
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03-AUG-2000; 2000JP-00236115
26-SEP-2000; 2000JP-00292483
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Les 21; Conservative
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                                                                                                                                                                                  WPI; 2002-195876/25.
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                                                                                                                        Kurane R,
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                                                                                                                                                                                                                                                            The present invention relates to nucleic acid probes, which are useful for assaying nucleic acids by hybridising with a target nucleic acid, in which a single-stranded oligonucleotide is labelled with a fluorescent
Fluorescently-labeled nucleic acid probes for assaying nucleic acids and their polymorphism and mutation, particularly useful in science and medicine for e.g. analytical applications, disease diagnosis and microbial identification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 12; Page 60; 152pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ62397 standard; DNA; 22
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18-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                   RESULT 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method for identifying a genetic marker for spider lamb syndrome (SLS). The method comprising, obtaining a sheep DNA sample, and analysing the sample DNA with a probe to determine the presence or absence of a polymorphism in fibroblast growth factor receptor 3 (FGFR). The invention is used for diagnosing if sheep carry the gene for SLS, used to eliminate carriers of the syndrome from a flock. SLS or hereditary chondrodyplasia is a semi-lefual congenital disorder in sheep causing severe skeletal abnormalities. The present sequence is a 5' PCR-RFLP primer used to detect nucleotide transversion in sheep FGFR3 gene. The FGFR3 gene is located on chromosome 6
          fequence. This fragment was then cloned as an ECORI/Blunt-HindIII fragment into NotI/Blunt- HindIII cut vector pRc/RSV to give pVACI. The single chain Fv for an individual patient can be inserted within the VH1 leader sequence. This plasmid when encoding a single chain murine antibody/retroviral envelope fusion protein can be used as a plasmid vaccine and it induces a strong humoral response to the antibody moiety in BALB/c mice. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a genetic marker for spider lamb syndrome, used to diagnose if sheep carry a gene for the syndrome, involves analyzing sheep DNA samples for mutations in fibroblast growth factor receptor 3.
encoding of an Sfil cloning site without modification of the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            5' PCR-RFLP primer used to detect nucleotide transversion in FGFR gene
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sheep; spider lamb syndrome; SLS; fibroblast growth factor receptor 3; FGFR; hereditary chondrodysplasia; semi-lethal congenital disorder; severe skeletal abnormality; genetic marker; PCR primer; RFLP; restriction length polymorphism; chromosome 6; ss.
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86.4%; Pred. No. 1e+03;
tive 0; Mismatches 3; Indels
                                                                                                                                                            0.5%; Score 17.2; DB 1; Length 22; 36.4%; Pred. No. 1e+03;
                                                                                                                                                                                         3; Indels
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                                                                                                                                Sequence 22 BP; 3 A; 3 C; 11 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                         1e+03;
                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                     853 GAGGAGGAGCTGGTGGAGGCTG 874
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                                                                                                                                                                         86.4%;
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                                                                                                                                                                                          19; Conservative
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                                                                                                                                                                            Best Local Similarity
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AAD21616
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sequence for the solute carrier family 6 neurotransmitter transporter, serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence complementary to the first sequence. The invention is used in producing a recombinant organism that can be used to express SLC6A4 for protein structure analysis and binding studies. A composition comprising a genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
                                                                                                                                                                                                                                                                                                                                                                                       Solute carrier family 6 neurotransmiter transporter; sectonin 4; SLC6A4; genotyping; allele specific oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide comprising a polymorphic variant for the solute carrier family 6 neurotransmitter transporter, serotonin member 9 gene for identifying drugs for treating disorders related to expression
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Pred. No. 1e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2395 TGCAGAGGTACCCTGGGTGTCC 2416
1852 TCCCCGTACCCCGGCATCCCTG 1873
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hes 19; Conservative
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                                                                                                                                                                                                                                    AAF74089;
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Duely maccon Best Local Similarity 86.4 Matches 19; Conservative

Query Match

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Alzhaimer and a disease, paratrinson's disease; graft-versus-host disease; scleroderma; hypertension; haemophilia; disease; triomboytopenic purpura; immunodeficiency; AIDS; dispathic thromboytopenic purpura; immunodeficiency; AIDS; dispathic triomboytopenic purpura; immunodeficiency; and dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia; cancer-associated cachexia; multiple sclerosis; fertility; primer.
                                                                                                                                                           Human; NOVX; PCR; 88; cancer; atherosclerosis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001US-0340390P.
2001US-0340440P.
2001US-0340565P.
2001US-034164P.
2001US-034147P.
2001US-0341477P.
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2001US-0342592P.
2001US-0344903P.
2002US-0353286P.
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2001US-033808P.
2001US-0339014P.
2001US-0339514P.
2001US-0339517P.
2001US-0339611P.
2001US-0340981P.
2001US-0341346P.
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2002US-0359914P.
2002US-0359956P.
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2002US-0361770P.
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                                                                   15-JUL-2004 (first entry)
                                                                                                               Human NOVX PCR primer #69.
                                                                                                                                                                                                                                                                                                                                                           US2004058338-A1.
                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2004
                         ADO42630;
    The invention relates to amplifying an unknown region that flanks a known region of a cancer-associated DNA sequence comprising providing a template polymucleotide, ligating a loop-forming oligonucleotide to the 3'-end of the sense strand, annealing the loop-forming oligonucleotide with the first portion to generate a panhandle structure, subjecting the panhandle structure control to person of a first primer homologous to the second cortion, where the unknown region is amplified. In the method of cortion, where the unknown region is amplified in the method of comprises a sense strand, comprising the known and unknown region of the known region is comprised a first tor second portion. The first portion is nearer the Unknown region than is the known region. The known collgonucleotide is complementary to the second portion is generated at the first portion is complementary to the second portion is generated at the free end of the comprises APFI (not defined) or BCR (B cell receptor). The method is cueful for amplifying an unknown region that flanks a known region of a cancer-associated DNA sequence. The cancer-associated DNA sequence the chromosomal breaks result in gene fusions with APF-4, CBK-6 and SEPIING and acute myseloid leukaemia, und acute myseloid leukaemia and acute myseloid leukaemia and soute myseloid leukaemia und acute myseloid leukaemia und acute myseloid leukaemi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amplifying an unknown region that flanks a known region of a cancerassociated DNA sequence by subjecting the panhandle structure to extension and to PCR in the presence of a first primer homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11q23. The present sequence is a PCR primer used the method of the invention to isolate the unknown region adjacent to the BCR cancer gene.
acute lymphoblastic leukaemia, AML, acute myeloid leukaemia,
chromosomal break point; chromosome 11q23, ATF; BCR; B cell receptor;
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97US-0065911P.
98US-00026033.
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Best Local Similarity 86.4%;
Marches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         (FELI/) FELIX C A.
(JONE/) JONES D H.
(RAPP/) RAPPAPORT E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-606415/57.
                                                                                                                                 US2003096255-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               second portion
                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                   9-FEB-1997;
                                            primer; PCR.
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2002US-0401788P

07-AUG-2002;

ADO42630 standard; DNA; 22 BP

RESULT 654 ADO42630 ID ADO426

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The sequences are useful for diagnosing, treating or

(AGEE/) (ALSO/) (ANDE/)

(BERG/) (BOLD/) (BURG/) (CATT/)

(EISE/)

(ELLE/) (GANG/) (GERL/) (GORM/) (ROTH/) (GUOX/)

(HALV/)

KHRA/) LARO/

KEKU/

(MACD/) (MILL/) (ORTT/) (PADI/)

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human NOVX polypeptides and nucleic acid molecules, useful for diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer, atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human NOVX polypeptides and the polymucleotides encoding them. The invention also relates to antibodies specific to the NOVX polypeptides. The polypeptides, polymucleotides and antibodies are useful for manufacturing a medicament for treating a syndrome associated with a human disease, such as a pathology associated with the NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guo XS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rook JP, Anderson DW, Berghs C, Boldog FL; tterton B, Dipippo VA, Edinger SR, Eisen A; mgolli EA, Gerlaan V, Gorman L, Rothberg BG, alvorsen Y, Ji W, Kekuda R, Khramtsov NV; Lepley DW, Li L, Macdougall JR, Miller CE, (tturajan M, Pena CEA, Peyman JA, Rieger DK; Shenoy SG, Smithson G, Spaderna SK, Spytek Kier RJ, Vernet CAM, Voss EZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example D; SEQ ID NO 485; 610pp; English.
            23-AUG-2002; 2002US-0405400P.
23-AUG-2002; 2002US-0405684P.
23-AUG-2002; 2002US-040568TP.
23-AUG-2002; 2002US-040568PP.
26-AUG-2002; 2002US-0406353P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burgess CE, Catterton E, D
Ellerman K, Gangolli EA, G
Herrmann JL, Halvorsen Y,
Larochelle WJ, Lepley DM,
Padigaru M, Patturajan M,
                                                                                                                                                                                                                                                                                                                                                    KEKUDA R.
KHRAMTSOV N V.
LAROCHELLE W J.
LEPLEY D M.
                                                                                                                                                                                                                                                                                                                                                                                                                  MACDOUGALL J R.
MILLER C E.
ORT T.
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Padigaru M, Patturajan
Rothenberg ME, Shenoy
Stone DJ, Taupier RJ,
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                                                                                              AGEE M L.
ALSOBROOK J. P.
ANDERSON D W.
                                                                                                                                                                                                               EISEN A.
ELLERMAN K.
GANGOLLI E A.
GERLACH V.
                                                                                                                                                                                                                                                                    GORMAN L.
ROTHBERG B G.
GUO X S.
HERRMANN J L.
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PATTURAJAN M.
PENA C B A.
PEYMAN J A.
RIEGER D K.
RIEGER D K.
SHENGY S G.
SMITHSON G.
SMITHSON G.
SPADERNA S K.
SPADERNA S K.
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TAUPIER R J.
VERNET C A M.
VOSS E Z.
                                                                                                                                   BERGHS C.
BOLDOG F L.
BURGESS C E.
CATTERTON E.
DIPIPPO V A.
EDINGER S R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZHONG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scleroderma
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(VERN/) (VOSS/) (ZHON/)

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preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host disease, soleroderma, hypertension, haemophilia, idiopathic thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia, obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated cachexia, multiple sclerosis or fertility. The nucleic acids may be used as hybridisation probes, in chromosome mapping, in tissue typing, in preventive medicine or in pharmacogenomics. This sequence represents a PCR primer used in analysis of expression of a human NOVX polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide derived from Trypanosomes, useful in preparing a medicament for suppressing the immune response in a mammal for treating autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypanosoma brucei; trypanosome suppressive immunomodulating factor; TSIF; immunomodulating activity; Trypanozoon infection; immunosuppressive; gene therapy; immune response; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

0.5%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22 BP; 8 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637 CTCAAGCACGTGGAGGTGAATG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma brucei TSIF PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   craaagcacarcaagcreaare 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Page 28; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-2003; 2003WO-EP051082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP74810 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-SEP-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-500278/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                               of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004056853-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-2004
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ВР.

(first entry)

(revised)

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Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus; g3p; binding; adsorption; gene VIII; diverse repertoire; specific binding pairs; replicable genetic display package; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                         Producing members of specific binding pairs - by expression in recombinant host cells with a secreting replicable genetic display
                                                                                           Primer HuVH3aBACK for human immunoglobulin VH chain.
                                                                                                                                                                                                                                                                                                                               (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                 Mccafferty J, Pope AR, Johnson KS,
Jackson RH, Holliger KP, Marks JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page ?; 209pp; English.
             AAQ23702 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                          (MEDI-) MED RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-056862/07
                                                          23-SEP-2004
21-MAY-1992
                                                                                                                                                                                                                                   10-JUL-1990;
                                                                                                                                                                                                                                                                                  L2-NOV-1990;
                                                                                                                                                                                                                                                                                                         15-MAY-1991;
                                                                                                                                                                                                                                                                       19-OCT-1990;
                                                                                                                                                                                                                                                                                            06-MAR-1991;
                                                                                                                                                                                       WO9201047-A
                                                                                                                                                                                                                                                           10-JUL-1990
                                                                                                                                                                                                             23-JAN-1992
                                                                                                                                                                Synthetic.
                                    AAQ23702;
   AAQ23702
                                     ö
                                                                                                                                                                                                                                                                                                 Heavy chain; light chain; antibody; chimeric; variable; constant; domain;
Fab; rescue; phagemid; PCR; ss.
a medicament for suppressing the immune response in a mammal for treating autoimmune disorders. The present sequence represents a PCR primer for TSIF, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Two prepns. of PCR-amplified VH genes were made. Both prepns. used an equimolar mixt. of the HUJHFOR primers; in one of the prepns, 6 separate PCR amplifications were performed with each of the HUYHBACK primers individually (1a-6a). The template was CDNA prepd. from RNA obtd. from B lymphocytes, and the prod. was further manipulated to yield the human VH domain. See also AAQ32260-349. (Updated on 25-MAR-2003 to correct PN
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodn. of specific binding pair members - by producing libraries of polypeptide chains displayed by a package, and selection.
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                                                                    0.5%; Score 17.2; DB 1; Length 22; 86.4%; Pred. No. le+03;
                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith AJH;
                                                Sequence 22 BP; 7 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                 Human heavy chain PCL primer HuVH3aBACK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Griffiths AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY. (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                    602 AGGTGTACAGTGACGCACAGCC 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 72; 117pp; English.
                                                                                                                                  1 AGGTATACACTGACGCACACCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                91WO-GB001134.
                                                                                                                                                                                                                                                                                                                                                                                                                92WO-GB000883
                                                                                                                                                                                                                                                                                                                                                                                                                                      91GB-00010549
                                                                                                                                                                                                  AAQ32277 Standard; DNA; 23
                                                                                                                                                                                                                                                            (first entry)
                                                                                 Local Similarity 86.4 nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson KS,
                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-415769/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-1991;
10-JUL-1991;
24-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                  WO9220791-A1
                                                                                                                                                                                                                                                                                                                                                                                                               15-MAY-1992;
                                                                                                                                                                                                                                               25-MAR-2003
22-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GP,
                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                         AAQ32277;
                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               field.)
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                                                                                              datches
                                                                                                                                                                             RESULT 6
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Hoogenboom HRJ, Griffiths AD;

90GB-00022845. 90GB-00024503. 91GB-00004744. 91GB-00010549.

90GB-00015198 90GB-00015198

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The primer was used to amplify the H chain V region from a human monoclonal anti Rh-D cell line Fog-1 (Ig-k). It is one of 6 VH Back monoclonal anti Rh-D cell line Fog-1 (Ig-k). It is one of 6 VH Back (AAQ23700-705) used together with the forward primer HulgG1-4CHIFOR (AAQ23716) for the H chain C region, to prepare a VH-CHI fragment. A corresponding light chain fragment, VK-CK, was prepd. C separately, then the two chains assmbled via a linker sequence to give an Fab construct. The PCR prod. was ligated into the vector, pJM-1-Fab D1.3 (AAQ23857) and the ligation mixt. used to transform E. coll cells. 96 of the resulting clones were screened for anti-Rh-D activity; 40% specifically agglutinated Rh-D positive but not Rh-D negative red blood cells, demonstrating a high frequency of successful splicing in the assembly process and the potential of this technique for one step cloning of human hybridomas. The pri-mers were also used to amplify a VH-CHI fragment to prepare an IgG-lambda monclonal anti-Rh-D Fab from a lymphoblastic cell line (ICL). To determine the diversity of the creating clones, VH and vlambda genes of 15 clones were PCR amplified. 3 different H chain and 2 different light chain families were PCR amplified. 3 clifferent A specific clones were identified out of 96 screened. The VH and Vlambda genes had identical nucleotide sequences in each clone and were typical of anti-Rh-D v-genes. The results demonstrate the potential of the technique to assemble, clone and solated human Ab fragments from the polyclonal cell populations. Sec also AAQ21092-100, 103-116, 126-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Revised record issued on 23-SEP-2004 : Correction to sequence location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polyclonal cell populations. See also AAQ21092-10
AAQ23463, 465-495, 693-719, 736-738, and 793-863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Gaps

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86.48;

Conservative

Best Local Similarity Matches 19; Conserv

Gaps

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3; Indels

0; Mismatches

86.4%;

19; Conservative

Best Local Similarity

Matches

Query Match

853 GAGGAGGAGCTGGAGGCTG 874

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0.5%; Score 17.2; DB 1; Length 23; 36.4%; Pred. No. 1.1e+03;

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WPI; 1993-117534/14.
                                                                                                                                    (MEDI-) MEDICAL RES
                                                                                                                                                                                                                             characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAR-1992;
15-MAY-1992;
                                                                                                24-MAR-1992;
24-MAR-1992;
15-MAY-1992;
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                         WO9306213-A1
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22-APR-1994
                                                             23-SEP-1992;
                                                                              23-SEP-1991;
25-SEP-1991;
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        Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                        pTK genes were identified using two sets of degenerative oligonucleotide primers: a first set which amplifies all pTK DNA segments (AAQ49743-44), and a second set which amplifies highly conserved sequences present in the catalytic domain of the c-kit subgroup of pTKs (AAQ49745-46). The pTK genes identified are described in AAQ49747-57 and AAR41897-02. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymerase chain reaction; murine; Mab12; monoclonal antibody; chimeric; mouse-human antibodies; antibody; prevention; human; anti-globulin response; PCR; ss.
                                                                                                                                                                                                                                                                                                                          New protein tyrosine kinase genes and proteins encoded by genes - are of human mega-karyocytic origin.
                                                                                                                                                     pTK; tyrosine kinase; catalytic domain; c-kit; amplification; primer; polymerase chain reaction; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 8 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                            Scadden D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VH domain PCR amplification primer HuVH3aBACK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                          (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1801 GACGICTGGICCTITGGGGICC 1822
          874
                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 14; 60pp; English.
                                                                                                                                                                                                                                                                                             Cowley S,
                          daggrecagericeredagrere 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 GACGTCTGGTCTTTGGAATTC 2
          GAGGAGGAGCTGGTGGAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ39335 standard; DNA; 23 BP
                                                                         ВР
                                                                                                                                                                                                                                        93WO-US000586
                                                                                                                                                                                                                                                         92US-00826935
                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Conservative
                                                                AAQ49744/c
ID AAQ49744 standard; DNA;
                                                                                                                                                                                                                                                                                             Groopman J,
                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                               WPI; 1993-320330/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                       pTK primer pTK2
                                                                                                                                                                                                                                       22-JAN-1993;
                                                                                                                                                                                                                                                          22-JAN-1992;
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26-JUL-1993
                                                                                                                                                                                                    WO9315201-A1
                                                                                                                     10-MAR-1994
                                                                                                           25-MAR-2003
                                                                                                                                                                                                                       05-AUG-1993
                                                                                                                                                                                                                                                                                             Avraham H,
                                                                                                                                                                                  Synthetic.
                                                                                           AAQ49744;
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          853
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AAQ39335
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The sequence is that of PCR primer HuVHJaBACK which was used, individually or in an equimolar mix of all 6 HuVHBACK primers (AAQ39333-Q39338), in the prepn. of PCR-amplified VH genes. It was used as part of a method of producing chimeric mouse-human antibodies or fragments which have the same binding specificity as a parent Ab but have increased human characteristics, preventing anti-globulin response in humans. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Producing human antibody polypeptide dimer specific for antigen comprises use of chain shuffling using phage expression, useful for reducing anti globulin responses in humans for increased human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03; 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                              Winter GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                              Jespers LSAT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multimeric (SBP) antibody chain primer.
                                                                                                                                                                                                                                                         (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              853 GAGGAGCTGGTGGAGGCTG 874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Page 29; 109pp; English.
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                                                  91GB-00020252.
91GB-00020377.
92GB-00006318.
92GB-00006372.
92WO-GB000883.
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92WO-GB000883.
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Local Similarity 86.4%;
les 19; Conservative (
92WO-GB001755
                                                                                                                                                                                                                                                                                                              Hoogenboom HRJM, Baier M,
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                                                                                                                                                                                                                                 COUNCIL
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Waterhouse P;

Smith AJH,

Griffiths AD,

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The primers (AAQ48987-Q49045) are used in the amplification of Kappa and lambda-chain genes of various antibodies. These genes are then recombined into the same replicon, resulting in very diverse libraries of antibody chains, e.g. from unimmunised donors. It is also useful for chain shuffling, mutagenesis, humanishng and CDR imprinting. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A set of degenerate primers (AAT03085-86) designed to amplify all protein tyrosine-kinase (pTK) sequences was used with a second set (AAT03087-88), which amplified highly conserved sequences present in the catalytic domain of the c-kit subgroup of pTKs, in a 2-step PCR to obtain probes used to screen cDNA libraries for the identification of novel pTK genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein tyrosine-kinase; agonist; cell growth; differentiation; polymerase chain reaction; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                Prodn. of specific binding pair members, e.g. antibody chains display on surface of replicable genetic display packages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
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                                          CAMBRIDGE ANTIBODY TECHNOLOGY. MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGAGGAGCTGGTGGAGGCTG 874
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il Similarity 86.4%;
19; Conservative
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                                                                                                                                                                                             Johnson KS, Winter GP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                  WPI; 1993-320739/40
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                                                                                         (MEDI-)
                                               CAMB-)
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1D AATO 3086/
1D XX AATO 3086/
NX AATO 14-F.
XX Prot.
XX API,
X
S X C C C C C C X S X L L X B X X B X X B X X B X X B X X B X X B X X B X 
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(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection and cloning of an antibody gene - using PCR, dissociating the gene into single strands and isolating the gene from a cDNA mixture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                Polymerase chain reaction; PCR; amplify; primer; detection; antibody gene; antigen specific antibody; activation; lymphocyte; heavy chain; light chain; variable region; immunoglobulin; ss.
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                             Length 23;
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                                                           Indels
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Sequence 23 BP; 8 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
                          Score 17.2; DB 1;
Pred. No. 1.1e+03;
0; Mismatches 3;
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0; Mismatches
                                                                                       1801 GACGTCTGGTCCTTTGGGGTCC 1822
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                                                                                                                                                                                               Bb
                                                                                                                                                                                                                                                                                       HuVH3a 5' heavy chain primer.
                             0.5%;
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                            Query Match 0.5
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 86.4
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                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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AAX76600
ID AAX7660
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DT 11-AUG-
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3; Indels

0; Mismatches

Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03;

Wood WI;

Matthews W, Tsai SP,

Lee JM,

95WO-US004228

Synthetic

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This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. ARZ4381-Z4388 represent primers used in the amplification of a human 1gG4 heavy chain which is used in the method of
                                                                                                                                                                                                                                             New polynuclectide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, serum albumin; HA; antiinflammatory; immunosuppressive; cardiant; nootropic; neuroprotective; gene therapy; immune disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nootropic; neuroprotective; gene therapy; immune disorder; wound heali
hyperproliferative disorder; renal disorder; cardiovascular disorder;
respiratory disorder; neurological disease; endocrine disorder;
reproductive system disorder; infectious disease;
gastrointestinal disorder; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                         Turenhout EAM
                                                                                                           (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING
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                                                                                                                                                         Voorberg JJ, Van Den Brink EN,
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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                   99WO-NL000285.
                                                                98EP-00201543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer Hu VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-616755/71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention
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                   07-MAY-1999;
                                                                08-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABA03074;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes methods of screening a DNA construct binding a transcriptional antibody fusion reagent capable of binding a transcriptional associated biomolecule in vivo. The antibodies are useful in treating Hepatitis A and B respiratory syncitial virus, HIV, Junin virus, Herpes simplex I and II, rubella, cytomegalovirus, Varicella-Zoster virus, Epstein-Barr virus, measles, hantavirus, dengue, Ebola inter alia and cancer. Expression vectors that encode the fusion antibodies may be used in gene therapy. The methods can be used to create and isolate the fusion antibodies. The monoclonal antibody fusion reagent represent specifically claimed PCR primers used in the construction of a human sFv library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibodies from libraries useful in treating viral infections and cancer.
                                                           Human, sFV library, single chain monoclonal antibody fusion reagent, transcription regulation, screening, diagnosis, HIV; Hepatitis A, Hepatitis B respiratory syncitial virus, Junin virus, cytomegalovirus, Herpes simplex virus, rubella; Varicella-Zoster virus, hantavirus, Epstein-Barr virus; measles; dengue; Ebola inter alia; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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hemophilia A; amplification; ss.
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                     Human sFv library construction PCR primer SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human IgG4 heavy chain PCR primer huVH3aback.
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                                                                                                                                                                                   gene therapy; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                               97WO-US021407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Russell M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INVI-) INVITROGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-371138/31.
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                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                  WO9928502-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-1997;
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AAZ43845;

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Query Match

Matches

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Gaps

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The present invention relates to albumin fusion proteins, which comprise a therapeutic protein and albumin. The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases/disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), renal disorders (e.g. childhood acute myeloid leukemia), renal disorders (e.g. childhood acute myeloid leukemia), renal disorders (e.g. childhood acute myeloid disorders (e.g. arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's disease), endocrine disorders (e.g. productive system disorders (e.g. syphilis), infectious diseases (e.g. masteles), gastrointestinal disorders (e.g. intritable bowel syndrome) and wound healing. In the present invention, human serum albumin (HA) see AAMS2567) was used to generate fusion human serum albumin (HA) see AAMS2567) was used to generate fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; albumin; HA; immune system disorder; transplant rejection; blood related disorder; myocardial infarction; glomerulonephritis; hyperproliferative disorder; childhood acute myeloid leukaemia; HH; heavy chain variable domain; renal cell carcinoma; antileukaemic; cardiovascular disorder; respiratory disorder; non-allergic rhinitis; pherorological disease; Alzheimer's disease; endocraine disorder; meaales; pheorytochroma; reproductive system disorder; neuroprotective; syphilis; infectious disease; gastrointestinal disorder; neuroprotective; syndrome; HIV; human immunodeficiency virus infection; cytostatic; antiinflammatory; gene therapy; immunosuppressive; cardiant; antiarthritic; antiinflammatory; renal disorder; antimicrobial; vulnerary; arrhythmia; melanoma; PCR primer; 88.
                   Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction) and hyperproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins. The present sequence was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                       Disclosure; Page 538; 606pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           853 GAGGAGGTGGTGGAGGCTG 874
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12-APR-2000; 2000US-0229358P. 25-APR-2000; 2000US-0199384P. 21-DEC-2000; 2000US-0256931P.

12-APR-2001; 2001WO-US011991

WO200179480-A1.

25-OCT-2001.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Haseltine WA;

Gaps

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The invention relates to human albumin (HA) fusion proteins and their corresponding nucleic acid sequences. Therapeutic proteins fused to albumin or its fragments have an extended shelf-life. The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases, disorders used as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. childhood acute myeloid infarction), hyperproliferative disorders (e.g. childhood acute myeloid cleuksemia, metastatic renal cell carcinoma), renal disorders (e.g. childhood acute myeloid cleuksemia, metastatic renal cell carcinoma), renal disorders (e.g. cardiovascular disorders (e.g. arrhythmias), crepiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's disease), endocrine disorders (e.g. pheocytochroma), reproductive system disorders (e.g. sproductive system) albumin fusion protein is used in gene therapy. The present sequence is a PCR primer used to amplify human heavy chain variable domain (VH) gene. Note: The present sequence is incorrectly reffered as compliance in the specification
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                                                Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma, renal cell carcinoma, HIV (human immunodeficiency virus) or infection.
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0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                             Example 60; Page 315; 394pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       853 GAGGAGGTGGTGGAGGCTG 874
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2000US-0187999P.
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WPI; 2001-616756/71
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09-MAR-2000;
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autoimmune

Li Y, Ruben SM;

Roschke V,

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Li Y, Ruben SM;

Roschke V,

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16-0CT-2001
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                             Rosen CA,
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Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimm diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human G-protein chemokine receptor (CCR5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 55; Page 438; 495pp; English.
                                                                                                             09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                     09-FEB-2001; 2001WO-US004152.
                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488965/53
                                                                                                                                                                                                                                                                                                      Rosen
The invention relates to human G-protein chemokine receptor (CCR5)

CC HOGNRIO polypeptides and polynucleotides. CCR5 HOGNRIO antibodies are

CC useful for treating, preventing or ameliorating a disease or disorder

associated with inflammation, defective or aberrant chemotaxis of immune

CC asrcoma) or defective or aberrant T-cell antigen presenting cell

interaction. The disease or disorder may also be an infections disease

CC cytomegalovirus infection such as an early stage HIV infection, a

CC cytomegalovirus infection, or a poxytrus infection, an autoimmune

CC cytomegalovirus infection, or a poxytrus infection, an autoimmune

CC cytomegalovirus infection, an early stage HIV infection, a

CC cytomegalovirus infection, as poxytrus infection, an autoimmune

CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The

disease or disorder may be associated with aberrant CCR5 expression, lack

conf CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand

ct increase or decrease storage capabilities. CCR5 HDGNRIO DNA are useful

CC function. CCR5 HDGNRIO protein is used as a food additive or preservative

ct increase or decrease storage capabilities. CCR5 HDGNRIO DNA,

CT or increase or decrease storage capabilities. CCR5 HDGNRIO DNA,

CT or increase or decrease storage capabilities. CCR5 HDGNRIO DNA,

CT or increase or decrease storage capabilities. CCR5 HDGNRIO DNA,

CT or increase or decrease storage capabilities. CCR5 HDGNRIO DNA,

CT or increase or decrease storage capabilities. CCR5 HDGNRIO DNA,

CT or increase or decrease storage capabilities are also useful in the

diagnosis, treatment and prevention of cancer (breast, ovary, adrenal

CC gland, bone, bone marrow, gastrointestinal tract, luver, lung,

curogenital); immune disorders (Addison's disease, alleries, autoimmune

CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colities)

CC cardiovascular disorders (Myocadial ischaemala) and wound healing. The

CC creations or UH domain appecifically binds to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                   Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor (CCRS) protein of the invention
                                                                                                                                                                                                                                                                                                          Example 55; Page 454; 518pp; English
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the inventation relaters to immune or procession chemically antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. aviral infection such as nearly stage HIV infection, a cytomegalovirus infection and as nearly stage HIV infection, a disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CRS expression, lack of CCRS function. CCRS HDGNR10 protein is used as a food additive or preservative function: CCRS HDGNR10 protein is used as a food additive or preservative function: CCRS HDGNR10 protein and in gene therapy. CCRS HDGNR10 DNA, cromedatobne, bone marrow, gastrointestinal tract, liver, lung, drenal contents, antibodies, agonists and antagonists are also useful in the disorders (myocardia) immune disorders (Myocardia) is diabetes mellitus, Crohn's curogenital); immune disorders (Myocardia) ischaemias) and wound healing. The cytomegaloviscular disorders (myocardia) ischaemias) and wound healing. The present sequence is a PCR primer used for amplifying human VH domain. The cycle) architical chemokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 17.2; DB 1; Length 23; 36.4%; Pred. No. 1.1e+03; Ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human VH domain PCR primer Hu VH3-5' SEQ ID NO:38.
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ABN87305
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AC AEN8730
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AC AEN8730
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Human;
XW Human;
XW ALWAN;
XW ALWAN;
XW ALWAN;
XW ALWAN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human VH domain amplifying PCR primer Hu VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   853 GAGGAGCTGGTGGAGGCTG 874
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Gaps

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albumin fusion protein; cytostatic; anorectic; immunosuppressive; antidiabetic; antirheumatic; antiarthritic; psoriatic; cancer; non-Hodgkin's lymphoma; obesity; transplant rejection; psoriasis; type I diabetes mellitus; rheumatoid arthritis; PCR primer; 88.

WO200158915-A2

growth hormone; hGH; albumin; human serum albumin; HSA;

WO200152904-A2

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where the iraginant of variant has alknown for therapeutic processity.

Abumin fusion proteins are stabilised therapeutic proteins a
Abumin proteins are stabilised therapeutic proteins e.g.

Athumin fusion proteins are stabilised therapeutic proteins e.g.

antidabetic, antirheumatic, antiarthritic and psoriatic activities.

Abumin fusion proteins are stabilised therapeutic proteins e.g.

clistical action, type I diabetes mellitus, rheumatoid arthritis and psoriasis.

Fusing albumin to therapeutic proteins stabilises the therapeutic protein, extends the shelf life and retains the in vitro or in vivo biological activity. It also reduces the need to formulate protein container abuntons with large excesses of carrier proteins to prevent loss of therapeutic proteins due to factors such as binding to the container. The fusion proteins are easily dispensed with a simple formulation requiring minimal post storage manipulation. The fusion of therapeutic proteins to albumin confers stability in aqueous or other solution. The present sequence represents a PCR primer which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an albumin fusion protein (I) comprising a therapeutic protein: X and (a fragment or variant of) albumin comprising a the fully defined sequence in ABB79006 of 585 amino acids, (where the fragment or variant has albumin or therapeutic protein: X
                                                                                                                                                                                                                                                                                                                                                                                           New albumin fusion proteins, useful for treating diseases and disorders such as cancer, comprise therapeutic protein fused to albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor; VEGF; antisense; angiogenesis; cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic; antisense therapy; RT-FCR; primer; VEGFR-1; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGFR-1 gene specific forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 60; Page 343; 413pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              853 GAGGAGGTGGTGGAGGCTG 874
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                                                                                                                                                                                           12-APR-2000; 2000US-0229358P.
25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                      12-APR-2001; 2001WO-US011850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 86.4%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                               Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-611723/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention
                                                                           WO200179442-A2.
                    sapiens.
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                                                                                                                25-OCT-2001
                                                                                                                                                                                                                                                                                                             Rosen CA,
                                      Synthetic.
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Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; findmune ceal chemotaxis; autoimmune disease; rheumatoid arthritis; neurodegeneration; viral infection; Kaposi sarcoma; cancer; hyperproliferative disease; neurological disease; PCR; primer; VH domain;
                                                                                                                                                                                                                                                                                                                                              The invention provides a composition comprising one or more antisense oligonucleotides directed against vascular endothelial growth factor (VEGF) Where the antisense oligonucleotides inhibits profileration of between 0.5-2.5 micro Ma. The antisense oligonucleotides and IC 5.0 concentration of against VEGF for inhibiting cancer cell proliferation and angiogenesis. Preferably the oligonucleotide AAM23032 (a modified version of AAM22984) is used and may be utilized to treat Kaposis sarcoma, ovarian cancer, prostrate cancer, pancreatic cancer or melanoma. Sequences AAM33012-023 represent gene-specific primers used in RT-PCR amplification of VEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                               Novel antisense oligonucleotides useful for inhibiting vascular endothelial growth factor expression, angiogenesis and for treating cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostrate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer #3 used to amplify human VH or VL domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23 BP; 6 A; 4 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1573 CAGGTGGCCCGGGGCATGGAGT 1594
                                                                                                                                                                                                                                                                                                                  Example 12; Page 56; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAAGTGGCCAGAGGCATGGAGT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK51873 standard; DNA; 23 BP.
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-2001; 2001US-00779879.
                                                                               19-JAN-2001; 2001WO-US000019
                                                                                                              19-JAN-2000; 2000US-00487023
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                                                                                                                                                                                                               WPI; 2001-451898/48
                                                                                                                                                                                Masood R;
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                                                                                                                                               (GILL/) GILL P S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2002048786-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VL domain; ss
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                                              26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptors
                                                                                                                                                                                Gill PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK51873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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ABK51873
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Matches
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Li Y, Ruben SM

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The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCR5) designated HDGNR10, and polynucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide chemokine receptor (CCR5) HDGNR10 and polynucleotide sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antipunpantion, defective or aberrant chemotaxis of immune cells and T-cell/antipunpantion and autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections (especially early-stage human immune deficiency virus (HIV), cytomegalovirus or pox virus infections, Raposi sarcoma, or conditions associated with aberrant or deficient expression of the CCR5 expression, cits ligands. The antibodies are also useful to determine CCR5 expression, cits ligands. The antibodies are also useful to determine CCR5 expression, cits ligands. The antibodies are also useful to determine CCR5 expression, cits ligands in the antibodies are also useful to determine CCR5 expression, cG-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the recombinant receptor, and in the treatment of a wide range of diseases (e.g. parkinson's disease), and hyperproliferative disorders (e.g. cancer). ABK51871-ABK51906 represent PCR primers used to amplify VH and VL domains
                                                                                                                                                                                                     New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the examples of the present invention
                                                                                                                                                                                                                                                                                                           Example 55; Page 150; 180pp; English.
                                                                                                   Roschke V,
                                                                                                                                                 WPI; 2002-434754/46.
ROSCHKE V.
                             LI Y.
RUBEN S M.
                                                                                                                                                                                                                                                             inflammation
                                                                                                      Rosen CA,
                        (LIYY/) I
(RUBE/) H
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Gaps ö 0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; ive 0; Mismatches 3; Indels Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other; Pred. No. 1.1e O; Mismatches 853 GAGGAGGAGCTGGTGGAGGCTG 874 GAGGTGCAGCTGGTGGAGTCTG 22 86.48; Best Local Similarity 86.4 Matches 19, Conservative

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ABS76647 standard; DNA; 23 (first entry) 12-DEC-2002 ABS76647;

Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatodi arthritis; acquired immunodeficiency syndrome; AlDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder; PCR; primer; ss. Novel metalloprotease MP1 associated primer #10.

WO200272751-A2 19-SEP-2002

metalloprotease (MP-1). (I) is useful for preventing, treating, or metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an aberrant glutamate transport or motor neuron disorder, such as amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders associated with MP-1 activity, e.g. diabetes, cancer, reproductive disorders (e.g. Klainfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Huntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis or sepsis), pulmonary diseases (e.g. pneumonia, emphysema or cystic fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents a primer associated with the novel human metalloprotease MPI polynucleotide New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders. The invention describes an isolated nucleic acid molecule (I) encoding Gaps ö Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03; 3; Indels Duclos F, Krystek S; Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other; 0; Mismatches Example 19; Page 301; 473pp; English. 853 GAGGAGGAGCTGGTGGAGGCTG 874 22 1 GAGGTGCAGCTGGTGGAGTCTG (BRIM) BRISTOL-MYERS SQUIBB CO. Chen J, Feder J, Nelson TC, 05-FEB-2002; 2002WO-US003353. 05-FEB-2001; 2001US-0266518P. Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative (WPI; 2002-723329/78. 유 ò

Capture agent; nested sorting; gene library; PCR primer; ss Human antibody VH gene amplifying sense primer, HuVH3aBACK. 19-JUL-2000; 2000US-0219183P. 18-JUL-2001; 2001WO-US022821 Ault-Riche D, Kassner PD; 07-MAY-2002 (first entry) (POIN-) POINTILLISTE INC. WO200206834-A2. 24-JAN-2002

AAD28818 standard; DNA; 23 BP

RESULT 673

AAD28818;

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                                                                                                                                        specifically bind to a polypeptide and, oligonucleotides that comprise a sequence that encodes a preselected polypeptide to which the agents bind. The anti-tag capture agents such as antibodies are used as tools for sorting proteins containing polypeptide tags for which the capture agents are specific and for a process of nested sorting. The agents are useful for functional surveys of large diversity libraries such as gene libraries. The present sequence is a PCR primer used to amplify human antibody heavy chain variable region (VH) gene. This primer is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human potassium channel beta-subunit, K+betaM3 polypeptide and polynucleotide for diagnosing, preventing and treating immune, metabolic, gastrointestinal, renal, neural and proliferative diseases or disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; potassium channel beta subunit; K+betaM3; cytostatic; anti-HIV; antiaddictive; antiarthritic; antiasthmatic; antirheumatic; antianaemic; antibacterial; immunosuppressive; antipsoriatic; dermatological; nootropic; neuroprotective; anticonvulsant; neuroleptic; antimanic; antidepressant; antiulcer; antiinflammatory; antidiarrheic; antipyretic; antiallergic; gene therapy; neural disorder; immune disorder; cancer; proliferative disorder; antibody; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes the human potassium channel beta-subunit
                                  Combination of capture agents used as tools for sorting proteins containing polypeptide tags for which the capture agents are specific.
                                                                                                                         The invention relates to a combination comprising capture agents which
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen J, Jackson DG, Ramanathan C, Siemers N;
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                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K+betaM3 antibody VH domain PCR primer SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                     Disclosure; Fig 13A; 159pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                         853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGGTGCAGCTGGTGGAGTCTG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ82763 standard; DNA; 23 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2002; 2002WO-US003986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-FEB-2001; 2001US-0267039P. 03-APR-2001; 2001US-0281224P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-682813/73.
WPI; 2002-155051/20
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feder J, Lee L,
Chang H, Ryseck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200268587-A2.
                                                                                                                                                                                                                                                                                               the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ82763;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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K+betaM3 protein (I). (I) has cytostatic, antiaddictive, antiarthritic, antiasthmatic, anti-HIV, antirheumatic, antibacterial, immunosuppressive, antipacratic, dermatological, antianaemic, nootropic, neuroprotective, antidarcheic, antidapressant, antiulcer, antidiarrheic, antidapressant, antiulcer, antidiarrheic, antiallergic and vulnerary activities, and can be used in gene therapy. (I) can be used for diagnosing a pathological condition (or susceptibility) in a subject, and for can the diam treating a medical condition, e.g. neural disorders related to aberrant neurotransmitter release or drug addiction, a disorder related to hyper potassium channel activity, an immune disorder related to berrant neutear factor KappaB (NF KB) activity, immune disorder related to transplant rejection, immune disorder, especially immuneumppression is desirable, a proliferative disorder, especially cancer, or a proliferative disorder related to an aberration(s) in the capual tion, a proliferative disorder related to an aberration(s) in the capual condition, a proliferative disorder related to an aberration(s) in the capual condition, a proliferative disorder related to an aberration(s) in the capual condition, a proliferative disorder related to an aberration(s) in the capual condition, a proliferative disorder related to an aberration(s) in the capual condition, and aberration(s) in the capual condition, and aberration(s) in the capual condition, and aberration(s) in the capual condition and condition, and condition and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin; variable heavy chain; variable light chain; human; G-procein chemokine receptor; CCR5; HDGNR10; cancer; inflammation; dimmunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease; histocytosis; chemotaxis; infectious disease; autoimmune disease; Addison's disease; dermatitis; rheumatoid arthritis; allergy; neurodegenerative disorder; viral infection; poxvirus infection; HIV; human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma; preumocystis carnii infection; cardiovascular disorder; atherosclerosis; lymphocytopenia; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.2; DB 1; Length 23; pred. No. 1.18+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunoglobulin variable heavy domain PCR primer #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roschke V, Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВЪ.
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2001US-0297257P.
2001US-0310458P.
2001US-0328447P.
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21-DEC-2001; 2001US-0341725P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2002; 2002WO-US003634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABS68573 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.5
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200264612-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-2001;
12-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABS68573;
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Barber L;

Cacace A,

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(BRIM ) BRISTOL-MYERS SQUIBB CO.
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27-MAR-2001; 2001US-0278983P.
                                                                                                                             Best_Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                         WO200272755-A2.
                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                               16-JAN-2003
                                                                                                                                                                                                                                19-SEP-2002.
                                                                                                                                                                        ABQ83145;
                                                                                                                          Query Match
                                                                                                                                                          RESULT 676
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The present invention describes a human G protein coupled receptor (GPCR), designated HGPRBMY27 (I). (I) has antiinflammatory, antiinfertility, pulmonary, cytostatic, nephrotropic, hormonal and circulatory activities, and can be used in gene therapy. (I) or the protein encoded by it can be used to prevent, treat, or ameliorate a medical condition, such as inflammatory disorders, reproductive disorders, pulmonary disorders, cancer, renal disorders, connective tissue disorders, endocrine disorders, or disorders involving aberrations in tubular tissues. They can also be used to diagnose a pathological condition or a susceptibility to (I). The protein can be used to screen for candidate compounds capable of modulating activity of a GPCR polypeptide. The present sequence represents a PCR primer for the VH domain of an antibody against human HGPRBMY27, which is used in an antibody against human HGPRBMY27, which is used in an
                                                                                                                                                               New polynuclectide encoding a human G-protein coupled receptor for preventing, treating, or ameliorating e.g. an inflammatory, reproductive, pulmonary, renal connective tissue, or endocrine disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                Example 34; Page 298; 356pp; English.
Ramanathan C, Feder J, Mintier G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             example from the present invention
                                                                                    WPI; 2002-657945/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of antibody at least 95-100% identical to a second antibody consisting of an antibody at least 95-100% identical to a second antibody consisting of an avaiable heavy (WH) or variable light (WL) domain of the antibody expressed by a hybridoma cell line consisting of XF2.5F1, XF21.1F8, XF27.28.18B5, X
                                                                                                                                        New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.
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                                                             WPI; 2002-643455/69
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Gaps

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Cytogratic; cardiant; neuroprotective; immunomodulator; antimigraine; sedative; gynaecological; potassium channel beta subunit; K+betaN6; gastrointeetinal; reproductive; neural; sleep; low DNA repair capacity; hyperpotassium channel activity, cardiovascular; melatonin synthesis; mammary cancer tumourigenesis; pineal gland associated disorder; mimune disorder; melatonic associated disorder; low free-radical buffering capacity; delayed sleep phase syndrome; circadian cycle; melatonin secretion; cancer; PCR; primer; ss.
Score 17.2; DB 1; Length 23;
Pred. No. 1.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                              K+beta M6 related VH domain PCR primer SEQ ID No 30.
                                                                          853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                              1 caccacciccicciccacitic 22
                                                                                                                                                                                                       ABT09824 standard; DNA; 23 BP
       86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2001; 2001US-0270132P.
27-MAR-2001; 2001US-0278953P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2002; 2002WO-US005674.
                                                                                                                                                                                                                                                                                 (first entry)
                        Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200270727-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                 05-DEC-2002
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                                                                                                                                                                                                                                               ABT09824;
                                                                                                                                                                         RESULT 677
                                                                                                                                                                                              ABT09824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinfertility; pulmonary; crtostatic; nephrotropic; hormonal; circulatory; gene therapy; inflammatory disorder; reproductive disorder; pulmonary disorder; cancer; renal disorder; connective tissue disorder; endocrine disorder; antibody; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G protein coupled receptor; GPCR; HGPRBMY27; antiinflammatory;
                                                                                                                                                                                              Gaps
                                                                                                                                                                                              ö
                                                                                                                                                        0.5%; Score 17.2; DB 1; Length 23; 66.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human HGPRBMY27 antibody VH domain PCR primer SEQ ID NO:40.
                                                                                                                     Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                  853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                         BP
                                                                                                                                                                             86.48;
                                                                                                                                                                                                                                                                                                                                                             ABQ83145 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Siemers N;

Ramanathan C,

Chen J, Jackson DG,

Lee L,

Feder J, Chang H;

WPI; 2002-713455/77.

(BRIM) BRISTOL-MYERS SQUIBB CO.

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The invention relates to an isolated polynucleotide encoding a potassium channel beta subunit (K+betaM6) polypeptide or its variants. The human dotassium beta subunit polynucleotide or polypeptide is useful for diagnosing, preventing, treating or ameliorating a pathological condition such as gastrointestinal, reproductive, neural, sleep, cardiovascular or activity, an immuned disorder related to hyperpotessium channel strivity, an immuned disorder related to aberrant NFB activity, pineal gland associated disorder migraine headaches, disorders associated with aberrant melatonin synthesis and/or release or with low DNA repair capacities or low free-radical buffering capacity, delayed sleep phase syndrome, aberrations in circadian cycle, mammary cancer tumourigenesis, age related disorders associated with decreased melatonin secretion, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer. This polynucleotide sequence represents a PCR primer relating to the potassium channel beta subunit (K+betaM6) of the invention
                                  polypeptide, useful for diagnosing, preventing, treating or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; diagestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antiinflammatory; antiulcer; ineuroporotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic; VH domain; PCR; primer; ss.
   New polynucleotide encoding human potassium channel beta subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer #3 for amplifying human antibody VH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                               Example 34; Page 281; 332pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2000; 2000US-0229358P.
25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK93297 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-010886/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200177137-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2001.
                                                                             e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
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ABK93297
XX
ABK93297
XX
DT 27-AUG-
XX
DE PCR pr:
XX
Albumin
XW
Albumin
Albumin
XW
Albumin
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8
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New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein.

Example 60; Page 512; 2102pp; English

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Gaps

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The present invention relates to albumin fusion proteins comprising a therageutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therageutic protein X. The albumin extends the schifts of protein X, and may increase its biological in vitro/in vivo activity. The protein Is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haemacropoietic disorders, neural disorders (e.g. Alzheimer's, schizophremia), and connective disorders (e.g. osteoporosis, arthritis). ABK93295-ABK93304 represent PCK primers used to amplify DNA encoding human antibody VH domains in the examples of the present invention
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer; inflammation; viral infection; autoimmune disease; neurodegeneration; rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma; hyperproliferative disease; heavy chain variable domain; PCR; primer; VH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human G-protein chemokine receptor (CCRS), HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5 antibodies are used for the treatment or prevention of inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also related antibodies.
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human HDGNR10 antibody VH domain amplifying PCR primer, Hu VH3-5'.
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                      Score 17.2; DB 1; Length 23;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                    Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0. Other;
                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 55; Page 171; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                               874
                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                                                 853 GAGGAGGAGCTGGTGGAGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                                                                                                                       0.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD42429 standard; DNA; 23
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86.4'
Matches 19, Conservative
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defective or aberrant chemotaxis of immune cells or T cell antigen-
presenting cell interaction, viral infections (specifically human immune
deficiency (including its early stages), cytomegalo or pox viruses),
autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
carinii infection, Kaposi's sarcoma or any condition associated with
aberrant expression of CCR5 or their ligands. They are also used for the
detection, diagnosis, prognosis and monitoring of cancers or other
hyperproliferative diseases. The present sequence is a PCR primer used to
amplify human HDGNR10 antibody heavy chain variable (VH) domain
                   88888888888888
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Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

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Match 0.5%; Score 17.2; DB 1; Length 23; Local Similarity 86.4%; Pred. No. 1.1e+03; es 19; Conservative 0; Mismatches 3; Indels
                                                                                       853 GAGGAGCTGGTGGAGGCTG 874
        Query Match
                              Best Loca
Matches
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Gaps

AAD46081 standard; DNA; 23 BP (first entry) 27-DEC-2002 AAD46081; RESULT 680

Human K+betaM2 antibody VH domain amplifying 5' PCR primer, VH3.

AAL49669 standard; DNA; 23 BP

AAL49669

RESULT

AAL49669;

Human; potassium channel beta-subunit; K+betaM2 protein; neural disorder; reproductive disorder; metabolic disorder; premature puberty; nephritis; endocrine disorder; memory disorder; neuroendocrine condition, asthma; spermatogenesis; renal disease; learning deficiency; Alzheimer's disease; neurodegenerative disease; learning deficiency; Alzheimer's disease; carcinoid tumour; blood coagulation disease; blood platelet disease; rheumatoid arthritis; allergy; hyperproliferative disease; gene therapy; graft-versus-host disease; organ rejection; antisterility; thrombolytic; antiinflammatory; neuroprotective; anti-Parkinsonian; immunosuppressive; nephrotropic; cytostatic; nootropic; hypotensive; vulnerary; PCR; primer;

Homo sapiens.

WO200266601-A2.

29-AUG-2002.

24-JAN-2002; 2002WO-US002332.

24-JAN-2001; 2001US-0263872P. 14-FEB-2001; 2001US-0269794P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Lee L, Chen J, Jackson D, Ramanathan C, Siemers N; Carroll P; Feder J, 1 Chang H, 0

WPI; 2002-691617/74.

New potassium channel beta-subunit, K+betaM2, proteins and nucleic acids, useful for diagnosing, treating and/or preventing e.g. reproductive, neural, metabolic, endocrine, memory, neurodegenerative disorders or

Example 19; Page 358; 366pp; English.

diseases.

The present invention relates to human potassium channel beta-subunit (K+betaM2) proteins and polynucleotides encoding such proteins. The FebrerM2 sequences are useful for diagnosing, treating and/or preventing reproductive disorders, neural disorders, disorders related to aberrant potassium regulation or hyper potassium channel activity, metabolic

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disorders (e.g. premature puberty), endocrine disorders (e.g. aberxant growth hormone synthesis and/or secretion), memory disorder, disorders of the testis (e.g. spermatogenesis), neuroendocrine condition related to aberrant thyroid hormone release, renal disease or disorders (e.g. capturints), disorders related to aberrant higher brain function (e.g. nephritis), disorders related to aberrant higher brain function (e.g. learning deficiencies), neurodegenerative diseases (e.g. Alzheimer's disease), prolliferative disorders (e.g. carcinoid tumour) and disorders (involving excessive smooth muscle tone or excitability (e.g. asthma).

They may be used to modulate haemostatic or thrombolytic activity, to treat or prevent blood coagulation diseases or disorders, blood platelet diseases, wounds, autoimmune diseases, disorders or conditions (e.g. rhemmatoid arthritis), allergic reactions (e.g. asthma), organ rejection or graft-versus-host disease, and hyperproliferative diseases. K+betaM2 or graft-versus also used in gene therapy. The present DNA sequence is a givented against human k+betaM2 DNA. This sequence is used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 86.4
Matches 19, Conservative
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Human; glycine receptor alpha subunit 4; HGRA4; HGRA4sv; splice variant; cardiovascular disorder; reproductive disorder; neural disorder; cardiant; antiarrhythmic; antianginal; antidiarrhieic; antilulcer; nootropic; neuroprotective; antibacterial; virucide; protozoacide; nervous system disorder; gatrointestinal disorder; gene therapy; infection; PCR; primer; ss. Anti-HGPR4 antibody VH domain PCR primer SEQ ID NO: 40. 27-NOV-2002 (first entry)

Unidentified.

#0200266606-A2.

29-AUG-2002

13-FEB-2002; 2002WO-US004329.

16-FEB-2001; 2001US-0269535P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Chen J, Jackson DG, Ramanathan C, Feder J, Chang H; Chang

WPI; 2002-674925/72.

New isolated nucleic acid molecules encoding human glycine receptor A4 (HGRA4) polypeptides, useful for preventing, treating and ameliorating conditions, e.g. neural or gastrointestinal disorders.

Example 24; Page 341; 349pp; English.

The present invention provides the protein and coding sequences of the human glycine receptor alpha 4 (HGRA4) and its splice variant HGRA4sv. The sequences can be used in the treatment of neural disorders, gastrointestinal disorders, disorders related to hyper glycine receptor

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activity, cardiovascular disorders, reproductive disorders, or bacterial, viral and parasitic infections. The present sequence is a PCR primer used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human humanized antibody that specifically binds to fibroblasts activating protein alpha, useful for treating cancer or tumor, and for imaging tumors associated with activated stromal fibroblasts, e.g. lung or breast cancer.
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, FAPalpha, fibroblast activating protein alpha, antibody, Ab, gene therapy, cancer, wound healing; inflammation, cytostatic, PCR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garin-Chesa P, Pfizenmaier K, Moosmayer D, Mersmann M;
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                                                                                                           0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
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                                                                         Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Human V gene library PCR primer HuVHB3.
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                                                                                                                                                                                   853 GAGGAGGAGCTGGTGGAGGCTG 874
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                                                                                                                                                                                                        1 GAGGTGCAGCTGGTGGAGTCTG 22
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11-SEP-2000; 2000GB-00022216
                                                                                                                                                                                                                                                                                                               AAK98428 standard; DNA; 23
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                                                                                                                                               19; Conservative
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                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer; ss
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                                                                                                             Query Match
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The present invention relates to a human or humanised antibody (Ab) which specifically binds to fibroblast activating protein alpha (FAPalpha). The antibodies are useful for preparing a composition for the treatment of cancer, and for imaging tumours associated with activated stronal fibroblasts, such as colorectal cancer, non-small-cell lung cancer, breast cancer, head and neck cancer, non-small-cell lung cancer, bladder cancer, pancreatic cancer and metastatic brain cancer, and diseases associated with the same, such as inflammation and wound healing. The present sequence is a PCR primer described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human humanized antibody that specifically binds to fibroblasts activating protein alpha, useful for treating cancer or tumor, and for imaging tumors associated with activated stromal fibroblasts, e.g. lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                              Human; FAPalpha, fibroblast activating protein alpha, antibody, Ab, gene therapy; cancer; wound healing; inflammation; cytostatic; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mersmann M;
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Pred. No. 1.1e+03;
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                                                                                                                                                                  Human V gene library PCR primer HUVHB3.
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1 GAGGTGCAGCTGGTGGAGTCTG 22
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                                                                          AAK98469 standard; DNA; 23
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Best Local Similarity 86.4
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                          WO200168708-A2
                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                    08-AUG-2002
                                                                                                                                                                                                                              primer; ss.
                                                                                                                                                                                                                                                                                                                      20-SEP-2001.
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                                                                                                        AAK98469;
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Schmidt 1
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                                             RESULT 683
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Gaps

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853 GAGGAGGAGCTGGTGGAGGCTG 874

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New isolated K+betaM4 or K+betaM5 nucleic acid molecule, useful for preventing, treating or ameliorating a medical condition related to hyper potassium channel activity such as cancer, immune, neural and
                                                                                       infectious disease; inflammatory disorder; cancer; Hepatotropic;
Cerebroprotective; Neuroprotective; Gastrointestinal; Gynecological;
Immunomodulator; Cardiovascular; Immunostimulant; Immunosuppressive;
Nephrotropic; Antiinflammatory; Cytostatic; Gene Therapy; human; VH; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K+berant and K+berans, CDNA sequences (I, ADJ33294 and ADJ33316), and senceded proteins sequences (II, ADJ33295 and ADJ33317). The invention is useful for preventing, treating or ameliorating a medical condition by administering (I) or (II) to a mammalian subject, where the medical condition is a disorder related to hyper potassium channel activity selected from a hepatic, neural, gastrointestinal, reproductive, immune, cardiovascular or renal disorder, or an immune disorder related to aberrant apoptosis or innate immunity, an infectious disease, an inflammatory disorder and cancer. The present sequence is a primer used in an example from the invention for amplifying VH domains, for k+betam6 proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human potassium channel beta subunits,
                                 hyper potassium channel activity; hepatic disorder; neural disorder; gastrointestinal disorder; reproductive disorder; immune disorder; cardiovascular disorder; renal disorder; immune disorder; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Siemers N;
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                   Potassium channel beta subunit; K+betaM4; K+betaM5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
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07-MAR-2001; 2001US-0274258P.
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Best Local Similarity
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                                                                                                                                                                                                                                           WO200268604-A2.
                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                06-SEP-2002
                                                                                                                                                                     primer; ss.
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ID ABT4
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This invention relates to an isolated nucleic acid molecule comprising a polynucleotide encoding a human G-protein receptor, including HGRBMY28, CC HGRBMY29, HGRBMY29, GDTPGENENY29/2 POLYPEPTIGES. THE HGRBMY28 OF HGRBMY29 polypeptides and nucleic acids are useful for treating, preventing or ameliorating a medical condition, e.g. an immune disorder, an inflammatory disorder, an inflammatory disorder, an inflammatory disorder, an inflammatory disorder, a neural disorder, a pastrointestinal disorder, a disorder a pulmonary coupled receptors are either disorder, a disorder a pulmonary coupled receptors are either disorder, a disorder a disorder related to aberrant p27 regulation, a disorder related to aberrant bNA repair regulation, a disorder related to aberrant DNA repair regulation, a disorder related to aberrant call cycle regulation, a disorder related to aberrant capptosis regulation, a disorder in disorder of the spleen, a disorder of the lymph capptosis regulation, a disorder of the spleen, a disorder of the injuder, a male or female reproductive disorder; an oesophageal disorder, a metabolic disorder, an endocrine disorder, a proliferative disorder afflicting the colon, cervix, lung, squamous cells or tissues, a renal disorder, a cardiovascular disorder, a placental disorder, and a disorder of the spleen, extense of the chestes, heart or lymph modes. The isolated polymucleotides of the invention may be used to treat disorders by gene therapy. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
HGPRBMY29v1; HGPRBMY29v2; HGRBMY28; HGRBMY29; immune disorder; pulmonary;
                   inflammatory; haematopoietic; gastrointestinal; small intestine; cancer; proliferative; aberrant p27 regulation; FEM1; cell cycle; DNA repair; pappicosis; spleen; lymph node; reproductive; oesophageal; metabolic; endocrine; colon; cervix; lung; squamous cell; renal; cardiovascular; placental; testis; heart; gene therapy; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New G-protein coupled receptors, HGRBMY28 and HGRBMY29, and their variants, useful for treating, preventing or ameliorating e.g. hematopoietic, neural, pulmonary, gastrointestinal, inflammatory or proliferative disorders.
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Pred. No. 1.18+03;
0; Mismatches 3; Indels
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03-MAY-2001; 2001US-0288468P.
25-JUN-2001; 2001US-0300619P.
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Best Local Similarity 86.4%;
Matches 19; Conservative (
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                                                                                                                                                                     Homo sapiens.
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AC AAL5
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Gaps

Neuroprotective; antiinflammatory; immunosuppressive; cytostatic; neural; nephrotropic; cardiant; human G-protein receptor; HGRBMY28; HGRBMY29;

Human GPCR related VH antibody cloning primer SEQ ID 142.

vivlemore401-10.rng

(first entry) 27-AUG-2003 Human antibody VH domain amplifying primer, Hu VH3-5'

Human, TNF-related apoptosis-inducing ligand; Kaposi's sarcoma, cancer, hyperproliferative disorder, rheumatoid arthritis, Parkinson's disease, neurodegenerative disorder; Alzheimer's disease; Hashimoto's disease; allergic disorder; acquired immune deficiency syndrome; ocular disorder; myasthenia gravis; autoimmune disorder; Huntington's disease, vaccine; septic shock; multiple sclerosis; inflammatory disorder; liver injury; infectious diseases; myelodysplastic syndrome; cardiovascular disorder; graft-versus-host disease; toxin-induced liver disease; cachexia; AIDS; errebrovascular disorder; thrombotic microangiopathy; aplastic anaemia; ischaemic injury; anorexia; diabetes; ulcerative colitis; psoriasis; asthma; AIDS; therapy; TRAIL receptor; tumour necrosis factor; TRAIL-R; PCR; primer; ss.

Homo sapiens.

WO2003042367-A2

22-MAY-2003.

13-NOV-2002; 2002WO-US036431

14-NOV-2001; 2001US-0331309P. 07-MAY-2002; 2002US-0377973P. 15-AUG-2002; 2002US-0403376P.

(HUMA-) HUMAN GENOME SCI INC

Rosen CA; Salcedo T, Roschke V, Ruben SM,

WPI; 2003-449572/42

Novel antibody against TNF-related apoptosis inducing ligand, useful for preventing, treating and ameliorating cancers and other hyperproliferative disorders, binds immunospecifically to TRAIL receptor polypeptide.

Example 5; Page 325; 405pp; English.

tumour necrosis factor (TRP)-related approximatory. This coult is a composed to the invention are useful for treating, preventing or ameliorating cancer (e.g. cancers of pancreas, uterine, breast, colon, lung and gastrointestine and Kaposi's sarcoma's and other hyperproliferative disorders, neurodegenerative disorders (e.g. neurodegenerative disorders (e.g. neurodegenerative disorders (e.g. lupus, rheumatoid arthritis, multiple sclerosis, myasthenia gravis, Hashimoto's disease and immunodeficiency syndrome; AIDS, herpes viral infections and other viral rheumatoid arthritis), infections diseases (e.g. acquired immune deficiency syndrome; AIDS, herpes viral infections and other viral confections), myelodysplastic syndromes (e.g. applastic anamia), graft-versus-host disease, ischaemic injury, liver injury, toxin-induced liver disease, septic shock, cachexia, anorexia and proliferative disorders. Antibodies of the invention are also useful for treating cardiovascular disorders associated with neovascularisation, speciasis, and ulcerative colitis and for wound healing. The invention is also used to prepare vaccines. The present sequence is a PCR primer used to amplify human antibody VH domain. This primer is used in the exemplification of The invention relates to antibodies that immunospecifically bind to the inventior

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

Gaps ö Query Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels

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1 GAGGTGCAGCTGGTGGAGTCTG 22 셤

ABQ76996 standard; DNA; 23

ABQ76996;

03-APR-2003 (first entry)

Human anti-VEGF2 antibody VH domain PCR primer HuVH3-5'.

cytostatic; cardiant; cardiovascular; antiinflammatory; antirheumatic; antiarthetic; antidiabetic; ophthalmological; antiallergic; vulnerary; immunosuppressive; dermatological; antipsoriatic; proliferative disorder; cancer; cardiovascular disorder; arrhythmia, cerebrovascular disorder; acrebral anoxia; inflammatory disease; infectious disease; angiogenesis; autoimmune disease; Systemic Lupus Erythematosus; wound healing; vascular tissue repair; gene therapy; vaccine; PCR; primer; ss. Human, VH domain; VL domain; vascular endothelial growth factor; VEGF-2;

Homo sapiens.

WO200283850-A2

24-OCT-2002

12-APR-2002; 2002WO-US011405.

13-APR-2001; 2001US-0283408P.

(HUMA-) HUMAN GENOME SCI INC.

Wager RE; Ruben SM, Rosen CA, Albert VR,

WPI; 2003-093008/08.

New isolated polynucleotide encoding an antibody which inhibits vascular endothelial growth factor (VEGF)-2 polypeptide, useful for diagnosing or treating diseases associated with aberrant VEGF-2 expression or function, e.g. cancer.

Example 32; Page 236; 344pp; English.

This invention describes a novel isolated polynuclectide encoding a first antibody comprising an amino acid sequence selected from at least one, two or three complementarity determining (CDR) region(s) of a VH and/or UL domain of a second antibody that immunospecifically binds to a vacular endothelial growth factor (VEGF)-2 polypeptide. The products of the invention have cytostatic, cardiovascular, antibheumatic, vulnerary, antiparamentory, antiarthritic, antidiabetic, ophthalmological, cardiant, antiallergic, immunosuppressive, dermatological and antipostiatic activity. The polynucleotide is useful in diagnosing, treating, preventing, prognosing, wellocating or monitoring diseases associated with aberrant VEGF-2 receptor expression or lack of VEGF-2 or VEGF-2 receptor function, such as cancer and other proliferative disorders (e.g. cerebral anoxia), inflammatory diseases, cerebrovascular disorders (e.g. cerebral anoxia), inflammatory diseases, infectious diseases, autoimmune diseases (e.g. rheumatoid arthritis, systemic Lupus Erythematosus, allergies), diabetic retinopathy or psoriasis. The polynucleotide, polypeptide and antibodies described in the invention may also be used to stimulate angiogenesis, wound healing, may also be used for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors and from the diagnostics and therapeutics e.g. gene therapy and in vaccines to treat human diseases. This sequence represents a PCR primer used in the isolation and amplification of polynucleotides described in the disclosure of the invention.

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

853 GAGGAGGAGCTGGTGGAGGCTG 874

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The invention relates to an isolated antibody comprising a first amino acid sequence having 95 % identity to a second amino acid sequence of either variable heavy chain or light chain-complementarity determining regions (VHCDR1)/VLCDR1, VHCDR2/VLCDR2 or VHCDR3/VLCDR3 appearing as ABG71906-ABG71911 being specific for human TRAIL receptors 1-4 (TNF (tumour necrosis factor) related apoptosis-inducing ligand receptor, also known as TR4, TR5, TR7 and TR10). Also included are an isolated cell that produces the antibody, an antibody that binds the same epitope on a TR4 polyapetide or detecting, diagnosing, prognosing or monitoring cancers, and other hyperproliferative disorders using the antibodies, a hybridoma cell line selected from the hybridoma cell line selected from the hybridoma cell lines selected from the hybridoma cell lines sontained in C ATCC Deposit No. PFA-3149, PFA-2687, PFA-3730, PFA-2739, PFA-2729, PFA-2729, PFA-2729, PFA-2731, PFA-2730, PFA-2729, PFA-2729, PFA-2731, APA-2731, APA-2731, APA-2731, PFA-2731, PFA-2732, PFA-2731, PFA-2732, PFA-2731, PFA-2732, PFA-2733, PFA-2733, PFA-2733, PFA-2733, PFA-2733, PFA-2733, PFA-2732, PFA-2733, PFA-
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                                                             Gaps
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0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
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                                                          Indels
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                                                          0; Mismatches
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                                                                                                                  853 GAGGAGGAGCTGGTGGAGGCTG 874
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16-NOV-2000; 2000US-0248847P.
27-NOV-2000; 2000US-025904P.
04-UTN-2001; 2001US-0255018P.
09-OCT-2001; 2001US-0327359P.
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                                                             19; Conservative
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                                Best Local Similarity
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     Query Match
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Byfurome (altob), on neurougenerative usolute (e.g., national, e.g., e.g., inflammatory diseases such as rhematoid arthritis, and psoriais, cardiovascular diseases, in promoting angiogenesis, wound healing, and in regulating immune response. Many other diseases and disorders are listed in the specification. The antibody is administered in combination with a chemotherapeutic agent selected from irinotecan, paclitaxel (TAXOL (RTW), and gencitabine. The antibody is useful as a diagnostic tool to monitor the expression of TRAIL receptor expression on cells, to detect, purify, and target the polypeptides, and in immunoassays for qualitatively and quantitatively measuring levels of TRAIL receptor polypeptides. The present sequence is a PCR primer used to amplify a nuclaic acid encoding the heavy chain variable region of an anti-TRAIL receptor antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; vascular endothelial growth factor; VEGF-2; inflammatory disease; proliferative disorder; tumour; breast; cancer; brain; prostate; colon; lymphangioma; infection; Kaposi's sarcoma; psoriasis; immunosuppressive; rheumatoid arthritis; diabetic retinopathy; gene therapy; antimicrobial; cytostatic; ophthalmological; autoimmune disease; VH; PCR; primer; ss.
decreased apoptosis, e.g. cancer (such as colon, breast, uterine, pancreatic, lung, gastrointestinal, and Kaposi's sarcoma), graft-versushost disease (GVHD), infectious disease, acquired immunodeficiency syndrome (AIDS), or neurodegenerative disorders (e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to vascular endothelial growth factor (VEGF)-2 antibodies. VEGF-2 antibodies are useful for treating, preventing or ameliorating a disease or disorder, such as inflammatory diseases or disorder, proliferative disorders, tumours, tumour metastasis, breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New vascular endothelial growth factor (VEGF)- 2 antibodies, for treating, preventing or ameliorating a disease or disorder, such as inflammatory diseases, proliferative disorders, autoimmune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               853 GAGGAGCAGCTGGTGGAGGCTG 874
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cancer, brain cancer, prostate cancer, colon cancer, lymphangioma, an infectious disease, Kaposi's sarcoma, an autoimmune disease, rheumatoid arthritis, psoriasis, diabetic retinopathy, a disease or disorder associated with aberrant VEGF-2 (receptor) expression, or a disease or disorder associated with the lack of VEGF-2 (receptor) function. The antibody is also useful for detecting, diagnosing, prognosing, or monitoring cancers and other hyperfoliferative disorders. VEGF-2 is also used in gene therapy. The present sequence is a PCR primer used for amplifying human VH gene. This sequence is used in the exemplification of
      88888888888888888
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Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

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Gaps
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0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels
                                                                     853 GAGGAGGAGCTGGTGGAGGCTG 874
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                   Local Similarity 86.4%;
les 19; Conservative
     Query Match
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ABX99237 standard; DNA; 23 (first entry) 21-MAY-2003 ABX99237; RESULT 690

Anti-CAN-12 antibody VH region PCR primer Hu VH3.

Human; ss; PCR; CAN-12; calpain; cysteine protease; cytostatic; protein co-ordinate data; antiinflammatory; neuroprotective; primer; immunosuppressive; inotropic; vulnerary; analgesic; gene therapy; vaccine; neurodegenerative condition; musculo-degenerative condition; cancer; multiple sclerosis; a blood disorder; autoimmune disorder; oseophagitis, oseophagitis, oseophagitis, cancer; and motility disorder; chromosome 2p16-p21. antibody; heavy chain variable region; light chain variable region.

Homo sapiens

WO200288303-A2.

07-NOV-2002

02-APR-2002; 2002WO-US010419.

04-MAY-2001; 2001US-0288768P. 06-JUN-2001; 2001US-0296180P. 25-JUN-2001; 2001US-0300620P. 03-APR-2001; 2001US-0281253P.

(BRIM) BRISTOL-MYERS SQUIBB CO

Chen J, Duclos F, Feder JN, Nelson TC, Seiler S,

WPI; 2003-156689/15.

New isolated nucleic acid molecule for diagnosing, treating or preventing disorders, e.g. neuro- and musculo-degenerative conditions or cancer, related to the CAN-12 or CAN-12v2 polypeptides.

Example 35; Page 454; 737pp; English.

The invention relates to an isolated nucleic acid molecule comprising a polynucleotide having a sequence that is at least 95% identical to the human cDNAs for CAN-12 or its variants (CAN-12v1 and CAN12v2), including various functional fragments defined in the specification CAN-12 is a calpain family cysteine processe, the gene for which is located on chromosome 2p16-p21. Also included are the encoded CAN-12 proteins (including fragments), CAN-12 recombinant vectors, host cells, anti-CAN-

a molecule or a molecule complex which comprises the structural coordinates of CAN-12 and CAN-12v2 models given in the specification, a method for identifying a mutant with altered biological properties, function or activity of CAN-12 and CAN-12v2 models given in the specification, a method for identifying a mutant with altered biological properties, function or activity of CAN-12 and CAN-12v2 and a method for designing or selecting compounds as potential modulators of CAN-12 and CAN-12v2. The nucleic acid molecule and the polypeptide are useful in diagnosing, treating and/or preventing various diseases and disorders related to the CAN-12 or CAN-12v2 polypeptides, particularly neuro- and musculo- degenerative conditions, such as cancer, multiple sclerosis, blood disorders, autoimmune disorders, oesophagitis or other ossophagaal motility disorders. Many other diseases and disorders are listed in the specification. The methods may be used in identifying agonists and antagonists of the above polypeptide and polynucleotide. The present sequence is a PCR primer used to clone DNAs encoding the VH and VL (heavy and light chain variable regions) molecules of anti_CAN-12 antibodies

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Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

.; 0 0.5%; Score 17.2; DB 1; Length 23; 16.4%; Pred. No. 1.1e+03; 3; Indels 0; Mismatches Best Local Similarity 86.4%; Matches 19; Conservative Query Match

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ACC48653 standard; DNA; 23 RESULT 691 ACC48653

BP.

ACC48653;

11-AUG-2003 (first entry)

Human antibody heavy chain variable region PCR primer Hu VH3-5'.

antianginal, neuroprotective; osteopathic; cytostatic; immunosuppressive; antibacterial; antipsoriatic; antiinflammatory; gynaecological; immunosupmessive; dermantantimulant; antirbanmatic; antiarthritic; antianaemic; haemostatic; dermatological; antiarteriosclerotic; virucide; vulnerary; antiasthmatic; gene therapy; antibody; PCR; primer; 88. Human; potassium channel; K+betaMB; cardiovascular; vasotropic; cardiant;

WO2003020910-A2.

13-MAR-2003

04-SEP-2001; 2001US-0317087P. 16-OCT-2001; 2001US-0329666P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Chang H; Lee LM, Feder JN,

WPI; 2003-290187/28.

New human potassium channel beta subunit (K+betaWB) polypeptide or polymucleotide, useful for preventing, treating or ameliorating e.g. breast or colon cancer, arthritis, asthma, multiple sclerosis, ostecarthritis or ischemia.

Example 32; Page 284; 308pp; English.

The present sequence is PCR primer Hu VH3-5', which is designed to amplify human antibody heavy chain variable regions (VH). It is one of a set of primers (see ACC48651-86) used in the identification and cloning of VH and VL domains of antibodies directed against the novel human

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companies can be used to generate expression vectors. Antibodies directed to KabetaMB are useful for affinity purification of the polypeptide, in diagnostic assays and imaging, in immunophenotyping, and in therapeutic applications, including the use of nucleic acids encoding the antibodies in antibody-based gene therapy. Disorders that may be treated include a male reproductive disorder, a testicular disorder, testicular cancer, a neural disorder, a disorder related to aberrant calcium, potassium or potassium channel regulation, a pullmonary disorder, an immune system disorder associated with mis-regulation of NPKB, an inflammatory disorder, an innate immunity disorder, a disorder associated with a failure to initiate and/or sustain an adequate inflammatory response, in the antibody and an antibody and an antibody and an antibody and an adequate inflammatory response, an innate immunity disorder, and innate                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell mediated autoimmune disease, or psoriasis
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Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

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Query Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels
                                                                                                                  853 GAGGAGGAGCTGGTGGAGGCTG 874
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Gaps ö

> RESULT 692 AAD54813

AAD54813 standard; DNA; 23 BP

AAD54813;

26-JUN-2003 (first entry)

Human TR4 antibody VH domain amplifying PCR primer, Hu VH3.

TRAIL receptor; TR4; cancer; Kaposi's sarcoma; cerebellar degeneration; hyperproliferative disorder; neurodegenerative disorder; immune disorder; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; Huntington's disease; amyotrophic lateral sclerosis; rheumatoid arthritis; multiple sclerosis; Sjogran's syndrome; asthma; biliary cirrhosis; multiple sclerosis; Sjogran's syndrome; asthma; biliary cirrhosis; Bencet's disease; Crohn's disease; allergic disorder; glomerulonephritis; immune deficiency syndrome; myasthenia gravis; polymyositis; inflammatory disorder; rheumatoid arthritis; septic shock; infections disease; acquired immunodeficiency syndrome; viral infection; ALDS; proliferative disorder; myelodysplastic syndrome; aplastic anaemia; ischaemic injury; myocardial infarction; reperfusion injury; cachexia; ancexia; stroke, cardiovascular disorder; peripheral artery disease; limb ischaemia; arrhythmia; congestive heart failure; neovascularisation; ocular disorder; wound healing; angiogenesis; transplantation; primer; PCR; human; ss

Homo sapiens

WO200297033-A2

05-DEC-2002.

2001US-0293473P. 2001US-0294981P. 07-MAY-2002; 2002WO-US014268 25-MAY-2001; 04-JUN-2001;

02-AUG-2001; 2001US-0309176P. 21-SEP-2001; 2001US-0323807P. 09-OCT-2001; 2001US-0327364P. 14-NOV-2001; 2001US-0331310P. 20-DEC-2001; 2001US-0341237P. 05-APR-2002; 2002US-0369860P. 2001US-0331044P 07-NOV-2001;

Human; antigen; platelet glycoprotein; GPIIIa; fibrin; ss; PCR; primer; anti-platelet binding protein; heavy chain variable region; phage display library; platelet aggregation thrombus formation; thromboembolism; unstable angina; asphenous vein bypass graft; percutaneous transluminal coronary angioplasty; atrial fibrillation; valvular heart disease; cerebrovascular disease; Trousseau's syndrome; peripheral vascular disease; arterial thromboembolism; acute diseaminated intravascular coagulation; extracorporeal device; prosthetic heart valve; auxiliary-subclavian venous thrombosis.

Human heavy chain variable region gene cDNA library PCR primer #3.

BP.

ACD28137 standard; DNA; 23

25-SEP-2003 (first entry)

ACD28137;

(HUMA-) HUMAN GENOME SCI INC.

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The present invention relates to novel antibodies that immunospecifically bind to TRAIL receptor (TR4). Sequences of the invention are useful for treating, preventing or amediorating cancer (e.g. colon, breast, uterine, pancreatic, lung, gastrointestinal or central nervous system cancer e.g. medulloblastoma, neuroblastoma, glioblastoma and Kaposi's sarcoma) in human. They are useful for detecting expression of TR4 polypeptide and detecting, diagnosing, prognosing or monitoring cancers and other hypercentation, diagnosing, prognosing or monitoring cancers and other hypercentating preventing or amediorating neurodespeneration are useful for treating, preventing or amediorating or monitoring cancers and other hypercentating preventing or amediorating or monitoring acancers (e.g. upons) prognosing or monitoring acancers and other hypercenting progneting or amediorating or anthiotopic lateral sclerosis, retinitis pigmentosa, cerebellar degeneration and Huntington's disease, retinitis pigmentosa, cerebellar degeneration and Huntington's disease, colymyositis, immune-related glomerulonephritis, monitorin's disease, polymyositis, immune-related glomerulonephritis, myasthenia sclarosis, inflammatory circlositis and immune deficiency syndrome (AlbS), infectious diseases (e.g. acquired immunodeficiency syndrome). Infections and other viral infections and other viral infections and cardiovascular diseases (such as that caused by stroke, anorexia and toxin-induced liver diseases (such as alcohol). They are also useful for treating cardiovascular diseases or disorders and contar diseases such as limb ischemmia, diseases or disorders and cardiovascular tuberculosis, diseases or disorders and cardiovascular tuberculosis, diseases or disorders and contaring and sequence is human TR4 antibody the propertion or recovery from s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                  Novel antibody useful for treating cancers and other hyperproliferative disorders, immunospecifically binds to TRAIL receptor and comprises variable heavy or light chain complementarity determining regions.
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Vaughan TJ
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Rosen CA, Albert VR, Dobson CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                   Example 5; Page 224; 301pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salcedo T, Ruben SM,
                                                        WPI; 2003-140454/13.
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1 GAGGTGCAGCTGGTGGAGTCTG 22

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27-FEB-2001; 2001US-00794189
   US2003027207-A1.
 Homo sapiens,
     06-FEB-2003
               Filpula DR;
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The invention relates to a nucleic acid molecule, or its complement, that encodes an anti-placele binding protein, isolated from a phage display encodes an anti-placele binding protein, isolated from a phage display concodes an anti-placele thing protein, isolated from a phage display of library by an in vitro selection process that comprises screening at class one human anti-play variable domain expression library against at class one human placelet antigen, and the human antibody variable domain expression library expresses single-chain proteins. Also included are an expression library expresses a single-chain proteins. Also included are an expression overcor comprising the week of an on-human mammal. Comprising the cells producing the anti-platelet binding protein encoded by the mucleic acid that binds to a placelet aggregation or thrombus formation), a substantially isolated and purified human antibody (or its fragment) that binds to a placelet binding protein, and a conjugate comprising a non-confident antigenic polywer covalently linked to the single-chain antigen-binding site of the anti-platelet binding protein, and a conjugate comprising and antigenic polywer covalently linked to the single-chain antigen-binding protein are useful for inhibiting platelet aggregation or platelet midding protein are useful for whole the blood vessel having an endothenial linking in need of treatment. The cottor, the host cell, the anti-platelet binding protein or platelet midding protein or platelet midding protein or platelet midding protein or platelet midding protein or sector sector of whose cell, the anti-platelet binding protein or platelet midding protein or platelet midding protein or sector. The host cell, the anti-platelet binding protein or the only are encodery preventing or treating conditions such as venous for conjugate of encodery preventing or treating thromboembolism, unstable angina, saphenous vain bypass graffs, valvular heart disease, cerebrowageular disease, secondary prevent conjugates of medical d Novel nucleic acid molecule encoding anti-platelet binding protein which is useful for inhibiting platelet aggregation or platelet mediated thrombus formation in blood and for treating venous thromboembolism. Example 1; Page 17; 30pp; English 29-FEB-2000; 2000US-0185628P. WPI; 2003-554858/52. FILP/) FILPULA D R.

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platelet binding protein antibodies
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0.5%; Score 17.2; DB 1; Length 23; 16.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels
Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                               86.48;
                                             Query Match
Best Local S
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Human, protein coordinate data; heavy chain variable domain; VH; cancer; complementarity determining region; CDR; light chain variable domain; VL; TRAIL receptor 7; TR7; tumour necesses factor; KILLER; death receptor 5; DR5; TRAIL receptor 2; TRAIL-R. FELST WF. related apoptosis-inducing ligand; Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma; glioblastoma; graft versus host disease; antibody therapy; nootropic; AIDS; acquired immune deficiency syndrome; neurodegenerative disorder; immunosuppressive; neuroprotective; antibody therapy; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated antibody or its fragments such as VHCDR1 (heavy chain variable domain complementarity determining region), vHCDR2 (Hight chain variable domain complementarity determining region), VLCDR2 or VLCDR3. The antibody or its fragment immunospecifically binds TRAIL (tumour necrosis factor; TNF-related apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The antibody or its fragment is useful for treating, preventing or amellorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or agastrointestinal cancer or Kaposi's sarcome or cancer of the central nervous system such as medulloblastomm, neuroblastomm or glioblastomm or graft versus host disease, AIDS (acquired immune deficiency syndrome) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibody or its fragment, useful for treating, preventing or ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy. The present sequence is human VH domain amplifying PCR primer
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a neurodegenerative disorder. The invention is useful in anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;
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                                                                                                                                                              Human VH domain amplifying PCR primer, Hu VH3-5'.
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                                        BP
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                                      AAL62799 standard; DNA; 23
                                                                                                                          (first entry)
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Best Local Similarity 86.44
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                        06-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-2003
                                                                                 AAL62799;
RESULT 694
                     AAL62799
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Local Similarity 86.4 les 19; Conservative

Matches

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Gaps

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BP.

inflammatory disease; arthritis, asthma; AIDS; psoriasis; graft-versus-host disease; systemic lupus erythematosus; reproductive disorder; varicocale; orchitis; neural disorder; Alzheimer's disease; Parkinson's disease; depression; schizohrenia; cardiovascular disorder; hypertension; acute heart failure; pulmonary disorder; endocrine disorder; obesity; diabetes; anorexia; bone disorder; osteoporosis; pain; cancer; chromosome identification; gene therapy; PCR; primer; ss; variable heavy chain; VH. Human; G-protein coupled receptor; HGPRBMY25; immune disease; Human heavy chain variable region related PCR primer #3. 1 GAGGTGCAGCTGGTGGAGTCTG 22 21-FEB-2002; 2002US-00081775 ACD91445 standard; DNA; 23 (first entry) US2003060409-A1. Homo sapiens. 22-SEP-2003 27-MAR-2003 cancer ACD91445; RESULT 695 셤

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The invention describes an isolated nucleic acid molecule comprising a sequence that is at least 95% identical to a polymoclectide encoding novel human G-protein coupled receptor HGPRBMY25. The nucleic acid molecule, polypeptide and antibody are useful in diagnosing, preventing, treating or ameliorating medical conditions where GPCR is directly or andirectly involved, such as immune or inflammatory diseases (e.g. arthritis, asthma, AIDS, graft-versus-host disease, psoriasis or systemic lupus erythematosus), reproductive disorders (e.g. varioccele or cribits), neural disorders (e.g. Alzheinmer's disease, Parkinson's disease, depression or schizophrenia), cardiovascular disorders (e.g. hypertension or acute heart failure), pulmonary disorders, endocrine disorders (e.g. obseity, diabetes or anorezial, bone disorders (e.g. osteoporosis), pain or cancer. The polymucleotide may also be used in identification, in identifying organisms from minute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule encoding a human G-protein coupled receptor (HGPRBMY25) is useful for diagnosing, preventing or treating diseases involving the receptor, e.g. inflammation, diabetes, asthma, hypertension
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21-FEB-2001; 2001US-0270134P. 27-MAR-2001; 2001US-0278952P.
                                                                                                                                                                                                                                                                                                                                                             Ramanathan CS, Feder JN,
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                                                                                                                                                                                                            (FEDE/) FEDER J N.
(MINT/) MINTIER G A.
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New human G-protein coupled receptor HGPRBMY26 polypeptides and nucleic acids, useful for preventing, treating or ameliorating e.g. testicular disorder, choriocarcinoma, infertility, viral orchitis, or Cushing's

Example 35; Page 106; 149pp; English.

syndrome

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The invention relates to an isolated nucleic acid molecule encoding a G protein-coupled receptor HGPRBWY26. The nuclectide sequence comprises sequential nuclectide deletions from either the C-terminus or the N-terminus. Also included are an isolated polypeptide encoded by the crecombinant host call comprising the nucleic acid, making a crecombinant host call comprising the nucleic acid, making a pathological condition or a susceptibility to a pathological condition in testicular tissue of a subject, identifying a compound that modulates the bological activity of a human G-protein coupled receptor HGPRBMY26 (and a member consisting of NPAT/GRE or NPAT G alpha 15, all undefined), and creening for candidate compounds capable of modulating activity of the HGPRBMY26 polypetide. The HGPRBMY26 polypetides, polypeutides, polypeutides, compounds or pharmaceutical preparations comprising HGPRBMY26 are useful for preventing, treating or ameliorating a male reproductive condition; can amine disorder or a condition where G-protein coupled receptors are (in) directly involved in disease progression, a testicular disorder, testicular cancer, choriocarcinoma, nonseminoma, seminoma,
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Query Match

Matches

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male reproductive condition; amine disorder; testicular disorder; male resticular cancer; choriticarcinoma; nonseminoma; seminoma; seminoma; spermatogenesis; infertility; filmfelter's syndrome; XX male; epididymitis; genital wart; germinal cell aplasia of the testis; cryptorchidism; varicocele; immotile cilia syndrome; viral orchitis; premature puberty; incomplete puberty; Kallman syndrome; Cushing's syndrome; hyperplaciniania; haemochromatosis; congenital adrenal hyperplacia; collicle stimulating hormone deficiency; granulomatous disease; PCR; primer; antibody; heavy chain; light chain;
                                                                                                                                         Human anti-HGPRBMY26 antibody heavy chain PCR primer Hu VH-3 5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barber LE;
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874
            1 GAGGTGCAGCTGGTGGAGTCTG 22
853 GAGGAGGAGCTGGTGGAGGCTG
                                                                                                                                                                                                                                                                                                                                                            07-MAR-2002; 2002US-00092771.
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27-MAR-2001; 2001US-0278927P.
                                                                          ADA09673 standard; DNA; 23
                                                                                                                    06-NOV-2003 (first entry)
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(RAMA/) RAMANATHAN C
(MINT/) MINTIER G A.
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                                                    RESULT 696
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spermatogenesis, infertility, Klinefelter's syndrome, XX male, epididymitis, genital warts, germinal cell aplasia of the testis, cryptorchidism, varicocele, immotile cilia syndrome, viral orchitis, premature puberty, incomplete puberty, Kallman syndrome, Cushing's syndrome, hyperprolactinaemia, haemochromatosis, congenital adrenal hyperplasia, follicle stimulating hormone (FSH) deficiency and granulomatous disease. The present sequence is a PCR primer used in the isolation sequences encoding heavy or light chains (VH or VL) of anti-HGPRBMY26 antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-protein coupled receptor; GPCR; HGPRBMY14; neuropeptide Y receptor; proliferative disorder; testicular cancer; NF-kB; diabetes mellitus; autoimmune disorder; male reproductive disorder; appetite disorder; VH; eating disorder; neurodegenerative disorder; human; PCR; primer; ss.
                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder e.g., testicular cancer, autoimmune or neurodegenerative disorders, or diabetes mellitus.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Human HGPRBMY14 antibody VH gene amplifying primer, Hu VH3-5'.
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Pred. No. 1.1e+03;
0; Mismatches 3; Indels
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Best Local Similarity 86.4%;
Matches 19; Conservative 0
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16-OCT-2001; 2001US-0329897P
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Barber LE;
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RAMANATHAN C S.
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KORNACKER M.
RYSECK R.
CACACE A.
BARBER L E.
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The invention relates to G-protein coupled receptor (GPCR), HGPRBMY14 and its corresponding nucleic acid sequence. HGPRBMY14 sequences are useful for preventing or treating a disorder directly linked to aberrant neuropeptide Y receptor activity or to aberrant DNA synthesis, an eating or appetite disorder, male reproductive disorder or proliferative disorder, andle reproductive disorder or proliferative disorder e.g., testicular cancer. These are useful for detecting a susceptibility to) a pathological condition. HGPRBMY14 is useful for

Example 30; Page 111; 166pp; English.

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identifying its binding partners, including agonists and antagonists. Antagonists to the polypeptide is useful in treating a disorder related to aberrant NF-NB activity or a proliferative disorder. HOPRBMY14 DNA and protein are also useful in treating neurodegenerative or autoimmune disorders, or diabetes mellitus. The present sequence is a RT-PCR primer used for amplifying human HGPRBMY14 antibody VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a human chemokine betal (Ckbl) protein (I) comprising a deletion in amino acid residues from the amino terminus and/or carboxy terminus of the 31 residue amino acid sequence (S1, see ADD06466). (I) has anti-HIV, neuroprotective, antithyroid, antiarthritic, antirheumatic, immunosuppressive, nootropic, antiinflammatory, antiathatic, antiallergic, osteophymic, nephrotrophic, tuberculostatic, virucide, antiatheroselerotic and antimicrobial activities. (I) is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiarthritic; antirheumatic; immunosuppressive; nootropic; antiinflammatory; antisthmatic; antiallargic; osteopathic; nephrotrophic; tuberculostatic; virucide; antialherosclerotic; antimicrobial; infection; HIV; immune disorder; haematopoietic disorder; autoimmune disorder; multiple sclerosis; Grave's disease; arthritis; ransplant rejection; neurodegenerative disorder; Alzheimer's disease; inflammatory disease; asthma; allergic disorder; inflammatory howel disease; glomerulomphritis; infectious disease; tuberculosis; hepatitis infection; herpes viral infectious disease; viral infection; viral infection; proliferative disorder; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human chemokine betal protein comprising deletion in amino acids from amino and/or carboxy terminus, and is a fusion protein further comprising human serum albumin, is useful for treating multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; chemokine betal; Ckbl; anti-HIV; neuroprotective; antithyroid;
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                         ö
                                                                                                                                                                              Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03;
                                                                                                                                                                                                                       Indels
                                                                                                                                        Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human serum albumin; HSA; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 46; SEQ ID NO 35; 423pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human VH domain PCR primer SEQ ID NO:35.
                                                                                                                                                                                                                                                            853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                     1 GAGGIGCAGCIGGIGGAGICIG
                                                                                                                                                                                                                                                                                                                                                                                                       ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2002; 2002WO-US016525.
                                                                                                                                                                                0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2001; 2001US-0293212P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                     ADD06499 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                       19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-140456/13.
                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bell A, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200297038-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD06499;
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                RESULT 698
                                                                                                                                                                                                                         Matches
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for preventing infection, preferably viral (human immunodeficiency virus (HIV)) infection, in a cell, by contacting the cell with (I). (I) is also useful for treating a disease, such as HIV infection or immune disorders, haematopoietic disorders, autoimmune disorders, multiple sclerosis, carve's disease, arthritis, rheumatoid arthritis, transplant rejection, grave's disease, arthritis, transplant rejection, asthma, allergic disorders, inflammatory bowel disease, osteoarthritis, collitis, inflammatory kidney diseases, glomerulonephritis, inflammatory disease, disease, tuberculosis, hepatitis inflammatory disease, userulosis, hepatitis inflammatory disease, cultammatory disease, userulosis, hepatitis infections, broliferative disorders or aberosclerosis, in an individual. (I) inhibits or abolishes the ability of HIV to bind to, viral infection, proliferative disorders or arberosclerosis, in an individual. (I) inhibits or abolishes the ability of HIV to bind to, viral also acts a CCRS agonists or antagonists, stimulate chemotaxis of CCRS-expressing cells, inhibit CCRS igand binding to a CCRS expressing cells, inhibit CCRS igand binding to a CCRS expressing colls, inhibit CCRS igand binding to a CCRS expressing cells, inhibit CCRS igand binding to a CCRS expressing cells, inhibit CCRS expression. (I) is useful as an immunological probe for the differential identification of the tissues or cell-types. (I)-human serum albumin (HSA) fusion proceins are useful for disquesing and preventing various disorders in mammals, cell-types. (I)-human serum albumin (HSA) fusion proceins are useful for electrophoresis techniques, for raising antibodies, and to test the electrophoresis techniques, for raising antibodies, and to test the biological activities of the CKbl protein. (I)-HSA fusion protein portein portein custing for molecules that bind to the CKbl protein portein custing for molecules that bind to the CKbl protein portein portein custing for molecules that bind to the CKbl protein in the contein contein custing for mol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTRPC3 VH domain PCR primer, SEQ ID 272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             853 GAGGAGGTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 caccrecrecrecrecres 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC83653 standard; DNA; 23 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003012063-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 699
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The present invention relates to novel proteins and their coding sequences (ADC83405) encoding human transient receptor potential sequences (ADC83400-ADC83405) encoding human transient receptor potential channels. The coding sequences are useful for preparing a medicament for preventing, treating or ameliorating a medical condition, such as renal disorders; a disorder related to abbarrant calcium regulation; neural disorders various choroid plexus neoplasms; prion disorder; cerebellum disorders, various choroid plexus neoplasms; prion disorders; movement disorders; a disorder that maps to or is misoriated with chromosome locus 9q21.11-21.31; amyotropic lateral calcionasis early onset pulverulent cataract; infantlle nephronophthisis; hypomagnesemia with secondary hypocalcemia; osteoporosis; DNA-repair deficiencies; xeroderma pigmentosum; UV sensitivity; gamma irridation sensitivity; pyrimidine dimer sensitivity; chemical mutagenesis; Bloom's conceased levels of apurinic/Apyrimidine/Abasic sites; disorders related to aberrant signal transduction; and disorders related to misregulation con the content of the content 
                                                                                                                                                           userul in preventing, treating or ameliorating a medical condition, such as renal disorder, neural disorder e.g., Alzheimer's disease, or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Albumin fusion protein; therapeutic protein; HIV; osteoporosis; cancer;
                                                                                                                               New human transient receptor potential channel (LTRPC3) nucleic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wound; autoimmune disease; cardiovascular disease; hepatitis; multiple sclerosis; psoriasis; graft-versus-host disease; stroke; atherosclerosis; inflammation; anti-HIV; osteopathic; cytostatic; vulnerary; cardiant; hepatotropic; neuroprotective; antipsoriatic; immunosuppressive; carebroprotective; antiarteriosclerotic; antiinflammatory; human; VH domain; PCR; primer; ss.
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  Bol
Lee L, Blanar MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which was used in an example from the invention
                                                                                                                                                                                                                                             Example 34; Page 436; 508pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human VH domain DNA, PCR primer #3.
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  Wu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD68036 standard; DNA; 23 BP
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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Feder JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2004 (first entry)
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                               Sun L;
                                                                               WPI; 2003-278394/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS2003125247-A1
     Chen J,
                                 Levesque PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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  Lee N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 700
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vivlemore401-10.rng

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New albumin fusion protein for diagnosing, preventing
                                                                                                                                                           Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 AAD61497 standard; DNA; 23 BP
                                                                                                                                                                                                                                                                                                                                                             26-APR-2002; 2002US-00133797
                                                                                                                                                                                                                                                                                                                                                                        26-APR-2001; 2001US-0286764P
                                                                                                                                                                           Best Local Similarity 86.4%;
Matches 19; Conservative
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     Haseltine WA;
                                         factor) and an albumin.
               WPI; 2003-810996/76
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CHEN J.
FEDER J N.
                                                                                                                                                                                                                                                                                                                                        US2003109021-A1
                                                                                                                                                                                                                                                                                                                  PCR; primer; 88
                                                                                                                                                                                                                                                                                                                             Ното варіеля
                                                                                                                                                                                                                                                                                                                                                   12-JUN-2003
    Rosen CA,
                                                                                                                                                                                                                                            AAD61497;
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                  (WUSS/) (CHEN/) (FEDE/) (LEEL/) I
                                                                                                                                                                                                                     RESULT 701
AAD61497
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The present invention relates to albumin fusion proteins comprising any of the therapeutic proteins listed in the specification, or their fragments or variants, and an albumin protein or its fragments or variants. The invention also discloses pharmaceutical compositions comprising the albumin fusion proteins, a kit comprising the albumin fusion proteins, and methods for treating a disease or disorder in a patient, that is modulated by the therapeutic protein or its fragment ovariant. The compositions and methods of the invention are useful in variant. The compositions and methods of the invention are useful in such as HIV, osteoporosis, cancer, wounds, autoimmune diseases or disorders, cardiovascular diseases, hepatitis, multiple sclerosis, psoriasis, graftversus-host diseases, stroke, atherosclerosis and inflammation. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence represents a PCR primer. Note: The present sequence is given in the Sequence listing but is not mentioned elsewhere in the specification. The present sequence given as SEQ ID No:38 in the Sequence
diseases (e.g. HIV, cancer, atherosclerosis or stroke) comprises a
therapeutic protein (e.g. cathepsin K or vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                listing differs from that given on page 129.
                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 38; 180pp; English
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0.5%; Score 17.2; DB 1; Length 23; 66.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels 853 GAGGAGGAGCTGGTGGAGGCTG 874 22 GAGGTGCAGCTGGTGGAGTCTG

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Gaps

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Human MMP-29 antibody VH domain amplifying 5' PCR primer, VH3.

Human; metalloprotease; MMP-29; immune disorder; reproductive disorder; testicular disorder; gastrointestinal disorder; cardiovascular disorder; ovarian disorder; hepatic disorder; pulmonary disorder; renal disorder; metabolic disorder; neural disorder; millammatroxy disease; sclerosis; skeletal muscle disorder; amportrophic lateral sclerosis; gene therapy; immunomodulatory; antiinfertility; cytostatic; hepatotropic; pulmonary; nephrotropic; cardiant; vascular; neuroprotective; nootropic; muscular;

LEE L.

and polymuclectides encoding such proteins. Sequences of the invention are used to diagnose a pathological condition or a susceptibility to a medical condition in a subject. They are useful for preventing, treating, or ameliorating medical conditions is such as immune condition or disorders, cancer, male reproductive disorders, male reproductive disorders, cancer, hepatic disorders, pulmonary disorders, metabolic disorders, cancer, hepatic disorders, pulmonary disorders, metabolic disorders, cancer, hepatic disorders, pulmonary disorders, metabolic disorders, renal disorders, pulmonary disorders, metabolic disorders, renal disorders, pulmonary disorders, metabolic disorders, inflammatory diseases inflammatory diseases where proteases are either directly or indirectly involved in disease progression, sclerosis, amyotrophic lateral sclerosis or a disorder associated with aberrations of chromosome 2q32. MMP-29 sequences are also useful in gene therapy. The present sequence is human MMP-29 antibody VH domain amplifying PCR primer. This sequence is used in the exemplification of the invention present invention relates to novel metalloprotease (MMP-29) proteins ..cm .uucieic acid encoding a metalloprotease (MMP-29) useful for diagnosing a pathological condition or a susceptibility to a medical condition in a subject. ö Query Match

0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other; Krystek SR; 853 GAGGAGGTGGTGGAGGCTG 874 Example 37; Page 134; Opp; English. Lee L, Chen J, Feder JN, (KRYS/) KRYSTEK S R. WPI; 2003-801269/75 Wu S, ઠે

Human antibody related PCR primer SEQ ID NO:14. 1 gaggrecageregregaerere 22 ADD67296 standard; DNA; 23 BP 15-JAN-2004 (first entry) ADD67296; RESULT 702 ADD67296

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Gaps

apparatus combination; binding site collection; pattern recognition; profiling; screening; ss; PCR primer.

Homo sapiens. Synthetic

WO2003062402-A2

31-JUL-2003

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24-JAN-2003; 2003WO-US002397.

24-JAN-2002; 2002US-0352011P.

(POIN-) POINTILLISTE INC.

Ault-Riche D,

WPI; 2003-636736/60.

New combination comprising an addressable collection of binding sites, software comprising instructions for pattern recognition and an imager for detecting patterns, useful for profiling a sample.

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The present invention describes a combination of apparatus (1)

comprising: (a) an addressable collection of binding sites; and (b)

software comprising instructions for pattern recognition and/or an imager

for detecting patterns. The addressable collection of binding sites

comprises: (a) capture agents, where each capture agent is preselected to

specifically bind to a pre-selected tags; and (b) tagged reagents, each

comprises a molecule and etags; where each locus in the

collection comprises the same capture agent, where the tagged reagent

comprises a molecule and a tag, each tag is pre-selected to specifically

bind to a capture agent, where each tag is bound to a capture agent,

comprises a molecule and a tag, each tag is bound to a capture agent,

comprises a molecule and a tag, each tag is bound to a capture agent,

comprises a molecule and a tag, each tag is bound to a capture agent,

comprises the ranged reagent with the capture agent, where

comprises a sample; (1) a system for profiling samples; (2) a method for profiling

comprising a capture system or computer readable medium comprising

the database produced by the method of profiling a sample; (4) a method

for preparing a capture system that displays a collection of binding

comprising capture agents bound to a solid support and tagged reagents;

and (6) a method for screening samples. The combination (1) is useful for

of the dramation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; HEAG2; potassium channel; aberrant amygdala function; autism; fear; neurodevelopmental disorder; psychopathological; schizophrenia; aggression; memory; emotional disorder; aberrant hypothalamus function; leptin receptor disorder; energy-expenditure disorder; motion sickness; food intake disorder; bone remodeling disease; bone disorder; nootropic; neurophysin-related disorder; appetite suppression; neuroleptic; therapy; neuroprotective; osteopathic; anorectic; antiemetic; VH domain; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer used to amplify human HEAG2 VH domain, Hu VR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                   Disclosure; SEQ ID NO 14; 309pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 cacerecaecreciceaerere 22
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25-JUN-2001; 2001US-0300614P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Conservative
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CHEN J.
JACKSON D.
RAMANATHAN C S.
SIEMERS N O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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(RAMA/)
(SIEM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR; ss.
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Gaps

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                                                                                                                                                                                                                                                                The present invention provides novel polynucleotides encoding HEAG2 (human potassium channel) polypeptides, fragments and homologues thereof. The invention is useful for producing three-dimensional representation of a molecule or molecular complex comprising the structural coordinates of the PAS domain of HEAG2. The invention is also useful for treating conditions such as disorder associated with aberrant amygdala function, fear, neurodevelopmental psychopathological disorders, softizophrenia, autism, aggression, memory, enotional disorders, aberrant hypothalamus function, leptin receptor disorders, food intake disorders, energy-expenditure disorders, bone camodeling disease, appetite suppression and motion sickness. The present sequence is PCR primer used to amplify human HEAG2 VH domain. This sequence is used in the exemplification of
                                                                                                                                             Computer for producing three-dimensional representation of molecule o molecular complex of PAS domain of potassium channel protein, useful designing compounds as potential modulators for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                   Siemers NO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     albumin fusion protein; albumin activity; human serum albumin; serum osmotic pressure; shelf-life; stability; antidiabetic; gene therapy; diabetes mellitus; PCR; primer; ss; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 0.5%; Score 17.2; DB 1; Length 23; l Similarity 86.4%; Pred. No. 1.1e+03; 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human albumin fusion protein-related PCR primer SeqID1058.
                                                                   Ramanathan CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                 Feder JN, Lee L, Chen J, Jackson D,
Chang H, Duclos F, Krystek SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                       Example 32; Page 108; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGGTGCAGCTGGTGGAGTCTG 22
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2002US-0378950P.
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                                                                                                                                                                                                      neurodevelopmental disorders
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(CHAN/) CHANG H.
(DUCL/) DUCLOS F.
(KRYS/) KRYSTEK S R.
                                                                                                                   WPI; 2003-810910/76.
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003060071-A2.
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24-JAN-2002;
28-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention
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Ruben SM;

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antibody (ABI) comprising an amino acid sequence of at least one, two or three complementarity determining regions (CDR) of a heavy chain variable (VH) domain of an antibody (AB2) that immunospecifically binds to a protein chemokine receptor (CCRS), at least one, two or three CDR regions of a light chain varaible (VL) domain of AB2 or at least one, two or three CDR regions of both a VH and a VL domain of AB2. The antibody is useful for detecting, diagnosing, prognosing or monitoring cancers and other hyperproliferative disorders and for treating, preventing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide comprising domains of an antibody that binds G-protein chemokine receptor CCRS is useful to detect, diagnose, prognose or monitor cancers and other hyperproliferative disorders and to treat or prevent a disease or disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ameliorating a disease or disorder. This sequence represents a primer used in the isolation of an immunoglobulin heavy chain variable region from antibodies of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a new isolated polynucleotide that encodes an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 17.2; DB 1; Length 23; 36.4%; Pred. No. 1.1e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
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                                                                                                                  09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                                                                                                                            Li Y,
           01-MAY-2002; 2002US-00135839.
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                                                                                                                                                                                        09-FEB-2001; 2001US-00779879.
                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                            Roschke V,
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-898066/82
                                                                                 09-FEB-2000;
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Matches
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           8 X X B X X B X X B X X B X X B X X B X X B X X B X X B X 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel albumin fusion protein having albumin or biological activity. Human serum albumin is responsible for a significant proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of the therapeutic protein. The albumin fusion protein of the invention may allow production of compositions with antidiabetic activity whilst the nucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating diabetes mellitus. The present sequence is that of a PCR primer which was used in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New albumin fusion protein, useful for preparing a composition for treating diabetes mellitus.
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28-MAY-2002; 2002US-0383123P.
05-JUN-2002; 2002US-0384625P.
10-JUL-2002; 2002US-0394625P.
24-JUL-2002; 2002US-0398008P.
09-AUG-2002; 2002US-041031P.
13-AUG-2002; 2002US-041135F.
18-SEP-2002; 2002US-0411426P.
02-OCT-2002; 2002US-0414984P.
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                                                                                                                                                                                                                                                                                                                     11-OCT-2002; 2002US-0417611P.
23-OCT-2002; 2002US-0420246P.
05-NOV-2002; 2002US-0423623P.
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Matches 19; Conservative
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(PRIN-) I
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Gaps

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874

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KW calpain superfamily; hepatotropic; nephrotropic; gynaecological;
KW antiinflammatory; Cytostatic; vasotropic; gynaecological;
KW andiinflammatory; Cytostatic; vasotropic; cardiant; ophthalmological;
KW auditory; gene therapy; vaccine; hypercalpain activity;
KW auditory; gene therapy; vaccine; hypercalpain activity;
KW female reproductive tract; amenorrhoea; primary dysmenorrhoea;
KW female reproductive tract; amenorrhoea; primary dysmenorrhoea;
KW female reproductive tract; amenorrhoea; primary dysmenorrhoea;
KW paccutal inflammatory disease; endomerriosis; pelvic aromatase deficiency;
KW chlamydial infection; neural disorder; hepatic disorder; immune disorder;
KW hardisonietic disorder; renal disorder; pulmonary disorder;
KW proliferative disorder; renal disorder; colon disorder;
KW proliferative disorder; colon; gastrointestinal tissue; colon cancer;
CM colon adenocarcinoma; ischaemia-reperfusion injury; hearing disorder;
KW primer; 88; VH domain.
                                                                                                                               Human protease-42 protein-related VH domain PCR primer SeqID70.
                                                                                      (first entry)
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cytostatic; CCRS modulator; antibody; G-protein chemokine receptor; CCRS; cancer detection; cancer diagnosis; cancer prognosis; cancer monitoring; cancer; hyperproliferative disorder; human; HDGNR10; PCR; primer; 88; immunoglobulin; heavy chain; variable region.

US2003166024-A1.

04-SEP-2003

Homo sapiens

Human immunoglobulin variable heavy chain primer seq id 25.

(first entry)

12-FEB-2004

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(RYSE/) F
(CACA/) C
(BARB/) F
(BOLD/) E
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(KORN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel DNA sequences encoding protease-42

Equally and the calpain superfamily. Calpains have been associated with numerous disease states. The invention may allow development of compounds with hepatotropic, pardiant, ophthalmological, antinflammatory, cardiant, ophthalmological, antinflammatory, activities. The sequences provided may be useful for gene therapy or development of a vaccine. The nucleic acids may be useful for preparing a composition for diagnosing, preventing, treating or ameliorating a composition for diagnosing, preventing, treating or ameliorating a composition for diagnosing, preventing, treating or ameliorating a disorder related to aberrant calpain activity, a disorder associated with deficiencies in calpain activity, a disorder associated with Mypercalpain activity, a disorder associated with Mypercalpain activity, a disorder related to aberrant calcium regulation, privice tract disorders, infertility, carcinomas of the female reproductive tract disorders, infertility, carcinomas cuterine bleeding dysfunction, pelvic aromatase deficiency, premature cuterine bleeding dysfunction, pelvic aromatase deficiency premature companse, placental dysfunction, pelvic aromatase deficiency placens, calpains, either directly or indirectly, are involved in disease to memopause, either directly or indirectly, are involved in disease calpains, either directly or indirectly, are involved in disease calpains, either directly or indirectly, are involved in disease calpains, either directly or indirectly, are involved in disease colon or gastrointestinal tissue, colon clon or gastrointestinal tissue, colon colon or gastrointestinal related to adenocarcinoma, ischaemia-reperfusion injury, hearing disorders, mailtiple sclerosis, cataracts or myocarditis.
                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding a human cysteine protease, useful for preparing
                                                                                                                                                                                                                                                                                                                                                                                                               a composition for diagnosing, preventing or treating e.g., neural, hepatic, immune, hematopoietic, renal or pulmonary disorders.
                                                                                                                                                                                                                                                                                     Nayeem A, Nelson TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 33; SEQ ID NO 70; 449pp; English.
                                                                                                                                                                                                                                     ဗ
                                                                                                                                                                                                                                                                                  Chen J, Feder JN,
                                                                                                                             14-MAR-2003; 2003WO-US007984.
                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB
                                                                                                                                                                               14-MAR-2002; 2002US-0364941P
                                                                                                                                                                                                                                                                                                                                  WPI; 2003-767513/72
                          WO2003078594-A2
                                                                          25-SEP-2003
                                                                                                                                                                                                                                                                                  Duclos F,
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RESULT 707
AAD63842
ID AAD63842 standard; DNA; 23
XX
AC AAD63842;
XX
DT 12-FEB-2004 (first entry)
XX
CX
KW Human HGPRBMY14 antibody VI
XX
XX
KW eating; appetite disorder;
KW autoimmune disorder;

뗦

12-FEB-2004 (first entry) Human HGPRBMY14 antibody VH domain amplifying PCR primer, Hu VH3-5'.

Human; G-protein coupled receptor; GPCR; hyper immune activity; melanoma; eating; appetite disorder; male reproductive disorder; testicular cancer; autoimmune disorder; hypercongenital condition; birth defect; vulnerary;

ADF18235 standard; DNA; 23 BP.

ΩI

RESULT 708 ADF18235

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid molecule encoding G-protein coupled receptor (GPCR). The methods and compositions of the present invention are useful for preventing, treating and/or ameliorating a disorder related to aberrant the spression or activity, a disorder fairecity linked to aberrant neuropeptide Y receptor activity, an eating or appetite disorder, a disorder linked to aberrant DNA synthesis, male reproductive disorder, immune activity, hypercongenital conditions, birth defects, necrotic lessions, wounds, disorder related to aberrant signal transduction, immuno compromised conditions, HIV infections, proliferative disorder of the skin, melanoma, foetal lung disorder, disorder of the breast, breast cancer, in addition to other proliferative diseases and/or disorders, in the call of the coll of th
necrotic lesion, signal transduction, proliferative disorder, anorectic, foetal lung disorder, proliferative disease, dermatological, anti-HIV, gene therapy, cancer, angiogenesis, gynaecological, relaxant, PCR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissues in the G1 or G2 phase of the cell cycle, disorders related to abnormal populations of cells or tissues in the S or M phase of the cell cycle, disorders related to aberrant smooth muscle contraction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiogenesis. The invention is useful in gene therapy. The present sequence is a PCR primer used to amplify human HGPRBMY14 antibody VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acids encoding G-protein coupled receptor polypeptide, useful for diagnosing, treating, ameliorating and/or preventing disorders, such as cancer, and autoimmune, gynecological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nelson TC, Kornacker MG, Ryseck R;
DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 30; Page 118; Opp; English
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                                                                                                                                                                                                                                                                                                                                                                         05-FEB-2001; 2001US-026525P.
16-OCT-2001; 2001US-0329897P.
05-FEB-2002; 2002US-00067649.
                                                                                                                                                                                                                                                                                                                    14-NOV-2002; 2002US-00295693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ramanathan CS,
Barber LE, Bol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEDER J N.
RAMANATHAN C S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NELSON T C.
KORNACKER M G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYSECK R.
CACACE A.
BARBER L E.
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                                                                                                                                                                                                     US2003198976-A1
                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                              23-OCT-2003
                                                                                         primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feder JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cacace A,
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                                                                               Human, TL5; cytostatic; anti-HIV; immunosuppressive; immunostimulant;
virucide; dermatological; antiinflammatory; antirheumatic; antiarthritic;
neuroprotective; muscular-gen.; antiasthmatic; antiallergic; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of PCR primer Hu VH3-5' for the human heavy chain variable region (VH). A set of primer sequences ADF18233-ADF18268 was used in the identification and cloning of VH and VL domains from antibody-expressing cell lines. The invention relates to antibodies that specifically bind to TL5. These are used in the diagnosis, prevention or rreatment of a disease or disorder such as an autoimmune disease, retamnent of a disease or disorder such as an autoimmune disease, transplant rejection, cancer (especially colon cancer, breast cancer, userine cancer, parceatic cancer, lung cancer, gastrointestinal cancer, and Kaposi's sarcoma), an immunodeficiency syndrome, or an inflammatory disease such as asthma or allergy.
                                                                                                                                                                                                                                                                                                                                                              New antibody that specifically bind to TLS, useful for diagnosing, preventing, treating or ameliorating diseases (e.g. cancer, autoimmune disease, inflammation or transplant rejection), and in immunophenotyping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TR2; orphan nuclear receptor; cytostatic; immunosuppressive; virucide; immunostimulant; dermatological; antiinflammatory; antirheumatic; antiathritic; neuroprotective; muscular; antiasthmatic; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 0.5%; Score 17.2; DB 1; Length 23; Local Similarity 86.4%; Pred. No. 1.1e+03; es 19; Conservative 0; Mismatches 3; Indels
                                                        Antibody heavy chain variable region PCR primer Hu VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-TR2 antibody VH domain amplifying primer Hu VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ.ID NO 13; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACF58403 standard; DNA; 23 BP
                                                                                                                                                                                                                  10-APR-2003; 2003WO-US010956
                                                                                                                                                                                                                                         15-APR-2002; 2002US-0372087P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                  12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                       WPI; 2003-854097/79
                                                                                                                                                                                                                                                                                                                                                                                                     epitope mapping.
                                                                                                                                                                 WO2003089575-A2.
                                                                                                                   PCR; gene; ss.
                                                                                                                                           Homo sapiens.
                                                                                                                                                                                          30-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACF58403;
           ADF18235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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The invention relates to an isolated antibody (A1) that specifically binds orphan nuclear receptor TR2 or that competitively inhibits the binding of an antibody to TR2. The antibody and methods are useful in inhibiting the growth of or Killing orphan nuclear receptor TR2 expressing cells and treating, preventing or ameliorating a disease or disorder selected from an autoimmune disease, graft-versus-host disease, transplant rejection, cancer, herpes simplex virus infection and an immunodeficiency, e.g. lupus erythematous, rheumatoid arthritis, multiple solatosis, mysathenia gravis, or inflammatory discorders (e.g. asthma or allergies). The antibody may also be used in immunoassays for qualitatively and quantitatively measuring levels of TR2 polypeptides in biological samples, in immunophenotyphing of cells lines and biological samples, or in epicope mapping. Sequences ACFS8401-436 represent PCR primers for amplifying the VM and VL domains of an anti-TR2 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibodies that specifically bind to orphan nuclear receptor useful for diagnosing, preventing, treating or ameliorating diseases, e.g. cancer, autoimmune diseases, inflammation or viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMAD; VH; CDR; complementarity determining region; VL; scFv; single chain antibody; antidiabetic; type II diabetes; human; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer Hu VH3-5' used to amplify human VH domain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
gene therapy; vaccine; scFv; TR01G03; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAGGTGCAGCTGGTGGAGTCTG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG30372 standard; DNA; 23 BP.
                                                                                                                                                                                                                                                                                                                                                                           12-APR-2002; 2002US-0371722P
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                                                                                                                                                                                                                                                                                                     10-APR-2003; 2003WO-US010955
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-853871/79.
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                                                                                                                                                  WO2003086301-A2
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                                                                                                                                                                                                                            23-OCT-2003
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                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG30372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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ADG30372
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Gaps

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The invention describes a new isolated nucleic acid molecule comprising:

a polynucleotide fragment or complement of the cDNA sequence;
by sequence; a polynucleotide fragment of the cDNA sequence; a

polynucleotide sequence comprising nucleotides 4-1404 or 1-1404 of the

1404-by sequence; or a polynucleotide sequence encoding a polypeptide, or

1404-by sequence; or a polynucleotide sequence encoding a polypeptide, or

1404-by sequence or comprising nucleotides sequence dees not

1404-by sequence; or a polynucleotide sequence encoding a polypeptide

1504-by sequence or comprising nucleotide sequence, or its

1505-by sequence or nucleotide sequence having only A or I residues. The

1505-by peptide comprises a fully defined 335-amino acid sequence, or its

1505-by sequence. The nucleic acid is useful for preparing a composition

1506-by sequence or its acid is acid is an enclorating a medical or

1507-by sequence or its acid is acid is a medical or

1508-by sequence or its acid is a disorder associated with deficiencies in

1509-by sequence or its accorder associated with deficiencies in

1509-by sequence or its accorder associated with deficiencies in

1509-by sequence or its accorder associated with hypermethionine activity,

1509-by sequence related to aberrant protease regulation, a disorder related to

1509-by sequence or its accorder accorders, metabolic disorders,

1509-by sequence or its accorder accorders, metabolic disorders,

1509-by sequence or its accorder accorders, an inflammancer or its accorder                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotide useful for detecting single nucleotide polymorphisms
                                  New nucleic acid encoding a human methionine aminopeptidase, useful for preparing a composition for diagnosing, preventing or treating e.g., neural, metabolic, vascular, immune or inflammatory disorders or ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variable domain of antibodies directed against novel human methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; single nucleotide polymorphism; microarray; side effect; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single nucleotide polymorphism detection primer, SEQ ID No 1688.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                          Example 34; SEQ ID NO 38; 183pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-2002; 2002JP-00034717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aminopeptidase, Protease-39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.5%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF88105/c
ID ADF88105 standard; DNA; 23
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WPI; 2003-900678/82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in human gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer; PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF88105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                The invention relates to a novel antibody that specifically binds to a GMAD polypeptide comprising a first amino acid sequence that is at least 95% identical to a second amino acid sequence of a VH CDR (complementarity determining region) or VL CDR of an scPv (single chain antibody molecule). The antibody of the invention demonstrates antidiabetic activity and may be useful for diagnosing, monitoring, treating, preventing or ameliorating type II diabetes. The current sequence is that of the PCR primer which was used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Naglich J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gynaecological, antiinflammatory; cytostatic; vasotropic; neuroprotective; gene therapy; vaccine; methionine activity deficiency; hypermethionine activity; protease regulation; cell cycle regulation; neural disorder; metabolic disorder; vascular disorder; immune disorder; inflammatory condition; proliferative disorder; colon cancer; varian encer; proliferative disorder; colon cancer; ovarian cancer; human; methionine aminopeptidase; protease-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                              New antibody that specifically binds to GMAD polypeptide, useful for diagnosing, monitoring, treating preventing or ameliorating type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 0.5%; Score 17.2; DB 1; Length 23; Local Similarity 86.4%; Pred. No. 1.1e+03; les 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bassolino DA, Krystek SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human heavy chain variable domain primer seq id 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heavy chain variable domain; primer; ss
                                                                                                                                                                                                                              Claim 2; SEQ ID NO 5; 410pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          853 GAGGAGGTGGTGGAGGCTG 874
                                                              Chowdhury P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 caccrecrecrecrecacrers 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feder JN, Nelson TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-2002; 2002US-0351251P.
08-MAR-2002; 2002US-0362872P.
                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JAN-2003; 2003US-00350516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG25299 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEDER J N.
NELSON T C.
BASSOLINO D A.
KRYSTEK S R.
                                                              Albert VR,
                                                                                                     WPI; 2003-804305/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ь.
                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS2003204070-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-2003
                                                              Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG25299;
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(NELS/)
(BASS/)
(KRYS/)
(NAGL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 711
ADG25299
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Matches
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New nucleic acid molecule encoding a human epidermal growth factor, BGS-8, useful for preventing, treating or ameliorating immune, hematopoietic, male or female reproductive, hepatic, cardiovascular, or proliferative
                                                                                                                                                                                                                                                                                                                                 Human growth factor protein BGS-8-related PCR primer SegID29.
                                                                                                                                                            Sequence 23 BP; 5 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                0; Mismatches
Claim 2; SEQ ID NO 1688; 704pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 32; SEQ ID NO 29; 330pp; English.
                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                 1652 CCGAGGACAACGTGATGAAGAT 1673
                                                                                                                                                                                                                           23 CTGAGAACGAGGTGAAGAT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                              ADG16167 standard; DNA; 23 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-2001; 2001US-0298340P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-2002; 2002WO-US019442.
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                     Local Similarity .86.4 es 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S, Feder J, Lee LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-167439/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2002102319-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                 26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                   primer; ss
                                                                                                                                                                                                                                                                                               ADG16167;
                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                             713
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                            RESULT 71
ADG16167
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This invention relates to a novel DNA sequence encoding a human growth factor with homology to epidermal growth factor-8 (BGS-8). The invention may be useful for the development of compounds with an immunosuppressive, haemostatic, gynaecological, antiinfertility, hepatotropic, cardiant or cytostatic activity which act as BGF agonists. In addition the genetic equences of the invention may be useful for gene therapy. The invention may be useful for preventing, treating or ameliorating medical conditions, such as immune disorder, haematopoietic disorder, a hepatic disorder, a male or female reproductive disorder, a hepatic disorder, a cardiovascular disorder, a proliferative disorder, cancer, or a disorder related to aberrant growth factor regulation, wound repair, a disorder related to aberrant growth factor regulation, wound repair, or regulation of the BGF receptor, or a proliferative condition involving one or more lymph node, uterus, liver, heart, stomach, lung and pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein; human serum albumin; HSA; therapeutic protein; shelf-life; in vitro biological activity; in vivo biological activity; metabolic disorder; endocrine disorder; diabetes; type 1; type 2; diabetes-related condition; hyperglycaemia; neural disorder; neuropathy; extinopathy; cardiovascular disorder; heart diseases; renal disorder; obesity; glucose level maintenance; weight loss; antidiabetic; cardiant; anorectic; ophthalmological; gene therapy; antibody; VH domain; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human antibody VH domain PCR primer Hu VH3-5', SEQ ID NO:344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   853 GAGGAGGTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH21547 standard; DNA; 23 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-0359370P.
2002US-0360000P.
2002US-0367500P.
2002US-0370227P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002US-0378950P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-2002; 2002WO-US040892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002US-0402131P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002US-0402708P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-2004 (first entry)
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08-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2002;
24-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH21547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADH21547
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                                                 The invention relates to a novel polymucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonucleotide containing single mucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1200 fully defined sequences as given in convention; a labelling probe containing the SNP containing oligo; and a microarray equipped with the SNP containing oligo. The isolated human a microarray equipped with the SNP containing oligo. The isolated human contains in human gene. The isolated human gene is also useful for detecting the single mucleotide colymorphisms in human gene is also effective in detecting single mucleotide polymorphism in a human gene. This polymucleotide sequence represents one of the PCR primers used in the single nucleotide polymorphism one of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human growth factor; epidermal growth factor-8; BGS-8; immunosuppressive; haemostatic; grasecological; antiinfertility; hepatotropic; cardiant; cytostatic; BGF agonist; gene therapy; immune disorder; cardiant; haematopoletic disorder; reproductive disorder; reproductive disorder; hepatic disorder; reproductive disorder; hepatic disorder; cardiovascular disorder; proliferative disorder; cancer; aberrant growth factor regulation; wound repair; angiogenesis regulation; epithelial cell growth regulation; epithelial, cell growth regulation; epidemal cell growth regulation; BGF receptor; proliferative condition; lymph node; uterus; pancreas; liver; heart; stomach; lung; human; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
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18-SEP-2002; 2002US-0411355P. 02-OCT-2002; 2002US-0414984P.

11-OCT-2002; 23-OCT-2002; 05-NOV-2002; 2002US-0423623P

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Haseltine WA;

2002US-0420246P

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Gaps

RESULT 715 ADG68058 Matches 셤 8

The invention relates to fusion proteins comprising human serum albumin and therapeutic polypeptide such as a therapeutic protein, antibody or peptide or their variants or fragments. The therapeutic protein protein may be fused to the N-terminus, the C-terminus or both termin of albumin via a linker. The albumin component of the fusion proteins or prological activity of the proteins compared with those of the corresponding thesapeutic proteins on their own. The invention also relates to nucleic acids the proteins on their own. The invention also relates to nucleic acids albumin fusion protein, vectors and host cells comprising an albumin fusion protein, the method of extending the shelf-life of a lusing an albumin fusion protein with albumin fusion protein mucleic acid, compositions and kits comprising an albumin fusion protein with albumin fusion proteins may be used in the treatment of metabolic/endocrine disorders, diabetes and diabetes. The albumin fusion proteins may be used to treat type 1 and type 2 diabetes, hyperglycaemia, neural disorders (especially heart disease, renal disorders and obseity. The proteins may also be used in a method of maintaining a basal glucose level in a patient and in a method for losing weight. The present sequence is related to the invention. New albumin fusion protein, useful for preparing a composition for Example 91; SEQ ID NO 344; 1086pp; English. treating diabetes mellitus. WPI; 2003-598501/56

0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; 3; Indels Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other; 0; Mismatches Local Similarity 86.4 les 19; Conservative Query Match

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Gaps

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neuron degeneration; neurogenic inflammation; allergy; immunodeficiency; excessive immune activation; visual defect; hearing disorder; pain; cancer; hypertension; cardiovascular disease; Calcium homeostasis; osteoporosis; hypercalcuric stone disease; chronic renal failure; prollferative disorder; ischaemia-reperfusion injury; heart failure; immuno-compromised condition; HIV infection; NF-kappa-B regulation; apoptosis regulation; NF-kappa-B activity; human; PCR; primer; ss. TRP-PLIK2; transient receptor potential channel; antiinflammatory; gynaecological; immunomodulatory; cardiant; cytostatic; neuroprotective; antiviral; anti-HIV; gene therapy; immune disorder; haematopojetic disorder; inflammatory disorder; renal disorder; secondary hypocalcaemia familial haemophagocytic lymphohistiocytosis; Human TRP-PLIK2 gene-related Ab VH domain PCR primer SeqID274. hyper transient receptor potential activity, prostate cancer; testicular cancer, chromosome 9q21 aberration; amyotrophic lateral sclerosis, frontotemporal dementia; early-onset pulverulent cataract; infantile nephronophthisis; reproductive disorder; hepatic disorder; ADG68058 standard; DNA; 23 BP (first entry) hypomagnesaemia; 11-MAR-2004 ADG68058

Homo sapiens

WO200294999-A2

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Blanar M,
                                Lee L,
                                Chang H,
                                Chen J, Feder J, Wu S,
                         BRIM ) BRISTOL-MYERS SQUIBB CO
       22-MAY-2002; 2002WO-US016164.
              22-MAY-2001; 2001US-0292599P. 08-MAR-2002; 2002US-0362944P.
                                       WPI; 2003-148463/14.
28-NOV-2002
                                Lee N,
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New TRP-PLIK2 nucleic acid and its splice variants, useful for manufacturing a medicament for preventing, treating or ameliorating a medical condition, e.g. renal, inflammatory or reproductive disorders.

Example 33; SEQ ID NO 274; 457pp; English.

This invention relates to a novel isolated human TRP-PILK2 (transient receptor potential channel) nucleic acid sequence and the protein encoded by it. The invention may be useful for the development of compounds with an antiinflammatory, gramecological, immunomodulatory, cardiant, cytostatic, neuroprotective, antiviral or anti-HIV activity. In addition, the DNA sequence may be useful for gene therapy. The invention may therefore be useful for manufacturing a medical condition, for preventing, contexting or ameliorating a medical condition, for example immune cisorders, hepstucks, hepstuck disorders, repair in a disorders, renal disorders, reproductive disorders, hepstuck disorders, negorders, respirate cancer, consistent cancer, diseases related to chromosome. 9q21.2-22 aberrations, testicular cancer, diseases related to chromosome. 9q21.2-22 aberrations, amyotrophic lateral scalerosis with frontotemporal dementia, early-onset curveruphic ataract, infantile nephronophthisis, hypomagnesaemia with secondary hypocalcaemia familial hemophagocytic lymphohistiocytosis, neuron degeneration, neurogenic inflammation, allergy, conset immunodeficiency/excessive immune activation, visual defects, hearing ciscorder, pain, cancer, hypertension, cardiovascular diseases, diseases associated with disturbances in Calcium homeostasis including costeoporosis, hypercalciuric stone disease, chronic renal failure, immuno-compromised conditions, HIV infection, disorders associated with aberrant compromised conditions, HIV infection, disorders associated with aberrant caperiation, disorders in which decreasing of increasing NF-kappa-B activity would be therapeutically desirable and disorders in which activity would be therapeutically desirable and disorders in which activity would be therapeutically desirable and disorders in which activity would be therapeutically desirable.

Gaps ö 0.5%; Score 17.2; DB 1; Length 23; Indels Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other; 1.1e+03; 0; Mismatches Pred. No. 86.4%; Query Match 0.5 Best Local Similarity 86.4 Matches 19; Conservative

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853 GAGGAGGAGCTGGTGGAGGCTG 874 1 GAGGTGCAGCTGGTGGAGTCTG 22 ö 셤

ABT17138 standard; DNA; 23 BP

RESULT 716

ABT17138;

Cytostatic; cardiant; cardiovascular; antiinflammatory; antirheumatic; antiarthritic; antidiabetic; ophthalmological; antiallergic; immunosuppressive; dermatological; antipsoriatic; vulnerary; antibody; CDR.region; VH domain; VL domain; immunospecific; VBGF-2; cancer; proliferative disorder; cardiovascular disorder; arrhythmia; cerebrovascular disorder; cerebral anoxia; inflammatory disease; Human VEGF-2 related PCR primer SEQ ID No 38. (first entry) 10-APR-2003

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New isolated polynucleotide encoding an antibody which inhibits a VEGF-2 polypeptide, useful for diagnosing, treating or preventing diseases associated with aberrant VEGF-2 expression or function, e.g. cancer or
infectious disease; autoimmune disease; rheumatoid arthritis; Systemic Lupus Erythematosus; allergy; diabetic retinopathy; psoriasis; angiogenesis; wound healing; vascular tissue repair; human; PCR; primer;
                                                                                                                                                                                 Wager RE;
                                                                                                                                                                                                                                                                         Example 32; Page 240; 425pp; English
                                                                                                                                                                                Albert VR, Ruben SM,
                                                                                                             L2-APR-2002; 2002WO-US011474.
                                                                                                                               13-APR-2001; 2001US-0283385P.
24-JAN-2002; 2002US-0350366P.
                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                    WPI; 2003-092991/08.
                                                                    WO200283704-A1.
                                                 Unidentified.
                                                                                                                                                                                                                                                      inflammation.
                                                                                         24-OCT-2002.
                                                                                                                                                                                Rosen CA,
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The invention relates to an isolated polynuclectide encoding a first antibody at least 95-100% identical to a second antibody comprising an amino acid sequence selected from at least on, two or three CDR region(s) of a VH or VL domain where the first antibody immunospecifically inhibits a VBGF-2 polypeptide. The isolated polynucleotide.is useful in diagnosing, preventing, preventing, prognosing, ameliorating or monitoring diseases associated with aberrant VBGF-2 or VBGF-2 receptor expression or lack of VBGF-2 or VBGF-2 receptor function, such as cancer and other proliferative disorders (e.g. cerebral anoxia), inflammatory diseases, infectious diseases, autoimmune diseases anoxia), inflammatory diseases, infectious diseases, alteringises), diabetic retinopathy or psoriants. The polynucleotide, polypeptide and antibodies may also be used to stimulate angiogenesis, wound healing, and promoting vascular tissue repair. The polynucleotide and polypeptide may also be used for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors, and for the production of diagnostics and therapeutics to treat human diseases. This polynucleotide sequence represents a PCR primer used in the exemplification of the invention

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

Gaps ö Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03; 3; Indels 0; Mismatches 86.48; 19; Conservative Query Match Best Local Similarity Matches

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ACA54716 standard; DNA; 23 ACA54716; RESULT 717 244444444 4444444

Human NF-kappaB associated antibody VH domain PCR primer #3. 05-JUN-2003 (first entry)

Human; nuclear factor-kappaB; NP-kappaB; immune disorder; cancer; inflammatory disorder; apoptosis; hepatic disorder; Hodgkin's lymphoma;

atherogelerosis, cachexia; euthyroid sick syndrome; stroke; EAE; experimental allergic encephalomyelitis; autoimmune disorder; wound; hyper immune activity; acute phase response; hypercongenital condition; birth defect; necrotic lesion; organ transplant rejection; pancreas; signal transduction; hyperproliferative disorder; diabetes mellitus; vitamin B12 malabsorption; neurological disorder; Huntington's chorea; Turner's syndrome; bacterial infection; cardiovascular disorder; infertility; psoriasis; haemolytic anaemia; antinflammatory; anti-HIV; cytostatic; hepatotropic; virucide; antirdalematic; antialteria antialteria neuropyressive; vinderaty; antialergic; neuropyressive; vulnerary; antialergic; antianaemic; antiinfertility; antianaemic; antipsoriatic; cerebroprotective; cardiant; antiinfertility; antianaemic; antipsoriatic; cerebroprotective; cardiant; antianteriosclerotic; PCR; primer; ss. haematopoietic tumour; hyper-IgM syndrome; viral infection; asthma; hypohidrotic ectodermal dysplasia; human immunodeliciency virus; HIV; X-linked anhidrotic ectodermal dysplasia; al incontinentia pigmenti; influenza; rheumatoid arthritis; inflammatory bowel disease; colitis;

Homo sapiens.

WO200286076-A2

31-OCT-2002

19-APR-2002; 2002WO-US012636,

19-APR-2001; 2001US-0284962P. 26-APR-2001; 2001US-0286645P.

09-JAN-2002; 2002US-0346986P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Carman J, Feder J, Nadler S;

WPI; 2003-093119/08

Novel NF-kappaB-associated polypeptides and polynucleotides useful for diagnosing, treating and preventing cancer, hepatic disorders, aberrant apoptosis, viral infections, autoimmune disorders, asthma and stroke.

Example 33; Page 407; 608pp; English.

The present invention relates to the isolation of human nuclear factorkappaB (NP-kappaB) associated polypeptides and polynucleotides. The NFkappaB associated polypeptide and polynucleotide sequences are useful for
preventing, treating or ameliorating various disorders including immune
disorders, inflammatory disorders, cancers, disorders relating to
aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas,
hematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal
dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, al
immunodeficiency virus (HIV), human T-cell lymphotropic virus (HTLV),
hepatitis B, hepatitis C, Epstein Barr virus (EBN), influenza),
rheumatoid arthritis, inflammatory bowel disease, colitis, asthma,
cheumatoid arthritis, antharmatory bowel disease, colitis, asthma,
altergic encephalomyelitis (EAB), autoimmune disorders related
to hyper immune activity, disorders related to aberrant acute phase
cesponses, hypersongenital conditions, birth defects, necrotic lesions,
wounds, organ transplant rejection, disorders related to aberrant signal
centerior of the panorease encourage encourages encoura disorders (e.g. Huntington's chorea), Turner's syndrome, bacterial infections, cardiovascular disorders, infertility, psoriasis and haemolytic anaemia. The present sequence represents a PCR primer used in the examples of the present invention

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

Gaps ö 0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; tive 0; Mismatches 3; Indels 19; Conservative Best Local Similarity Matches

1 GAGGTGCAGCTGGTGGAGTCTG 22

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The present invention relates to the isolation of a novel member of the immunoglobulin (Ig) superfamily, human antigen presenting cell expression (APEXX4, and variants (APEXX401) thereof.

The polypeptides of the invention are useful for treating, preventing or ameliorating medical conditions, such as immunological disorders (e.g. rheumatoid arthritis, inflammatory bowel disease, sepsis, acne or hostversus grateful disease, sepsis, acne or hostversust leukocyte proliferation, differentiation, migration or activation, disorders related to aberrant activation of disorders related to aberrant activation of natural killer cells, disorders of the spleen, inflammatory disorders, and proliferative disorders (e.g. neoplasms). APEX4, APEX41 and APEX41 polypeptides, and polymucleotides encoding them are useful for modulating proliferation, dispration and activation in various cells, tissues and conferentiation, migration and activation in various cells, themanone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New APEX (antigen presenting cell expression) 4 and APEX4v1 proteins and nucleic acids, useful for treating or preventing e.g. immunological disorders, hematopoeitic and/or proliferative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organisms. The polynucleotides sequences are are useful in chromosome identification, chromosome mapping, as molecular weight markers, and if gene therapy. The present sequence represents a PCR primer used in the examples of the present invention
                                                                                                                                                                                                                                                  PCR primer #3 for DNA encoding VH domain of anti-APEX4 human antibody.
                                                                                                                                                                                                                                                                                          Human; immunoglobulin superfamily; Ig; APEX4; sepsis; acne; antiqen presenting cell expression 4; immunological disorder; rheumatoid arthritis; inflammatory bowel disease; activation; host-versus-graft disease; haematopoietic disorder; migration; leukocyte proliferation; differentiation; T-cell activation; B-cell activation, natural killar cell; splean disorder; inflammatory disorder; proliferative disorder; inflammatory disorder; antinflammatory; antiarthritis; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 28; Page 296; 368pp; English.
GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dermatological; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-2001; 2001US-0278037P. 03-APR-2001; 2001US-0281223P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-2002; 2002WO-US008721
                                                                                                                                                                                                                (first entry)
                                                                                                                             ABX08633 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200277173-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                20-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2002.
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The invention comprises the amino acid and coding sequence of B7-related (BSL2) fusion proteins. The B7-related fusion proteins of the invention are useful for modulating the activation of immune or inflammatory response cells (e.g. T cells). The B7-related fusion proteins are useful for treating or preventing: transplantation rejection, graft versus host disease; asthma; chronic obstructive pulmonary disease; cancers; viral infections (e.g. HIV, herpes or encephalitis); and autoimmune disease (e.g. rheumatoid arthritis, multiple sclerosis or psoriasis). The present DNA sequence represents a PCR primer that was used to amplify the DNA encoding the variable domain of an antibody that is specific for a B7-
                                                                                                                                         PCR; ss; gene therapy; B7-related fusion protein; BSL2; viral infection; immune response modulation; inflammatory response modulation; cancer; transplantation rejection; graft versus host disease; asthma; herpes; chronic obstructive pulmonary disease; HIV; encephaltits; psoriasis; autoimmune disease; rheumatoid arthritis; multiple sclerosis; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated B7-related nucleic acid fusion molecules and fusion polypeptides, useful for diagnostic applications, modulating the activation of immune or inflammatory response cells, preventing ctreating cancer or psoriasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; tive 0; Mismatches 3; Indel8
                                                                                                       B7-specific antibody VH domain PCR primer - SEQ ID No 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    853 GAGGAGGAGCTGGTGGAGGCTG 874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BRIM ) BRISTOL-MYERS SQUIBB CO.
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ABT15964 standard; DNA; 23 BP
                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-2001; 2001US-00875338.
15-FEB-2002; 2002US-00077023.
                                                                                                                                                                                                                                                                                                                                                                    06-JUN-2002; 2002WO-US018049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACC78591 standard; DNA; 23
                                                                        28-MAR-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mikesell GE, Shen H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related protein
                                                                                                                                                                                                                                                                                               WO200299119-A2
                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                               12-DEC-2002.
                                    ABT15964;
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ACC78591
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Query Match 0.5%; Score 17.2; DB 1; Length 23; Best Local Similarity 86.4%; Pred. No. 1.1e+03; Matches 19; Conservative 0; Mismatches 3; Indels

Gaps

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The invention relates to an albumin fusion protein comprising a
therapeutic protein:X, and albumin, its variant or fragment. The albumin
there fusion protein has the formula R1-L-R2, R2-L-R1, or R1-L-R2-L-R1 where R1
therapeutic protein:X or fragment, Lis a peptide linker and R2 is
albumin. The albumin fusion protein is useful for treating a disease or
disorder that is modulated by therapeutic protein:X (claimed), such as
cancer; infections (bacterial, viral, fungal, parashito); or immune
CC (AIDS, asthma); hematopoietic (leukemia, sepsis); reproductive (cystic
fibrosis, endometriosis); musculoskeletal (osteoporosis, osteoarthritis);
cardiovascular (congestive heart failure, alterosolerosis); neural/
candiovascular (congestive heart failure, alterosolerosis); neural/
censory (ataxia, attention deficit disorders, autism); respiratory
dispative (ulcer, cirrhosis); or connective/epithelial (lupus, keloids)
disorders. Sequences ACC78589-634 represent PCR primers for amplifying
human VH and VL domains, that can be used to create multifusion proteins
                                                                        Albumin, HA; cytostatic; antibacterial; virucide; fungicide; anti-HIV; antiasthmatic; osteopathic; antiarthritic; antiinflammatory; nootropic; neuroprotective; anti-thyroid; anti-ulcer; hepatotropic; vulnerary; protein therapy; growth hormone; hGH; VL; VH; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; ss; PCR; VEGF; vascular endothelial growth factor; human; cancer; angiogenesis; neoplastic proliferation; primer; RT-PCR; reverse transcriptase PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New albumin fusion protein comprising a therapeutic protein:X, and albumin, its variant or fragment, useful for treating a cancer, AIDS asthma, leukemia, sepsis, endometriosis, osteoporosis, atherosclerosis, autism, or emphysema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 17.2; DB 1; Length 23; 36.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indel8
                                       Human VH domains amplifying forward primer VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 60; Page 391; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGGTGCAGCTGGTGGAGTCTG 22
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                                                                                                                                                                                                                                                                                              04-OCT-2002; 2002WO-US031794.
                                                                                                                                                                                                                                                                                                                                       05-OCT-2001; 2001US-0327281P.
                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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Matches 19; Conservative
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                   Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-468174/44.
                                                                                                                                                                                                                  WO2003030821-A2.
                                                                                                                                                                               Homo sapiens.
18-AUG-2003
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                                                                                                                                                                                                                                                           17-APR-2003
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Gaps ;

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The invention relates to a composition comprising an antisense oligomucleotide directed against vascular endothelial growth factor (VEGF). The antisense oligomucleotide is useful for preparing a composition treating cancer, neoplastic proliferation, abnormal cellular proliferation and preventing angiogenesis. The present sequence is a proliferation and preventing angiogenesis. The present sequence is a carearse transcriptase (RT)-PCR primer for a VEGF or related gene, used to clone the coding region for expression in tumour cell lines. The cell lines were used to test prospective antisense oligonucleotides
                                                                                                                                                                                                                                                                                                                                            New composition comprising an antisense oligonucleotide directed against vascular endothelial growth factor, useful for preparing a composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; se; G-protein coupled receptor; HGPRBMY39; cancer; PCR; primer; male reproductive disorder; testicular disorder; immune disorder; inflammatory disorder; developmental disorder; leukaemia; VH; bone marrow disorder; testicular cancer; proliferative disorder; neural disorder; Alzheimer's disease; prion disorder; antibody; bone metabolism disorder; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human HGPRBMY39 antibody VH domain PCR primer Hu VH3-5'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 6 A; 4 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1573 CAGGTGGCCCGGGCCATGGAGT 1594
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 12; Page 19; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 caagregecagagecargaagr 22
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                                                                                                                                    31-JAN-1997; 97US-0037004P.
30-JAN-1998; 98US-00016541.
2AN-2000; 2000US-00487023.
19-JAN-2001; 2001WO-US000193.
                                                                                                   13-MAR-2001; 2001US-00805761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2002; 2002WO-US028582.
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27-NOV-2001; 2001US-0333658P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACA61414 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                for treating cancer.
                                                                                                                                                                                                                                                                                                             WPI; 2003-255224/25
                                                                                                                                                                                                                                                                           Masood R;
                                                                                                                                                                                                                        (GILL/) GILL P S. (MASO/) MASOOD R.
                              US2002165174-A1.
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 Homo sapiens.
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                                                                  07-NOV-2002
                                                                                                                                                                                                                                                                         Gill PS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 722
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Homo sapiens.

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The invention relates to. an isolated nucleic acid encoding a human G-
protein coupled receptor HGPRBMY39 (or its fragment domain or epitope),

tis complement or a polynucledide capable of hybridising under stringent

conditions to it. Also included are a HGPRBMY39 recombinant vector, a

conditions to it. Also included are a HGPRBMY39 recombinant vector, a

recombinant host cell comprising the vector sequences (used to express

and make the protein), an isolated HGPRBMY39 polypeptide, and an anti-
HGPRBMY39 antibody. The HGPRBMY39 polypeptide, and an anti-
HGPRBMY39 antibody. The HGPRBMY39 polypeptide is

useful for preventing, treating or ameliorating e.g. a (male)

creproductive disorder; a testicular disorder or cancer; a disorder related to aberrant G-

protein coupled receptor dependent phosphatidylinositol-calcium

creproductive adisorder related to aberrant G-

protein coupled receptor dependent phosphatidylinositol or calcium second messenger activation; an inflammatory disorder; a developmental disorder; a

clasorder that would benefit from inhibition of a leukotriene B4-dependent

creproduction; a disorder associated with below normal neutrophil activation; a disorder associated with below normal neutrophil activation;

activation; a disorder associated to aberrant superoxide generation;

coxidation states; a disorder related to aberrant neutrophil activation;

coxidation states; a disorder related to aberrant neutrophil activation;

coxidation states; a disorder related to aberrant meutrophil activation;

coxidation states; a disorder related to aberrant superoxide generation;

coxidation states; a disorder related to aberrant neutrophil activation;

coxidation states; a disorder related to aberrant superoxide generation;

coxidation states; a disorder related to aberrant meutrophil activation;

coxidation states; a disorder related to aberrant superoxide generation;

coxidation states; a disorder related to aberrant superoxide generation;

coxidation states; a disorder activation;

coxidation states
                                                                                                                                                                                                              New human G-protein coupled receptor, HGPRBMY39, useful for treating or preventing e.g. immune, inflammatory, developmental, proliferative, neural, reproductive, bone marrow or prion disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                      Gopal S, Mintier G, Feder JN;
                                                                                                                                                                                                                                                                                                                                                 Example 37; Page 313; 359pp; English
                              (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                      WPI; 2003-313245/30.
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0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; 3; Indels 0; Mismatches 86.48; Query Match 0.5 Best Local Similarity 86.4 Matches 19; Conservative

Gaps .. 0

> 853 GAGGAGGAGCTGGTGGAGGCTG 874 1 GAGGTGCAGCTGGTGGAGTCTG 22 g

ADJ79912 standard; DNA; 23 ADJ79912;

BP.

06-MAY-2004 (first entry)

Primer #3 for VH region of anti-human K channel K+alphaM2 antibody gene.

immunosuppressive, antidepressant; nephrotropic; tranquilizer; antidadictive; nootropic; antinfertility; virucide; cytostatic; antidatheric; antidatheric; antidatheric; antidatheric; antidiaberic; antidiaberic; antidiaberic; antidiaberic; antidiaberic; antidiaberic; antidiamatory; antidiponic; osteopathic; potassium agonis; potassium antagonist; gene therapy; potassium cannel alpha subunit; diagnosis; rheumatoid arthritis; asthma; leukemia; psoriasis; neutropenia; diabetes; panoreatitis; osteoporosis; hypertriglyceridemia; infertility; testicular cancer; viral orchitis; memory disorder; obsessive/compulsive disorder; addiction; dopamine regulation; serotonin regulation; dysphoria; depression; irritability; anxiety; immunophenotyping; phosphorylation; BB; primer ADJ79912
XX
XX
AC ADJ7991
XX
AC ADJ7991
XX
DT 06-MAY
XX
XX
XX
XX
XX
Immunos
XW
Antiart
X

(BRIM) BRISTOL-MYERS SQUIBB CO. 19-JUL-2001; 2001US-0306577P. 19-JUL-2002; 2002WO-US023407. Feder J, Lee L, Chang H; WPI; 2003-577292/54. WO2003050235-A2. 19-JUN-2003

New isolated human potassium channel alpha subunit, KalphaM2 polypeptide, useful for diagnosing, preventing, treating or ameliorating a medical condition, for example a neural disorder, an immune disorder or a metabolic disorder.

Example 31; SEQ ID NO 43; 313pp; English.

The invention relates to an isolated human potassium channel alpha
subunit, K+alphaMZ polypeptide. The K+alphaMZ polypeptide and
subunit, K+alphaMZ polypeptide. The K+alphaMZ polypeptide and
colymucleotide are useful for diagnosing, preventing, treating or
ameliorating a medical condition, such as a neural disorder, an immune
disorder (e.g. rheumatoid arthritis, AIDS, asthma, leukemia, psoriasis or
centropenia), a disorder related to aberrant potassium regulation,
metabolic disorder (e.g. diabetes, pancreatitis, osteoporosis or
hypertriglyceridemia), a reproductive disorder, a renal disorder, a male
creproductive disorder (e.g. infertility, testicular cancer or viral
orchitis), a memory disorder, an obsersative/compulsive disorder, an
addiction, a disorder related to aberrant dopamine or serotonin
regulation, depression, irritability, anxiety, or depression,
irritability or anxiety associated with treating drug addiction, learning
irritability or anxiety associated with treating drug addiction,
irritability or price the affective disorders. Antibodies against
the polypeptides from recombinant cell culture, in diagnostic assays to
detect the presence or quantification of the polypeptides, or for
immunophenotyping. Vectors and host cells containing the gene are useful
containing the polypeptides. This sequence corresponds
corrections and host cells containing the gene are useful to a PCR primer to amplify a heavy chain variabl human potassium channel K+alphaM2 antibody gene.

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

Gaps ö 0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; ve 0; Mismatches 3; Indels Query Match 0.5%; Best Local Similarity 86.4%; Matches 19; Conservative

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853 GAGGAGGAGCTGGTGGAGGCTG 874 1 GAGGTGCAGCTGGTGGAGTCTG 22 ò

RESULT 724 ADJ93146

ADJ93146 standard; DNA; 23 BP 06-MAY-2004 (first entry) ADJ93146;

ds; gene; immunosuppressive; cardiant; antiinflammatory; cytostatic; anti-HIV; antirheumatic; antiarthritic; antibacterial; antiseborrheic; dermacological; antipsoriatic; neuroprotective; nootropic; antiparkinsonian; antidiabetic; ophthalmological; antiasthmatic; antidepressant; neuroleptic; hypotensive; tranquilizer; hypertensive; anorectic; metabolic; virucide; osteopathic; antianginal; vulnerary; Anti-human GCRP HGPRBMY30 antibody VH region PCR primer Hu-VH3

vivlemore401-10.rng

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The invention relates to an isolated human G-protein coupled receptor, HGPRBMY30 polypeptide or a sequence having 95% identity to the above mentioned sequences. (I) is useful for preventing or treating a medical condition, selected from an immune disporder; a cardiovascular disorder; an inflammatory disorder in which G-protein coupled receptors are either disorder; a reproductive disorder; a metabolic disorder; a neural disorder; an endocrine disorder; a metabolic disorder; a neural disorder; an endocrine disorder; cesticular cancer; a neural disorder; an endocrine disorder; an entabolic gastrointestinal disorder; an endocrine disorder; cesticular cancer; an eneral disorder; an endocrine disorder; castoming, preventing, treating, and/or ameliorating the diseases such as hematopoietic and pulmonary disorders, Alzheimer's Parkinson's diseases, diabetes, dwarfism, color blindness, retinal pigmentosa, as hematopoietic and pulmonary disorders, Alzheimer's, Parkinson's diseases, diabetes, dwarfism, color blindness, retinal pigmentosa, stress, renal failure, acute heart failure, hypotension, obesity, stress, renal failure, acute heart failure, hypotension, obesity, anorexia, HIV infections, osteoporosis, angina pectoris, and myocardial infarction. (I) and (II) are useful for modulating signal transduction activity; (I) and (II) are useful for modulating signal transduction of food additive or preservative, and for modifying the activities of (I).

(I) and (II) also useful to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size and shape, to change a mammal's mental state or physical state by influencing biorhythms, caricadic rhythms, capabilities, hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities. This sequence corresponds to a preservative or physical state by an endocrine levels appetite, libido, memory, proper, and proper an antibody targeted to the novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human G-protein coupled receptor, HGPRBMY30 polypeptide useful for preventing and treating e.g. immune disorders, cardiovascular disorders
     immune disorder; cardiovascular disorder; inflammatory disorder; metabolic disorder; reproductive disorder; inflammatory disorder; metabolic disorder; reproductive disorder; testicular cancer; neural disorder; endocrine disorder; gastrointestinal disorder; Alzheimer's disease; Parkinson's diseases; diabetes; dwarfism; asthma; schizophrenia; obesity; anorexia, osteoporosis; angina pectoris; myocardial infarction.
gene therapy; G-protein coupled receptor protein; HGPRBMY30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 37; SEQ ID NO 49; 343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ramanathan C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2002; 2002WO-US017085.
                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2001; 2001US-0294411P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mintier GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-140445/13.
                                                                                                                                                                                                                                                                        WO200296946-A1.
                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                           05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feder JN,
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30-APR-2003; 2003WO-US013414. 01-MAY-2002; 2002US-0376561P. (HUMA-) HUMAN GENOME SCI INC.

WO2003092597-A2.

13-NOV-2003

Homo sapiens.

Synthetic

Rosen CA, Ruben SM;

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Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
primer for the var
HGPRBMY30 protein
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Gaps ö 0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.18+03; tive 0; Mismatches 3; Indels 19; Conservative Local Similarity Query Match Matches

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GAGGAGCTGGTGGAGGCTG 874
                   853
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ADE83880 standard; DNA; 23 BP RESULT 725 ADE83880 ID ADE8386 XX

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antipsoriatic; dermatological; antiinflammatory; immunosuppressive; antirheumatic; antiarthritic; cerebroprotective; cytostatic; anti-HIV; vulnerary; dermatitis; autoimmune disease; rehumatoid arthritis; systemic lupus erythematoaus; autoimmune encephalitis; cancer; HIV infection; wound; inflammatory disorder; human; psoriasis;
                        Chemokine beta-4 binding antibody PCR primer Hu VH3-5' SEQ ID NO:39
                                    chemokine beta-4; CK-B4; single chain Fvs; scFvs;
            29-JAN-2004 (first entry)
                                                                          PCR primer; ss
                                     antibody;
ADE83880;
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New antibody that specifically binds to a chemokine beta-4 polypeptide, useful for diagnosing, treating, preventing or ameliorating psoriasis, rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection WPI; 2004-022614/02. and wounds

Example 2; SEQ ID NO 39; 181pp; English.

The present invention describes an antibody (I) that specifically binds to a chemokine beta-4 (CK-B4) polypeptide. Where (I) comprises a first to a chemokine beta-4 (CK-B4) polypeptide. Where (I) comprises a first camino acid sequence at least 95% identical to a second amino acid acid comprising a VH complementarity determining region (CDR) or VL CDR of any of the single chain Fvs (scFvs) from any of 17 fully defined sequences of 245-253 amino acids (ADEB3861 to ADEB3877). Also described: (I) a kit comprising the isolated nucleic acid of (2); (4) a host coll comprising the vector of (3); (5) a cell line engineered to express (I); (3) a vector comprising the isolated nucleic acid of (2); (4) a host cell comprising the vector of (3); (5) a cell line engineered to express (I); (6) an antibody that binds the same epitope as (I); (7) an antibody that competitively inhibits the binding (I) to a CK-B4 polypeptide; (8) a method for detecting aberrant expression of CK-B4 polypeptide; (7) and comparing the same pitope as (I); and comparing the camper of CK-B4 polypeptide expression or level of CK-B4 polypeptide expression or level of CK-B4 polypeptide expression or level of CK-B4 collogical sample with a second, normal biological sample, where an increase or decrease in the assayed level of CK-B4 polypeptide in the first of a blological sample comparing to the standard level in the first of a blological sample comparing to the standard level in the companion of the standard level of CK-B4 polypeptide companion or level of CK-B4 plolypeptide companion or level of CK-B4 plolypeptide companion or level of che standard level of CK-B4 polypeptide companion or level of CK-B4 plolypeptide companion or level of CK-B4 plolypetide companion or level of CK-B4 plolypetide companion or level aberrant expression, and (9) a method of treating, preventing or amellorating pooriasis, dermatitis or an autoimmune disease, comprising administering (1) to the animal. (1) has antipsoriatic, dermatological, antiinflammatory, immunosuppressive, antirheumatic, antiarthitic, cerebroprotective, cytostatic, anti-HIV and vulnerary activities. The methods and compositions of the present invention are useful for diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or an autoimmune disease such as rheumatoid arthritis, systemic lupus erythematous and autoimmune encephalitis. They can also be used in cancer, HIV infection, wounds and inflammatory disorders. The present sequence is used in the exemplification of the present invention.

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; Best Local Similarity Query Match

Wager RE;

Ruben SM,

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The invention comprises a DNA sequence encoding an antibody which immunospecifically inhibits vascular endothelial growth factor 2 (VEGF-2) protein. The antibody of the invention is useful for detecting, diagnosing, monitoring, treating or preventing cancers or other hyperproliferative disorders, inflammatory disorders, autoimmune disease, rheumatoid arthritis, psoriasis, and diabetic retinopathy. The present DNA sequence represents a PCR primer that was used in an example of the
                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide encoding VEGF-2 antibody, useful in detecting, diagnosing, prognosing, monitoring, treating or preventing e.g. cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 32; SEQ ID NO 38; 410pp; English
                                                                                                                                                     19-AUG-2002; 2002WO-US026246.
                                                                                                                                                                                              12-APR-2002; 2002WO-US011474.
                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                      Albert VR,
                                                                                                                                                                                                                                                                                                                               WPI; 2004-022839/02.
                                                                WO2003097660-A1.
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                    Unidentified.
                                                                                                         27-NOV-2003
                                                                                                                                                                                                                                                                                        Rosen GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG75494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4DG75494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or precedence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; vascular endothelial growth factor 2; VEGF-2; cancer; hyperproliferative disorder; inflammatory disorder; autoimmune disease; rheumatoid arthritis; psoriasis; diabetic retinopathy; PCR; ss; primer; VH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
    Gaps
                                                                                                                                                                                                                                                                                                                                                                             antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
hypertension; pre-eclampsia; NKB; ss; PCR; primer.
                                                                                                                                                                                                                                                                                                                                    Human neurokinin B antibody VH PCR primer HuVH3-5' SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Score 17.2; DB 1; Length 23; 36.4%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human VEGF-2-specific antibody VH domain PCR primer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; SEQ ID NO 43; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         853 GAGGAGCTGGTGGAGGCTG 874
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                                                853 GAGGAGGAGCTGGTGGAGGCTG
                                                                                            1 GAGGTGCAGCTGGTGGAGTCTG
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                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-2003; 2003WO-US016802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                        ADG34320 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                             (first entry)
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      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-053456/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003102136-A2.
                                                                                                                                                                                                                                                                                             26-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-DEC-2003
      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
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      Matches
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IID ADG3

XX ADG4

XX ADG3

XX ADG4

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                                                                                                                                                              RESULT
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                                                                                                                                         Gaps
                                                                                                                                             ö
                                                                 Score 17.2; DB 1; Length 23;
Pred. No. 1.1e+03;
0; Mismatches 3; Indels
Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-HLLRCR-1 antibody VH domain PCR primer #3.
                                                                                                                                                                                                                      853 GAGGAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2002; 2002US-00271078.
                                                                        Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG75494 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-2004 (first entry)
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Isolated nucleic acid molecule for e.g. diagnosing and treating cardiovascular condition, comprises polynucleotide encoding human leucine-rich repeat cardiac receptor-1 protein having amino acid sequence of Mintier G; 11-OCT-2001; 2001US-0328478P. Feder JN, Ramanathan CS, (FEDE/) FEDER J N. (RAMA/) RAMANATHAN C S. WPI; 2004-031999/03. MINTIER G. specific length. (RAMA/) (MINT/)

Example 34; SEQ ID NO 55; 164pp; English.

The invention relates to an isolated nucleic acid molecule comprises a polynucleotide encoding the full-length human leucine-rich repeat cardiac receptor-1 (HLLRCH-1) protein appearing as ADG75441and ADG75443. Also included are a recombinant vector comprising the isolated nucleic acid molecule, a recombinant vector comprising the vector sequences, the isolated polypeptide, an isolated antibody that binds condition in the isolated polypeptide, making an isolated polypeptide, and recovering the polypeptide, making an isolated polypeptide or specifically to the isolated polypeptide, making an isolated polypeptide or disolated polypeptide, and recovering the polypeptide, diagnosing a pathological condition or a susceptibility to a pathological condition in a subject (by determining the presence or absence of a mutation in the polymericoride, and diagnosing a pathological condition or a subsence of the mutation) and preventing, treating or ameliorating a medical condition by administering a polypeptide or its modulator to a manmalian subject. The HLLRCR-1 protein and nucleic acid are used for diagnosing, preventing, treating or ameliorating a cardiovascular caberrant apoptosis modulation, enural disorder, disorder related to aberrant call acides modulation, a disorder, neural disorder, disorder related proliferated condition of the colon, memory, catablishment of short term memory, establishment of short term memory disorder associated with the brain, particularly memory disorders, movement coll disorder associated with the brain, particularly memory disorders, movement disorders that accompany severe trauma to the brain, disorder seculation, aberrant call transfers on the province that encurisment of memory of the disorder including parkinson's other forms of ataxia, disorder associated with the brain, particularly memory disorders that encurisment (many other diseases and specification). The invention provides human sequence that encodes a leucine-rich repeat containing protein with homology to the leucine-rich repeat containing protein known as NoGo receptor that is primarily expressed in the brain and is thought to be responsible for modulating neurite growth. The present sequence is a PCR primer used to isolate nucleic acid encoding a VH or VL chain of an anti-HLLRCR-1 antibody.

Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

0.5%; Score 17.2; DB 1; Length 23; 86.4%; Pred. No. 1.1e+03; 3; Indels 0; Mismatches 853 GAGGAGGAGCTGGTGGAGGCTG 874 Query Match 0.5%; Best Local Similarity 86.4%; 19; Conservative Matches

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Gaps ö

> RESULT 729 ADH61821 ID ADH6 XX AC ADH6

ADH61821 standard; DNA; 23 ADH61821

(first entry)

Human G protein chemokine receptor-related PCR primer SegID15.

G-protein chemokine receptor; HSATU68; cytostatic; anti-HIV; anti-HIV; anti-Hibbetic; immunosupressive; noctropic; neuroprotective; vaccine; gene therapy; infectious disease; silicosis; sarcodosis; adult respiratory syndrome; ARD5; brain tumour; hyperproliferative disorder; lymphoblastic leukaemia; brain tumour; breast cancer; Raposi's sarcoma; Hodgkin's sarcoma; myeloid leukaemia; urethral cancer; gastrointestinal disorder; gastric reflux; peptic oesophagitis; liver disorder; intrahepatic cholestasis; hepatorenal syndrome; pancreatic disease; neoplasm; pancreas cell tumour; sallbladder disease; bile duct tumour; cardiac oedema; pulmonary heart disease; cardiovascular disease; cardiovascular disease; cardiovascular disease; testicular atrophy; gonorrhoea; renal disorder; kidney failure; interpretation disorder; diabetes mellitus; diabetes insipidus; immunoresponsiveness; B-cell function; lymphoid tissue regeneration; protein co-ordinate data; PCR; primer; ss.

Unidentified.

US2003224426-A1. 04-DEC-2003

11-APR-2003; 2003US-00411284.

11-JAN-1996; 96WO-US000499. 21-DEC-1998; 98US-00101518. 12-APR-2002; 2002US-0371725P.

(LIYY/) LI Y.

Li Y;

WPI; 2004-033959/03.

Novel isolated human G-protein chemokine receptor HSATU68 polypeptide, useful for preventing, treating or ameliorating medical conditions such as leukemia.

Example 13; SEQ ID NO 15; 168pp; English.

invention may also be used for the development of treatments for adult respiratory syndrome (ARDS), hyperproliferative disorders such as acute childhood lymphoblastic leukaemia, brain tumours, breast cancer, Kaposi's carlidhood lymphoblastic leukaemia, brain tumours, breast cancer, Kaposi's carcoma, Hodgkin's sarcoma, myeloid leukaemia and urethral cancer, gastrointestinal disorders such as intrahepatic cholestasis and cosophagitis, liver disorders such as intrahepatic cholestasis and islet cell tumours, gallbladder diseases such as intrahepatic cholestasis and nislet cell tumours, gallbladder diseases such as bile duct tumour, neurological diseases such as Alzheimer's disease, cardiovascular chearing such as cardiac oedema, pulmonary heart disease, reproductive disorders such as testicular atrophy, gonorrhoea, renal disorders such as testicular atrophy, gonorrhoea, renal disorders such as diabetes kidney failure, uninary disorders, endocrine disorders such as diabetes insipidua, for stimulating B-cell responsiveness to pathogens, an agent to increase serum immunoglobulin concentrations, to boost immunoresponsiveness among individuals having an acquired loss of B This invention relates to a novel isolated human G-protein chemokine receptor polypeptide (HSATU68) and the DNA sequence which encodes it. The invention may be useful for the development of compounds with a cytostatic, anti-HUV, antiinflammatcry, anti-diabetic, immunosuppressive, nootropic or neuroprotective activity which act as agonists or anti-HUV, and the invention. In addition, the invention may be useful for the development of a vaccine or for gene therapy. The invention is useful for diagnosing a pathological condition or a susceptibility to a pathological condition and for developing methods for treating, preventing diseases, disorders or conditions associated with aberrant expression and/or activity of the receptor of the invention such as infectious diseases which includes silicosis, sarcoidosis. The

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-cell function and as therapy for generation and/or regeneration of lymphoid tissues following surgery, trauma or genetic defect. The present sequence is that of a degenerate PCR primer which was used to amplify a region of a VH or VL gene during the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosuppressive; neuroleptic; neuroprotective; hypotensive; phypotrensive; phypotensive; and algesic; anorectic; anabolic; antiparkinsonian; noctropic; tranquilizer; antiaddictive; hypnotic; gene therapy; dopamine; opicid peptide; serotonin; GABA; glutamate; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human neurotransmitter transporter polypeptides and nucleic acid molecules useful for diagnosing, preventing or treating for e.g. disorders related to aberrant neurotransmitter transport or affective or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human neurotransmitter transporter; HNTTBMY1; PTA-4803; antidepressant;
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                  Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee LM;
                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                 Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feder JN,
                                                                                                                                                                                                                                           Score 17.2; DB 1;
Pred. No. 1.1e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HNTTBMY1 antibody VH domain primer, SEQ ID 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 30; SEQ ID NO 61; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Westphal R,
                                                                                                                                                                                                                                                                                                                                                                                               853 GAGGAGCTGGTGGAGGCTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-2001; 2001US-0340436P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-2002; 2002US-00319315.
                                                                                                                                                                                                                                                      0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH76560 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sharma R, Ramanathan CS,
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 86.4°
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHARMA R.
RAMANATHAN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               psychotic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-010866/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WESTPHAL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEDER J N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003219774-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEE L M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH76560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SHAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WEST/)
(FEDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LEEL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RAMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH76560

IID ADH77

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pathological condition or a susceptibility to a pathological condition in a subject. The human neurotransmitter transporter nucleic acid has the following activities: antidepressant, immunosuppressive, neuroleptic, neuroprotective, hypotensive, hypertensive, analgesic, anciectic, anabolic, antiparkinsonian, nootropic, tranguilizer, antiaddictive, and hypotensive in thuman neurotransmitter transporter nucleic acid can be used in gene therapy to treat disorders. The composition and methods are useful in diagnosing, preventing or treating a pathologic or medical condition selected from a disorder related to abbrrant neurotransmitter transport; affective disorders, immune-related disorders, hypotension, condition, endocrinal diseases, growth disorders, neurological disorders, metabolic disorders, immune-related disorders, hypotension, obesity, anorexia, bullmia, Parkinson's disease, dementias, behavioral disorders; cognitive disorders associated with aberrant serotonin expression and/or activity; anxiety, fear, depression, sleep, pain, disorders associated with aberrant maintenance of an attentive or alert state; attention deficit disorders; and sick and centre of the brain; disorders and field of the brain; disorders and alsorders 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
condition; and methods of diagnosing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody; regeneration IV; Reg IV; single chain antibody fragment; scFv; inflammatory bowel disorder; ulcerative colitis; Crohn's disease; diabetes; non-insulin dependent diabetes; insulin dependent diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antibody, useful for treating, preventing or ameliorating inflammatory bowel disorder, cancer of the gastrointestinal tract or diabetes (non-insulin dependent diabetes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antecting and or effecting the release of neurotransmitters such as dopamine, opioid peptides, serotonin, GABA, and glutamate; addictive dopamine, opioid peptides, serotonin, GABA, and glutamate; addictive alsorders; homeostatic disorders; neuroendocrine disorders; disorders affecting the establishment of long term potentiation; circadian rhythm disorders; disorders associated with the establishment of aberrant sleep/wake cycles; dopaminergic functional disorders; neuronal transmission system disorders, and pain. This polymucleotide sequence represents a primer used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reg IV-specific single chain antibody fragment (scFv) PCR primer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.2; DB 1; Length 23; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23 BP; 3 A; 3 C; 12 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      853 GAGGAGGAGCTGGTGGAGGCTG 874
                          or ameliorating a medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGGTGCAGCTGGTGGAGTCTG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; human; PCR; ss; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-2003; 2003WO-US019908.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%;
ilarity 86.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI58176 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-071976/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
Les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004003144-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADI58176
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